

GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: October 7, 2003, 19:04:06 ; Search time 112.61 Seconds

(without alignments)
258.946 Million cell updates/sec

Title: US-09-988-013a-2

Perfect score: 1 DIGUQSPSSILAVSAGENVT.....CHQTLSSWTGCGTKLEIKR 113

Sequence: 1 DIGUQSPSSILAVSAGENVT.....CHQTLSSWTGCGTKLEIKR 113

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_PROTOZOA:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	418.5	70.5	107	11	Q9ER29
2	392	66.0	109	4	Q9UL78
3	386	65.0	107	4	Q96SA9
4	383.5	64.6	108	4	Q9UL77
5	375.5	63.2	108	4	Q9UL70
6	373	62.8	107	4	Q9UL81
7	371	62.5	107	4	Q99M37
8	370	62.3	109	4	Q9UL85
9	368	62.0	239	4	Q9UL86
10	367	61.8	109	4	Q9UL86
11	366	61.6	238	11	Q8VC56
12	362.5	61.0	108	4	Q9UL83
13	360.5	60.7	99	11	Q9UL74
14	360.5	60.7	108	4	Q9UL79
15	359.5	60.5	234	4	Q8NEK1
16	359	60.4	239	11	Q8VC55

17	356.5	60.0	111	11	Q920E9	Q920E9 mus musculus
18	355.5	59.8	113	4	Q9UL80	Q9UL80 homo sapien
19	353.5	59.5	234	11	Q91WS9	Q91WS9 mus musculus
20	350	58.9	239	11	Q8K0F8	Q8K0F8 mus musculus
21	349.5	58.8	108	11	Q8V100	Q8V100 mus musculus
22	348	58.6	239	4	Q8RCDO	Q8RCDO mus musculus
23	346.5	58.3	109	11	Q920B6	Q920B6 mus musculus
24	342.5	57.7	214	11	Q91R15	Q91R15 mus musculus
25	339	57.1	104	11	Q9JL82	Q9JL82 mus musculus
26	336.5	56.6	298	11	Q9QYF0	Q9QYF0 mus musculus
27	333.5	56.1	234	11	Q8V0D0	Q8V0D0 mus musculus
28	333	56.1	134	11	Q8VDD0	Q8VDD0 mus musculus
29	332	55.9	112	11	Q8K1F3	Q8K1F3 mus musculus
30	330	55.6	114	11	Q8K1F1	Q8K1F1 mus musculus
31	322.5	54.3	107	11	Q9JL84	Q9JL84 mus musculus
32	319.5	53.8	103	11	Q9JL80	Q9JL80 mus musculus
33	319.5	53.8	116	4	Q96PF6	Q96PF6 mus musculus
34	319.5	53.8	234	11	Q8VCP0	Q8VCP0 mus musculus
35	318.5	53.6	234	11	Q91WP8	Q91WP8 mus musculus
36	317	53.4	112	11	Q8K1F2	Q8K1F2 mus musculus
37	314	52.9	106	5	Q9U410	Q9U410 schistosoma
38	306.5	51.6	148	11	Q8K122	Q8K122 mus musculus
39	305.5	51.4	97	11	Q9JL76	Q9JL76 mus musculus
40	301.5	50.8	101	11	Q9JL78	Q9JL78 mus musculus
41	301	50.7	241	11	Q921A6	Q921A6 mus musculus
42	298	50.2	112	11	Q8K1F0	Q8K1F0 mus musculus
43	294	49.5	235	11	Q91W12	Q91W12 mus musculus
44	293.5	49.4	127	11	Q925S9	Q925S9 mus musculus
45	270.5	45.5	109	6	Q9N0W5	Q9N0W5 oryctolagus

ALIGNMENTS

RESULT 1
Q9ER29 PRELIMINARY; PRT: 107 AA.
ID Q9ER29
AC Q9ER29;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DR 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
OS Anti human TNF-alpha light chain variable region (Fragment).
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;
RT "Cloning and sequencing of the light chain fragment of variable region
genes of an anti-TNF-a monoclonal antibody.";
RL J. Cell. Mol. Immunol. 12:21-26(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RT "Construction and sequencing of the single-chain antibody gene of a
human TNF-alpha specific monoclonal antibody.";
RL Ti 4 Chun i Ta Hsueh Hsueh Pao 19:373-376(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RT Submitted (MAR-2000) to the EMBL/Genbank/DBD databases.
RL Human TNF-alpha specific monoclonal antibody.";
DR HSSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig-MHC.
DR InterPro; IPR003596; Ig-V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
FT NON_TER 107 107
SO SEQUENCE 107 AA; 11784 MW; 2B15E8A6604A26C3 CRC64;

Query Match 70.5%; Score 418.5; DB 11; Length 107;
Best Local Similarity 76.6%; Pred. No. 2.6e-38;
Matches 82; Conservative 10; Mismatches 14; Indels 1; Gaps 1;

OY 4 LTQSSSLAVSAGENVYTMCKSSQSVLYSANHKNYLAWYQKPGOSPKLLIYMASTR 63
DB 1 MTQSSSLAVSAGENVYTMCKSSQSVLYSANHKNYLAWYQKPGOSPKLLIYMASTR 60
OY 64 VPDRTFTGSGSGTDFTLTISRVOVEDLAIYCHQ-YLSSWTGSGTKL 109
DB 61 VPDRTFTGSGSGTDFTLTISRVOVEDLAIYCHQ-YLSSWTGSGTKL 107

RESULT 2

OY 09UL78 PRELIMINARY; PRT; 109 AA.
AC 09UL78
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RT Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035036; AAD56272.1;
DR HSP; P80362; 1MPL.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 66.0%; Score 392; DB 4; Length 109;
Best Local Similarity 66.7%; Pred. No. 2.2e-35;
Matches 76; Conservative 18; Mismatches 14; Indels 6; Gaps 2;

OY 1 DIQLTQSPSSSLAVSAGENVYTMCKSSQSVLYSANHKNYLAWYQKPGOSPKLLIYMASTR 60
DB 1 EIVLTQSPGTLISLSPGERATLSCASQSV-----SSYLAWYQKPGQAPRLIYGAASR 55
OY 61 ESGVPRFTGSGSGTDFTLTISRVOVEDLAIYCHQYLS-WTFGGTKLEIKR 113
DB 56 ATGIPDFSGSGSGTDFTLTISRLEPEDCAVYICQYGGSPPLTFGGTKVEIKR 109

RESULT 3

OY 096SA9 PRELIMINARY; PRT; 107 AA.
AC 096SA9
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain variable region (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal monoclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin antibody v region genes";
RT J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1;
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 65.0%; Score 386; DB 4; Length 107;
Best Local Similarity 65.5%; Pred. No. 9.7e-35;
Matches 74; Conservative 17; Mismatches 16; Indels 6; Gaps 1;

OY 1 DIQLTQSPSSSLAVSAGENVYTMCKSSQSVLYSANHKNYLAWYQKPGOSPKLLIYMASTR 60
DB 1 DIQLTQSPSSSLAVSAGENVYTMCKSSQSVLYSANHKNYLAWYQKPGOSPKLLIYMASTR 60
OY 61 ESGVPRFTGSGSGTDFTLTISRVOVEDLAIYCHQYLSWTGSGTKLEIKR 113
DB 55 QSGVPRFTGSGSGTDFTLTISRLOPEDCAVYICQYGGSPPLTFGGTKVEIKR 107

RESULT 4

OY 09UL77 PRELIMINARY; PRT; 108 AA.
AC 09UL77
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RT Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1;
DR HSP; P01607; 1REI.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 108 AA; 11738 MW; C06681716CAD1E3 CRC64;

Query Match 64.6%; Score 383.5; DB 4; Length 108;
Best Local Similarity 64.9%; Pred. No. 1.8e-34;
Matches 74; Conservative 17; Mismatches 16; Indels 7; Gaps 2;

OY 1 DIQLTQSPSSSLAVSAGENVYTMCKSSQSVLYSANHKNYLAWYQKPGOSPKLLIYMASTR 60
DB 1 DIQLTQSPSSSLAVSAGENVYTMCKSSQSVLYSANHKNYLAWYQKPGOSPKLLIYMASTR 60
OY 61 ESGVPRFTGSGSGTDFTLTISRVOVEDLAIYCHQ-YLSSWTGSGTKLEIKR 113

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DB      55 QSGVPSRFGSGSGTDFLTITSLQPEDFATYCCOOSYSTSWTFEGTKVEIKR 108
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 5
ID      Q9UL70      PRELIMINARY;      PRT;      108 AA.
AC      Q9UL70;
DR      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      Myosin-reactive immunoglobulin light chain variable region
      (Fragment).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_Taxid=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98277139; PubMed=9614934;
RA      Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RT      Young D.C.;
RT      *Myosin-reactive autoantibodies in rheumatic carditis and normal
      fetus*.;
RL      Clin. Immunol. Immunopathol. 87:184-192(1998).
DR      EMBL; AF035044; AAD56280.1; -.
DR      HSSP; P01607; IREI.
DR      InterPro: IPR007110; Ig_1like.
DR      InterPro: IPR003006; Ig_MHC.
DR      InterPro: IPR003596; Ig_v.
DR      Pfam: PF00047; Ig; 1.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG_LIKE; 1.
FT      NON_TER
FT      SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;
SQ
Query Match
Best Local Similarity 63.2%; Score 375.5; DB 4; Length 108;
Matches 75; Conservative 15; Mismatches 17; Indels 7; Gaps 2;

QY      1 DIQLQSPSSSLAVSAGENTMCKSSQSYLSANHNKNTLAWYQKRGOSPKLLIYASTR 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      1 DIQMTQSPSSLSASVGDRTITCRASQGI-----SNTLAWYQKRGKAPKSLIYAASTL 54
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      61 ESGVDPDRFTGSGSGTDFLTITSRVVEDLAIYCHQYLS-SWTFGGGTLEIKR 113
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      55 QSGVPSRFGSGSGTDFLTITSLQPEDFATYCCOOSYSTSWTFEGTKVEIKR 108
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 6
ID      Q9UL81      PRELIMINARY;      PRT;      107 AA.
AC      Q9UL81;
DR      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      Myosin-reactive immunoglobulin light chain variable region
      (Fragment).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_Taxid=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98277139; PubMed=9614934;
RA      Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RT      Young D.C.;
RT      *Myosin-reactive autoantibodies in rheumatic carditis and normal
      fetus*.;
RL      Clin. Immunol. Immunopathol. 87:184-192(1998).
DR      EMBL; AF035033; AAD56269.1; -.
DR      HSSP; P01607; IREI.

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DR      InterPro: IPR007110; Ig_1like.
DR      InterPro: IPR003006; Ig_MHC.
DR      InterPro: IPR003596; Ig_v.
DR      Pfam: PF00047; Ig; 1.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG_LIKE; 1.
FT      NON_TER
FT      SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;
SQ
Query Match
Best Local Similarity 62.8%; Score 373; DB 4; Length 107;
Matches 71; Conservative 18; Mismatches 18; Indels 6; Gaps 1;

QY      1 DIQLQSPSSSLAVSAGENTMCKSSQSYLSANHNKNTLAWYQKRGOSPKLLIYASTR 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      1 DIQMTQSPSSLSASVGDRTITCRASQGI-----SNTLAWYQKRGKAPKSLIYAASTL 54
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      61 ESGVDPDRFTGSGSGTDFLTITSRVVEDLAIYCHQYLS-SWTFGGGTLEIKR 113
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      55 QSGVPSRFGSGSGTDFLTITSLQPEDFATYCCOOSYSTSWTFEGTKVEIKR 107
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 7
ID      Q99M37      PRELIMINARY;      PRT;      238 AA.
AC      Q99M37;
DR      01-JUN-2001 (TREMBLrel. 17, Created)
DT      01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      Hypothetical 26.3 kDa protein.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX      NCBI_Taxid=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      Strausberg R.;
RL      Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BC002035; AAH02035.1; -.
DR      HSSP; P01679; 2FBJ.
DR      InterPro: IPR007110; Ig_1like.
DR      InterPro: IPR003006; Ig_MHC.
DR      InterPro: IPR003596; Ig_v.
DR      Pfam: PF00047; Ig; 2.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG_LIKE; 2.
DR      PROSITE; PS00290; IG_MHC; 1.
KW      Hypothetical protein.
SQ      SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;
Query Match
Best Local Similarity 62.5%; Score 371; DB 11; Length 238;
Matches 74; Conservative 14; Mismatches 24; Indels 2; Gaps 2;

QY      1 DIQLQSPSSSLAVSAGENTMCKSSQSYLSANHNKNTLAWYQKRGOSPKLLIYASTR 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      20 DVVMQTFPLSLVPSLGDQASISCRSSQSYVHS-NGNTYLEWLVQKRGOSPKLLIYKVSNR 78
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      61 ESGVDPDRFTGSGSGTDFLTITSRVVEDLAIYCHQYLS-SWTFGGGTLEIKR 113
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      79 FSGVDPDRFTGSGSGTDFLTITSRVVEDLAIYCHQYLS-SWTFGGGTLEIKR 132
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 8
ID      Q9UL85      PRELIMINARY;      PRT;      109 AA.
AC      Q9UL85;
DR      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      Myosin-reactive immunoglobulin kappa chain variable region
      (Fragment).

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[illegible]

Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
EMBL: BC019760; AAH19760.1; -
InterPro: IPR003006; Ig_MHC.
Accession: Z98002000

Best Local Similarity 64.08; Pred. No. 6.2e-32;
Matches 73; Conservative 14; Mismatches 20; Indels 7; Gaps 2;

Best Local Similarity 64.08; Pred. No. 6.2e-32;
Matches 73; Conservative 14; Mismatches 20; Indels 7; Gaps 2;

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QY 1 DILTQSPSSSLAAGAGNVTMSCKSSSVLYLSANHKNTLAWTQKRGOSPKLLIYASTR 60
Db 1 DIYVTOGSPSLSLASTGDRVTISCRMSGI-----SLLAWTQKRGKRPDELLIYASTL 54
QY 61 ESGVPPDFETSSGSGDTFTLISRYQVEDLAIYCHYLS-SWTFGGCTLEIKR 113
Db 55 QSGVPSRFSSGSGSGDTFTLISCLQSEDPATYTCQOQYIFPPTFGGSTVAEIKR 108

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QY 1 DILTQSPSSSLAAGAGNVTMSCKSSSVLYLSANHKNTLAWTQKRGOSPKLLIYASTR 60
Db 1 DIYVTOGSPSLSLASTGDRVTISCRMSGI-----SLLAWTQKRGKRPDELLIYASTL 54
QY 61 ESGVPPDFETSSGSGDTFTLISRYQVEDLAIYCHYLS-SWTFGGCTLEIKR 113
Db 55 QSGVPSRFSSGSGSGDTFTLISCLQSEDPATYTCQOQYIFPPTFGGSTVAEIKR 108

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QY 1 DILTQSPSSSLAAGAGNVTMSCKSSSVLYLSANHKNTLAWTQKRGOSPKLLIYASTR 60
Db 1 DIYVTOGSPSLSLASTGDRVTISCRMSGI-----SLLAWTQKRGKRPDELLIYASTL 54
QY 61 ESGVPPDFETSSGSGDTFTLISRYQVEDLAIYCHYLS-SWTFGGCTLEIKR 113
Db 55 QSGVPSRFSSGSGSGDTFTLISCLQSEDPATYTCQOQYIFPPTFGGSTVAEIKR 108

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```

QY 1 DILTQSPSSSLAAGAGNVTMSCKSSSVLYLSANHKNTLAWTQKRGOSPKLLIYASTR 60
Db 1 DIYVTOGSPSLSLASTGDRVTISCRMSGI-----SLLAWTQKRGKRPDELLIYASTL 54
QY 61 ESGVPPDFETSSGSGDTFTLISRYQVEDLAIYCHYLS-SWTFGGCTLEIKR 113
Db 55 QSGVPSRFSSGSGSGDTFTLISCLQSEDPATYTCQOQYIFPPTFGGSTVAEIKR 108

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RESULT 15
Q9NEY1

ID	Q8NEK1	PRELIMINARY;	PRT;	234	AA.
AC	Q8NEK1;				

ID	Q8NEK1	PRELIMINARY;	PRT;	234	AA.
AC	Q8NEK1;				

DT	01-OCT-2002	(TREMBlere)	22	1st 300
DT	01-OCT-2002	(TREMBlere)	22	1st 300

DT	01-OCT-2002	(TREMBlere)	22	1st 300
DT	01-OCT-2002	(TREMBlere)	22	1st 300

DT	01-OCT-2002	(TREMBlere)	22	1st 300
DT	01-OCT-2002	(TREMBlere)	22	1st 300

DT	01-OCT-2002	(TREMBlere)	22	1st 300
DT	01-OCT-2002	(TREMBlere)	22	1st 300

DT	01-OCT-2002	(TREMBlere)	22	1st 300
DT	01-OCT-2002	(TREMBlere)	22	1st 300

DT	01-OCT-2002	(TREMBlere)	22	1st 300
DT	01-OCT-2002	(TREMBlere)	22	1st 300

DT	01-OCT-2002	(TREMBlere)	22	1st 300
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DT	01-OCT-2002	(TREMBlere)	22	1st 300
DT	01-OCT-2002	(TREMBlere)	22	1st 300

DT	01-OCT-2002	(TREMBlere)	22	1st 300
DT	01-OCT-2002	(TREMBlere)	22	1st 300

DT	01-OCT-2002	(TREMBlere)	22	1st 300
DT	01-OCT-2002	(TREMBlere)	22	1st 300

DT	01-OCT-2002	(TREMBlere)	22	1st 300
DT	01-OCT-2002	(TREMBlere)	22	1st 300

DT	01-OCT-2002	(TREMBlere)	22	1st 300
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DT	01-OCT-2002	(TREMBlere)	22	1st 300
DT	01-OCT-2002	(TREMBlere)	22	1st 300

DT	01-OCT-2002	(TREMBlere)	22	1st 300
DT	01-OCT-2002	(TREMBlere)	22	1st 300

DT	01-OCT-2002	(TREMBlere)	22	1st 300
DT	01-OCT-2002	(TREMBlere)	22	1st 300

DT	01-OCT-2002	(TREMBlere)	22	1st 300
DT	01-OCT-2002	(TREMBlere)	22	1st 300

DT	01-OCT-2002	(TREMBlere)	22	1st 300
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DT	01-OCT-2002	(TREMBlere)	22	1st 300

DT	01-OCT-2002	(TREMBlere)	22	1st 300
DT	01-OCT-2002	(TREMBlere)	22	1st 300

DT	01-OCT-2002	(TREMBlere)	22	1st 300
DT	01-OCT-2002	(TREMBlere)	22	1st 300

DT	01-OCT-2002	(TREMBlere)	22	1st 300
DT	01-OCT-2002	(TREMBlere)	22	1st 300

DT	01-OCT-2002	(TREMBlere)	22	1st 300
DT	01-OCT-2002	(TREMBlere)	22	1st 300

Query Match	60.58; Score 359.5; DB 4; Length 234;
Best Local Start/end	20.23; 10.23; 10.23; 10.23; 10.23; 10.23;

Query Match	60.58; Score 359.5; DB 4; Length 234;
Best Local Start/end	20.23; 10.23; 10.23; 10.23; 10.23; 10.23;

Query Match	60.58; Score 359.5; DB 4; Length 234;
Best Local Start/end	20.23; 10.23; 10.23; 10.23; 10.23; 10.23;

Conservative 16; Mismatches 16; Indels 9; Gaps 3;

Conservative 16; Mismatches 16; Indels 9; Gaps 3;

Conservative 16; Mismatches 16; Indels 9; Gaps 3;

Conservative 16; Mismatches 16; Indels 9; Gaps 3;

Search completed: October 7, 2003, 19:19:53
Job time : 114.61 secs

Search completed: October 7, 2003, 19:19:53
Job time : 114.61 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 19:07:11 ; Search time 42.0828 Seconds
(without alignments)
258.231 Million cell updates/sec

Title: US-09-988-013A-2

Perfect score: 594
Sequence: 1 DIQLTQSPSSLAVSAGENVNT.....CHQYLSSWTFGGTKLEIKR 113

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 segs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_76:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	531	89.4	111	2	G30502
2	494	83.2	103	2	PHI054
3	492	82.8	112	2	S41393
4	491.5	82.7	120	2	S51147
5	488	82.2	138	2	S26040
6	487	82.0	113	2	PT0407
7	485	81.6	118	2	PT0356
8	483	81.3	133	2	PS0023
9	482	81.1	101	2	S26337
10	482	81.1	112	2	S09970
11	482	81.1	112	2	S43103
12	480	80.8	133	1	K4HUJ1
13	479.5	80.7	240	2	S06084
14	477.5	80.4	145	2	PL0014
15	474.5	79.9	114	1	K4HULN
16	473.5	79.7	134	2	PC1214
17	472.5	79.5	134	2	S48531
18	469	79.0	113	2	PT0408
19	469	79.0	113	2	A53261
20	468.5	78.9	113	2	S34002
21	468	78.8	112	2	PL0265
22	467.5	78.7	113	2	S34003
23	465.5	78.4	214	2	S68212
24	464.5	78.2	114	2	S44119
25	462.5	77.9	113	2	A49260
26	461.5	77.7	113	2	S30523
27	461.5	77.7	113	2	PL0263
28	461.5	77.7	134	1	K4HUJ7
29	457.5	77.0	220	2	A31790

30	456.5	76.9	113	2	S30520	Ig kappa chain V r
31	454.5	76.5	109	2	S26336	Ig light chain V r
32	454.5	76.5	114	2	S44116	Ig kappa chain V r
33	452.5	76.2	132	2	S46373	Ig kappa chain V r
34	451.5	76.0	112	2	F30538	Ig kappa chain V r
35	450.5	75.8	112	2	E30538	Ig kappa chain V r
36	450.5	75.8	113	2	JC2270	PL7-6 antibody 11g
37	449.5	75.7	135	2	S38807	Ig light chain V r
38	446	75.1	104	2	PH1104	Ig light chain V r
39	445.5	75.0	113	2	PL0264	Ig kappa chain V r
40	444.5	74.8	111	2	S03304	Ig kappa chain V r
41	443.5	74.7	96	2	G38601	Ig kappa chain V r
42	443.5	74.7	124	2	S40364	Ig kappa chain V r
43	443	74.6	104	2	PH1102	Ig light chain V r
44	442	74.4	104	2	PH1101	Ig light chain V r
45	441	74.2	103	2	PH1047	Ig light chain V r

ALIGNMENTS

RESULT 1

G30502

Ig kappa chain V region (A52) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000

C:Accession: G30502

R:Ellat, D.; Webster, D.M.; Rees, A.R.

J. Immunol. 141, 1745-1753, 1988

A:Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1:

A:Reference number: A30502; MUID:88315787; PMID:2457627

A:Accession: G30502

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-111 <EIL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterocyclamer; immunoglobulin

F:16-96/Domain: immunoglobulin homology <IMM>

Query Match Best Local Similarity 89.4%; Score 531; DB 2; Length 111;

Matches 99; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLAVSAGENVNTMCKSSQSVLYSANRKNYLAHYQKPGSPKLLIYMASTR 60

Db 1 NIMTQSPSSLAVSAGEKVTMCKSSQSVLYSNOKNYLAHYQKPGSPKLLIYMASTR 60

QY 61 ESGVDRFTGSGSGDTFTITRSQVEDLAITYCHQYLSSWTFGGTKLEI 111

Db 61 ESGVDRFTGSGSGDTFTITRSQVEDLAITYCHQYLSSWTFGGTKLEI 111

RESULT 2

PHI054 Ig light chain V region (clone 202.135) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C:Accession: PHI054

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PHI054

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-103 <TTI>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:16-96/Domain: immunoglobulin homology <IMM>

Query Match Best Local Similarity 83.2%; Score 494; DB 2; Length 103;

Matches 90.3%; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 19:03:46 ; Search time 22.9897 Seconds

(without alignments)
231.148 Million cell updates/sec

Title: US-09-988-013a-2

Perfect score: 594
Sequence: 1 DIQLTQSPSPSLAVSAGENVY.....CHOYLSSWTFGGGKLEIKR 113

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	480	80.8	133	1	KV4B_HUMAN
2	474.5	79.9	134	1	KV4C_HUMAN
3	473.5	79.7	114	1	KV4A_HUMAN
4	434	73.1	121	1	KV4D_HUMAN
5	420.5	70.8	109	1	KV4M_HUMAN
6	392	66.0	129	1	KV3M_HUMAN
7	386.5	65.1	114	1	KV1A_MOUSE
8	382	64.3	110	1	KV3P_MOUSE
9	382	64.3	129	1	KV3L_HUMAN
10	380.5	64.1	108	1	KV1M_HUMAN
11	379	63.8	129	1	KV3H_HUMAN
12	378	63.6	109	1	KV3B_HUMAN
13	377	63.5	109	1	KV3D_HUMAN
14	375	63.1	109	1	KV3E_HUMAN
15	369.5	62.2	108	1	KV1V_HUMAN
16	368.5	62.0	111	1	KV3O_MOUSE
17	368	62.0	133	1	KV2E_HUMAN
18	365.5	61.5	111	1	KV3L_MOUSE
19	365.5	61.5	136	1	KV5B_MOUSE
20	364.5	61.4	149	1	KV5A_MOUSE
21	364	61.3	117	1	KV2E_HUMAN
22	362.5	61.0	128	1	KV3K_HUMAN
23	362	60.9	108	1	KV3A_HUMAN
24	361.5	60.9	108	1	KV1V_HUMAN
25	361	60.8	109	1	KV3G_HUMAN
26	360.5	60.7	108	1	KV1H_HUMAN
27	360.5	60.7	108	1	KV1R_HUMAN
28	360.5	60.7	111	1	KV3O_MOUSE
29	360.5	60.7	115	1	KV2A_MOUSE
30	359.5	60.5	108	1	KV1B_HUMAN
31	359	60.4	109	1	KV3F_HUMAN
32	359	60.4	113	1	KV2G_MOUSE
33	358.5	60.4	129	1	KV1W_HUMAN

34	358	60.3	107	1	KV1D_HUMAN	P01596	homo sapien
35	358	60.3	113	1	KV2D_HUMAN	P01617	homo sapien
36	357.5	60.2	108	1	KV1K_HUMAN	P01603	homo sapien
37	357.5	60.2	111	1	KV3M_MOUSE	P01665	mus musculus
38	352.5	59.3	108	1	KV1F_MOUSE	P01598	homo sapien
39	352.5	59.3	108	1	KV1O_HUMAN	P01607	homo sapien
40	352.5	59.3	111	1	KV3N_MOUSE	P01666	mus musculus
41	351.5	59.2	111	1	KV3R_MOUSE	P01670	mus musculus
42	351.5	59.2	111	1	KV3U_MOUSE	P01673	mus musculus
43	351.5	59.2	131	1	KV3I_MOUSE	P01661	mus musculus
44	351	59.1	113	1	KV2B_HUMAN	P01615	homo sapien
45	350.5	59.0	112	1	KV2C_HUMAN	P01616	homo sapien

ALIGNMENTS

```

RESULT 1
KV4B_HUMAN          STANDARD;          PRT;          133 AA.
ID   KV4B_HUMAN
AC   P06313;
DT   01-JAN-1988 (Rel. 06, Created)
DI   01-JAN-1988 (Rel. 06, Last sequence update)
DE   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-IV region JI precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX   NCBI_TaxID:9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE:86041853; PubMed-2997712;
RA   Klobbeck H.G., Bornkamm G.W., Combrato G., Mocikat R., Pohlenz H.D.,
RA   Zachau H.G.;
RT   "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT   single germline gene."
RL   Nucleic Acids Res. 13:6515-6529(1985);
CC   -----
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CC   entities requires a license agreement (See http://www.isb.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----
DR   EMBL: Z00022; CAAT7317.1;
DR   PIR: A01904; KAHUT1.
DR   HSP: P80362; IWT1.
DR   GO: GO:0005576; C:extracellular; NAS.
DR   GO: GO:0003823; F:antigen binding activity; NAS.
DR   GO: GO:0006955; P:immune response; NAS.
DR   InterPro: IPR007110; Ig-like.
DR   InterPro: IPR003065; Ig_MHC.
DR   InterPro: IPR003596; Ig_V.
DR   Pfam: PF00047; Ig_1.
DR   SMART: SM00406; IGV_1.
DR   PROSITE: PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL          1
FT   CHAIN          20
FT   DOMAIN          21
FT   DOMAIN          21
FT   DOMAIN          44
FT   DOMAIN          61
FT   DOMAIN          76
FT   DOMAIN          83
FT   DOMAIN          115
FT   DOMAIN          123
FT   DOMAIN          123
FT   DOMAIN          133
FT   DISULFID        43
FT   NON_TER         133
SQ   SEQUENCE        133 AA; 14632 MW; 5FB3953066744AF4 CRC64;
Query Match          80.8%; Score 480; DB 1; Length 133;

```

[illegible]

RESULT 2

ID	KV4C_HUMAN	STANDARD;	PRT;	134 AA.
AC	P06314			

DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region B17 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=66041854; PubMed=2997713;
RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned
RT cDNA probe.";
RL Nucleic Acids Res. 13:6531-6544(1985).
RN [2]
RP REVISION TO 76.

Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.

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CC or send an email to license@isb-sib.ch).

DR	EMBL: X02990: CAA26733.1; .
DR	HSSP: P80362: IMTL.
DR	GO: GO:0005576; C:extracellular; NAS.
DR	GO: GO:0003823; F:antigen binding activity; NAS.
DR	GO: GO:0006955; P:immune response; NAS.
DR	InterPro: IPR007110; Ig-1-like.
DR	InterPro: IPR003006; Ig_MHC.
DR	InterPro: IPR003596; Ig_V.
DR	Pfam: PF00047; Ig; 1.
DR	SMART: SM00406; Igv_1.
DR	PROSITE: PS50835; IG_LIKE; 1.
KM	Immunoglobulin V region; Signal.
FT	SIGNAL
FT	CHAIN
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DISULFID
FT	NON_TER
SO	SEQUENCE
	134 AA; 14566 MW; 6413A22F00738832 CRC64;

Query Match	79.98%;	Score 474.5;	DB 1;	Length 134;
Best Local Similarity	77.28;	Pred. No. 2.3e-43;		
Matches 88;	Conservative 13;	Mismatches 12;	Indels 1;	Gaps 1.

[illegible]

RESULT 3

ID	KV4A_HUMAN	STANDARD;	PRT;	114 AA.
15	D0163E			

DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain V-IV region Len.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP
RX MEDLINE=76004342; PubMed=50995;
RA Schneider M., Hilschmann N.;
RT "The primary structure of a monoclonic immunoglobulin-L-chain of
RT subgroup IV of the kappa type (Bence-Jones protein Len).";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
RN [2]

RP REVISION TO 9
PA 10/10/00

Submitted (AUG-1996) to the SWISS-PROT data bank.
 -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER
 -1- MISCELLANEOUS: THIS IS A BENGE-JONES PROTEIN.
 POS. 1990-01-1990-01

DR	PDB:	1EEU:	03-FEB-01.		
DR	PDB:	1EEQ:	09-FEB-01.		
DR	PDB:	1EK3:	06-MAR-01.		
DR	PDB:	1LVE:	21-JAN-98.		
DR	PDB:	1LVE:	18-MAY-99.		
DR	PDB:	1LVE:	28-MAR-01.		
DR	GO:	GO:0005576:	C:extracellular:	NAS.	
DR	GO:	GO:0008823:	P:antigen binding activity:	NAS.	
DR	GO:	GO:0006955:	P:immune response:	NAS.	
DR	InterPro:	IPR007110:	Ig-like.		
DR	InterPro:	IPR003006:	Ig_MHC.		
DR	InterPro:	IPR003596:	Ig_v.		
DR	Pfam:	PF00047:	Ig: 1.		
DR	SMART:	SM00406:	IGV: 1.		
DR	PROSITE:	PS00835:	IG_LIKE: 1.		
KW	Immunoglobulin V region:	Bence-Jones protein; 3D-structure			
FT	DOMAIN	1	23	FRAMEOR-1	
FT	DOMAIN	24	40	COMPLEMENTARITY-DETERMINING-1	
FT	DOMAIN	41	55	FRAMEOR-2.	
FT	DOMAIN	56	62	COMPLEMENTARITY-DETERMINING-2	
FT	DOMAIN	63	94	FRAMEOR-3.	
FT	DOMAIN	95	101	COMPLEMENTARITY-DETERMINING-3	
FT	DISULFID	102	113	FRAMEOR-4.	
FT	NON_TER	23	94	BY SIMILARITY.	
SO	SEQUENCE	114 AA:	12640 MW:	0647F1D1F736485 CRC64:	

Query Match	79.7%;	Score 473.5;	DB 1;	Length 114;
Best Local Similarity	78.9%;	Pred. No. 2.5e-43;		
Matches 90;	Conservative 11;	Mismatches 12;	Indels 1;	Gaps 1;

OY	1	DIOITGSPSSLAWSAGANVYMSCKSSOSVLYS	SNHNHNYLTAWQOKGOSPKLLIYASNR	60
		: : : :		
Db	1	DIWMTGSPBDLAWSLGSRATINCKSSQSVLYS	NSNKNYLTAWQOKGOSPKLLIYASNR	60
OY	61	ESGVPDPAFTSSGSGTDPTLTISRQVEDLAITY	CHQYLS -WFGGCGTLEIKR	113
Db	61	ESGVPDPAFTSSGSGTDPTLTISRQVEDLAITY	CHQYLS -WFGGCGTLEIKR	114

```

RESULT 4
KV40_HUMAN
ID KV40_HUMAN STANDARD: PRT: 121 AA.
AC P06312;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-IV region precursor (Fragment).
GN IGKV4-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobek H.G., Bornkamm G.W., Combario G., Mochkat R., Pohlentz H.D.,
RA Zechan H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene."
RL Nucleic Acids Res. 13:6515-6529(1985).
CC 1- MISCELLANEOUS: THERE IS ONLY ONE IG KAPPA V-IV GENE.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; Z00023; CAAT7318.1; -.
DR PIR; A01902; KAHU.
DR HSSP; P80362; IMTL.
DR GENE; HGNC:5834; IGKV4-1.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
DR Immunoglobulin V region; Signal.
KW CHAIN
FT SIGNAL 1 20
FT CHAIN 21 >121 IG KAPPA CHAIN V-IV REGION.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 114 BY SIMILARITY.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13380 MM; 9586AD418BD33974 CXC64;

Query Match 73.1%; Score 434; DB 1; Length 121;
Best Local Similarity 80.0%; Pred. No. 4e-39;
Matches 80; Conservative % 10; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQLTSPSSILAVSAGENVMSCKSSQSVLYSAHHKNTLYAQKPGSPKLLIYMASTR 60
DB 21 DIWVTSQPSDLSIALGERATINCKSSQSVLYSSNNKNTLYAQKPGSPKLLIYMASTR 80
QY 61 ESGVPDFRFTSGSGCTDFTLTISRQVEDLAIYICHOYLS 100
DB 81 ESGVPDFRFTSGSGCTDFTLTISRQVEDLAIYICHOYLS 120

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ID	NAME	STANDARD	PRT	109 AA
RV4D	HUMAN			
AC	KVAD_HUMAN	STANDARD	PRT	109 AA
DT	15-SEP-2003 (Rel. 42, Created)			
DT	15-SEP-2003 (Rel. 42, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	IG kappa chain V-IV region 5'UTR (Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:			
OC	Mammalia: Eutheria: Primates: Catarrhini: Homiidae: Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Abdominal adipose tissue;			
RX	PubMed=958180;			
RA	Olsen K.E., Sletten K., Westmark P.;			
RT	"Extended analysis of AL-amyloid protein from abdominal wall			
RT	subcutaneous fat biopsy: kappa IV immunoglobulin light chain.";			
RL	Biochem. Biophys. Res. Commun. 245:713-716(1998).			
CC	-1- FUNCTION: May play an important role in fibrillogenesis.			
DR	InterPro: IPR003599; 1g.			
DR	InterPro: IPR007110; 1g-like.			
DR	InterPro: IPR003596; 1g_v.			
DR	Pfam: PF00047; 1g; 1.			
DR	PROSITE: PS50835; 1g_LIKE; 1.			
KW	Immunoglobulin V region.			
FT	DOMAIN 1 23			
FT	DOMAIN 24 40			
FT	DOMAIN 41 55			
FT	DOMAIN 56 62			
FT	DOMAIN 63 94			
FT	DOMAIN 95 101			
FT	DOMAIN 102 109			
FT	DISULEID 23 94			
FT	UNSURE 23 23			
FT	UNSURE 94 94			
FT	NOV_TER 109 109			
SO	SEQUENCE 109 AA; 12060 MW; 0C4F31EA11E12A0B CRC64;			
QY	Query Match 70.8%; Score 420.5; DB 1; Length 109;			
Db	Best Local Similarity 72.5%; Pred. No. 9.7e-38;			
Matches	79; Conservative 12; Mismatches 17; Indels 1; Gaps			
QY	1 DIOLITGPPSSILANSAGCHNTMSCKSSQSVLYISANKHNTLAWIQARKGSGPKLLITWASTR 60			
Db	1 DIWVTGSPDPLVYSLGERATINCRSSQSVLYSSNNKNTLAWYQKRGKAPKLLFWSASTR 60			
QY	61 EGGVDPDFGTSGSGCTDFTLTISVQVEDLAIVYCHQYLS-SWTFGGGTR 108			
Db	61 EGGVDPDFGTSGSGCTDFTLTITPGLQADVAIVYCOQYRPIPTFGGAK 109			
RESULT 6				
KV3M_HUMAN				
ID	KV3M_HUMAN	STANDARD;	PRT;	129 AA.
AC	P18136;			
DT	01-NOV-1990 (Rel. 16, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	IG kappa chain V-III region HIC precursor.			
OS	Homo sapiens (Human).			
OC	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:			
OC	Mammalia: Eutheria: Primates: Catarrhini: Homiidae: Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=88171307; PubMed=3127527;			
RT	Klapps T.J., Tomhave E., Chen P.P., Carson D.A.;			
RT	"Antibody-associated kappa light chain variable region gene			
RT	expressed in chronic lymphocytic leukemia with little or no somatic			
RT	mutation. Implications for etiology and immunotherapy.";			
J.	J. Exp. Med. 167:840-852(1988)			
-1-	DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M			

AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC LEUKEMIA.

CC PIR: PL0021; K3HGH1.
 DR HSP: P80362; 1MTL.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; 1g; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 1 129
 FT DOMAIN 21 43 IG KAPPA CHAIN V-III REGION HIC.
 FT DOMAIN 44 55 FRAMEWORK-1.
 FT DOMAIN 56 70 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 71 77 FRAMEWORK-2.
 FT DOMAIN 78 109 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 110 118 FRAMEWORK-3.
 FT DOMAIN 119 129 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 43 109 JKL SEGMENT.
 FT NON_TER 129 129 BY SIMILARITY.
 SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2B74D6 CRC64;

Query Match 66.0%; Score 392; DB 1; Length 129;
 Best Local Similarity 65.8%; Pred. No. 1.2e-34;
 Matches 75; Conservative 18; Mismatches 15; Indels 6; Gaps 2;

QY 1 DIQLQSPSSSLAVSAGENTVMSCKSSQSVLYSANHKNTLAWYQKPGSPRLIITYMASTR 60
 ID KVA1_MOUSE STANDARD; PRT; 114 AA.
 AC P01632;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region S107A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81241357; PubMed=6788890;
 RA Kwan S.-P., Rudloff S., Seidman J.G., Leder P., Schaff M.D.;
 RT "Nucleic acid and protein sequences of phosphocholine-binding light
 chain";
 RT J. Exp. Med. 153:1366-1370(1981).
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 or send an email to license@sib-sib.ch).

DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; 1g; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 40 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 41 55 FRAMEWORK-2.
 FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 63 94 FRAMEWORK-3.
 FT DOMAIN 95 103 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 104 113 FRAMEWORK-4.
 FT DISULFID 23 94 BY SIMILARITY.
 FT NON_TER 114 114
 SQ SEQUENCE 114 AA; 12717 MW; 32008CE89DBE67B CRC64;

Query Match 65.1%; Score 386.5; DB 1; Length 114;
 Best Local Similarity 70.4%; Pred. No. 4e-34;
 Matches 81; Conservative 12; Mismatches 19; Indels 3; Gaps 3;

QY 1 DIQLQSPSSSLAVSAGENTVMSCKSSQSVLYSANHK-NYLAWYQKPGSPRLIITYMAST 59
 ID KVA3_MOUSE STANDARD; PRT; 110 AA.
 AC P01668;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region PC 7210.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gaumattian L., Ioh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 diversity";
 RT Nature 276:785-790(1978).
 RL Nature 276:785-790(1978).
 DR HSP: P01679; 2PRT.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; 1g; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 39 53 FRAMEWORK-2.
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 61 92 FRAMEWORK-3.
 FT DOMAIN 93 100 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 101 110 FRAMEWORK-4.
 FT DISULFID 23 92 BY SIMILARITY.
 FT NON_TER 110 110
 SQ SEQUENCE 110 AA; 11950 MW; 69F1ASCE886B1249 CRC64;

Query Match 64.3%; Score 382; DB 1; Length 110;
 Best Local Similarity 67.0%; Pred. No. 1.2e-33;
 Matches 75; Conservative 11; Mismatches 24; Indels 2; Gaps 1;

QY 1 DIQLQSPSSSLAVSAGENTVMSCKSSQSVLYSANHKNTLAWYQKPGSPRLIITYMASTR 60

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Db      1 DIVLTQSPASIAVLSAGQRAITISCKASQSIDYDGD--STANNYQOKPQGPCKLLITYAASNL 58
Oy      61 ESGVDPRTGSGSGDTFTLTISRVOVEDIAYYCHQYLSWTFGGGKLEIKR 112
        59 ESGIARFSGSGSGDTFTLTISRLEPEDEAVYCCQYIGSPRTFGGKLEIKR 110

RESULT 9
KV3L_HUMAN  STANDARD; PRT; 129 AA.
ID   KV3L_HUMAN
AC   P18135;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-II region HAW precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX   NCBI_Taxid=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88171307; PubMed=3127527;
RA   Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT   "Autoantibody-associated kappa light chain variable region gene
RT   expressed in chronic lymphocytic leukemia with little or no somatic
RT   mutation. Implications for etiology and immunotherapy."
RL   J. Exp. Med. 167:840-852(1988).
CC   -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC   LEUKEMIA.
CC   ANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC   LEUKEMIA.
DR   HSP: P80022; K3H0HA.
DR   HSP: P80362; 1MTL.
DR   GO: GO:0005576; C:extracellular; NAS.
DR   GO: GO:0003823; F:antigen binding activity; NAS.
DR   GO: GO:0006955; P:immune response; NAS.
DR   InterPro: IPR007110; Ig-like.
DR   InterPro: IPR003006; Ig_MHC.
DR   InterPro: IPR003596; Ig_V.
DR   Pfam: PF00047; Ig_1.
DR   SMART: SM00406; IGV; 1.
DR   PROSITE: PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL 1..20
FT   CHAIN 21..129 IG KAPPA CHAIN V-III REGION HAW.
FT   DOMAIN 21..43 FRAMEWORK-1.
FT   DOMAIN 44..55 COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN 56..70 FRAMEWORK-2.
FT   DOMAIN 71..77 COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN 78..109 FRAMEWORK-3.
FT   DOMAIN 110..118 COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN 119..129 JKL SEGMENT.
FT   DISULFID 43..109 BY SIMILARITY.
FT   NON_TER 129
SQ   SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;

Query Match 64.3%; Score 382; DB 1; Length 129;
Best Local Similarity 64.9%; Pred. No. 1.4e-33;
Matches 74; Conservative 18; Mismatches 16; Indels 6; Gaps 2;

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DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Lay.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX   NCBI_Taxid=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=7308198; PubMed=824717;
RA   Capra J.D., Klapper D.G.;
RT   "Complete amino acid sequence of the variable domains of two human
RT   Igm anti-gamma globulins (Lay/Pom) with shared idiotypic
RT   specificities."
RL   Scand. J. Immunol. 5:677-684(1976).
CC   -1- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC   CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POK V-III KAPPA CHAIN,
CC   WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC   -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC   GLOBULIN ACTIVITY.
DR   HSP: P01607; 1REI.
DR   HSP: A01871; K1H0LY.
DR   GO: GO:0005576; C:extracellular; NAS.
DR   GO: GO:0003823; F:antigen binding activity; NAS.
DR   GO: GO:0006955; P:immune response; NAS.
DR   InterPro: IPR007110; Ig-like.
DR   InterPro: IPR003006; Ig_MHC.
DR   InterPro: IPR003596; Ig_V.
DR   Pfam: PF00047; IGV; 1.
DR   SMART: SM00406; IGV; 1.
DR   PROSITE: PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN 1..23 FRAMEWORK-1.
FT   DOMAIN 24..34 COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN 35..49 FRAMEWORK-2.
FT   DOMAIN 50..56 COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN 57..88 FRAMEWORK-3.
FT   DOMAIN 89..97 COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN 98..107 FRAMEWORK-4.
FT   DISULFID 23..88 BY SIMILARITY.
FT   NON_TER 108
SQ   SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 64.1%; Score 380.5; DB 1; Length 108;
Best Local Similarity 65.2%; Pred. No. 1.6e-33;
Matches 75; Conservative 17; Mismatches 14; Indels 9; Gaps 3;

```

RA Goldfien R., Carson D.A.;
 RT "Cloning and sequence determination of a human rheumatoid factor
 RT light-chain gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
 CC -----
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 CC -----
 DR EMBL: M12740; AA:58992.1; -
 DR HSSP: P80362; IWTL.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG LIKE; 1.
 DR Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 1 20
 FT DOMAIN 21 129 IG KAPPA CHAIN V-III REGION CLL.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 69 FRAMEWORK-2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 77 108 FRAMEWORK-3.
 FT DOMAIN 109 118 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 119 129 JK1 SEGMENT.
 FT DISULFID 43 108 BY SIMILARITY.
 FT NON_TER 129 129
 SO SEQUENCE 129 AA; 14275 MW; 5C13B411BE6CC14 CRC64;
 Query Match 63.8%; Score 379; DB 1; Length 129;
 Best Local Similarity 63.5%; Pred. No. 2.9e-33;
 Matches 73; Conservative 18; Mismatches 16; Indels 8; Gaps 2;
 OY 1 DIQTQSPSSLAIVSAGENVMTSCSKSSQSVLYSANHKRYLWYQKPGQSPKRLITYMASTR 60
 DB 21 EIVWTQSPGTLSPGKRAFLSCRAASQV-----SNLWYQKPGQAPRLITYGASSTR 74
 OY 61 ESGVDPRTGSGCTDFTLTISRQVEDLAITYCHQYLS--SWTFGGTKLEIKR 113
 DB 75 ATGIPARFSGSGCTDFTLTISRQVEDLAITYCHQYLS--SWTFGGTKLEIKR 129
 RESULT 12
 KV3D_HUMAN STANDARD; PRT; 109 AA.
 ID KV3D_HUMAN STANDARD; PRT; 109 AA.
 AC P01620;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region SIE.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=82046598; PubMed=6794615;
 RA Andrews D.W., Capra J.D.;
 RT "Amino acid sequence of the variable regions of light chains from two
 RT idiotypically cross-reactive human Igm anti-gamma-globulins of the Wa
 RT group.";
 RL Biochemistry 20:5816-5822(1981).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
 CC GLOBULIN ACTIVITY.

DR PIR: A01892; K3HUST.
 DR HSSP: P80362; IWTL.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG LIKE; 1.
 DR Immunoglobulin V region.
 FT DISULFID 23 89
 FT NON_TER 109 109 BY SIMILARITY.
 SO SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;
 Query Match 63.6%; Score 378; DB 1; Length 109;
 Best Local Similarity 64.0%; Pred. No. 3.1e-33;
 Matches 73; Conservative 20; Mismatches 15; Indels 6; Gaps 2;
 OY 1 DIQTQSPSSLAIVSAGENVMTSCSKSSQSVLYSANHKRYLWYQKPGQSPKRLITYMASTR 60
 DB 1 EIVWTQSPGTLSPGKRAFLSCRAASQV-----SNLWYQKPGQAPRLITYGASSTR 55
 OY 61 ESGVDPRTGSGCTDFTLTISRQVEDLAITYCHQYLS--WTFGGTKLEIKR 113
 DB 56 ATGIPARFSGSGCTDFTLTISRQVEDLAITYCHQYLS--WTFGGTKLEIKR 109
 RESULT 13
 KV3D_HUMAN STANDARD; PRT; 109 AA.
 ID KV3D_HUMAN STANDARD; PRT; 109 AA.
 AC P01622;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region TL.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72188439; PubMed=5027703;
 RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
 RT T1). IV. The complete amino acid sequence and its significance for
 RT the mechanism of antibody production.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR: A01895; K3HUT1.
 DR HSSP: P80362; IWTL.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG LIKE; 1.
 DR Immunoglobulin V region; Bence-Jones protein.
 FT DISULFID 23 89 BY SIMILARITY.
 FT NON_TER 109 109
 SO SEQUENCE 109 AA; 11788 MW; 8C35058CDCT7499C CRC64;
 Query Match 63.5%; Score 377; DB 1; Length 109;
 Best Local Similarity 64.0%; Pred. No. 3.9e-33;
 Matches 73; Conservative 20; Mismatches 15; Indels 6; Gaps 2;
 OY 1 DIQTQSPSSLAIVSAGENVMTSCSKSSQSVLYSANHKRYLWYQKPGQSPKRLITYMASTR 60

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Db      1 EIVYTGSPGLSLSPGKRAFLSCRAQSV-----SMSFLAWYQKQKQAPRLLIYASSR 55
QY      61 ESGVPDRFTFGSGSGTDFTLISRVOYEDLAIIYCHQYLSS-WTFGGGTRLEIKR 113
Db      56 ATGIPDRFSSSGGTDPTLLISLPEDPDAFYVYCCQYGSSPFTFGGTVAELKR 109

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OM protein - protein search, using sw model

Run on: October 7, 2003, 19:03:26 ; Search time 142.224 Seconds

(without alignments)
126.112 Million cell updates/sec

Title: US-09-988-013A-2

Perfect score: 594
Sequence: 1 DIDLTPSSSLAVSAGENV.....CHQYLSWTFGGTKLEIKR 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

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3: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
4: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
5: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
6: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
7: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
8: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
9: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
10: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	594	100.0	113	17	AA92215
2	594	100.0	113	18	AAW27695
3	556	93.6	263	20	AAW90226
4	556	93.6	268	20	AAW90228
5	556	93.6	268	20	AAW90222
6	556	93.6	273	20	AAW90224
7	556	93.6	556	20	AAW90218
8	556	93.6	580	20	AAW90217
9	547	92.1	112	15	AA954933

10	540	90.9	112	23	AAE29266
11	533	89.7	112	23	AAE29264
12	531	89.4	112	23	AAE29268
13	531	89.4	113	17	AA92217
14	530	89.2	272	23	ABG31024
15	527	88.7	112	23	AAE29270
16	523	88.0	115	18	AAW27697
17	513	86.4	238	23	ABG70744
18	508	85.5	112	23	ABG70739
19	506.5	85.3	110	13	AA930012
20	504	84.8	130	24	AAE34366
21	502.5	84.6	113	15	AAE50322
22	502.5	84.6	251	22	AAE47933
23	502.5	84.6	258	22	AAE47944
24	502.5	84.5	259	21	AAE09779
25	501	84.3	112	13	AAE28807
26	499.5	84.1	134	22	AAE47922
27	497	83.7	112	15	AAE49322
28	497	83.7	301	18	AAW11507
29	497	83.7	301	20	AAW73217
30	497	83.7	301	22	AAE85454
31	497	83.7	301	22	AAE61959
32	497	83.7	352	20	AAE06272
33	497	83.7	553	18	AAW15508
34	497	83.7	553	20	AAW73223
35	497	83.7	553	22	AAE85455
36	497	83.7	553	22	AAE61960
37	490.5	82.6	113	13	AAE25407
38	490.5	82.6	220	18	AAW07528
39	490	82.5	134	18	AAW06206
40	486.5	81.9	113	21	AAW90819
41	485.5	81.7	139	17	AAE99469
42	485	81.6	113	22	AAE62769
43	485	81.6	288	20	AAE82743
44	485	81.6	673	20	AAE82742
45	484.5	81.6	137	18	AAW21653

ALIGNMENTS

RESULT 1					
ID	AA92215	standard; Protein: 113 AA.			
AC	AA92215;				
XX					
DT	28-MAY-1996	(first entry)			
XX					
DE	LL2 MAb VR region.				
XX					
KW	Humanised antibody; monoclonal antibody; MAb; LL2; B-cell lymphoma;				
KW	leukaemia; therapy; diagnosis; complementarity determining region;				
KW	CDR; antibody engineering.				
XX					
OS	Mus musculus.				
XX					
FT	Key	Location/Qualifiers			
FT	Region	24..40			
FT		/label= CDR1			
FT		/note= "claim 6, page 44"			
FT	Region	56..62			
FT		/label= CDR2			
FT		/note= "claim 7, page 44"			
FT	Region	95..103			
FT		/label= CDR3			
FT		/note= "claim 8, page 44"			
PN	WO9604925-A1.				
XX					
PD	22-FEB-1996.				
XX					
PF	11-AUG-1995;	95WO-US09641.			

S. aureus ClfA spe
S. aureus ClfA spe
S. aureus ClfA spe
Humanised LL2 MAb
Synthetic mouse fu
S. aureus ClfA spe
Variable kappa cha
Mouse/human chimera
Variable chain of
light chain variat
Escherichia coli 1
MAb NF52 light cha
Single chain antib
Single chain antib
Antiviral scfv-ant
5A8 VL. Synthetic
Anti-CA125 bifunct
Fc receptor human
Single chain, huma
Multispecific sing
Single chain human
Single chain human
Anti-Fc gamma rece
Single chain anti-
H22-anti-CEA antib
Bispecific single
Bispecific single
light chain variat
Anti-HGF receptor
Xenograft antibody
260F9 hybridoma VL
Monoclonal antibod
Human HIV-1 monocl
Fusion protein PNG
Plasmid pNG4/55.15
Mouse MAb 15 light

XX	12-AUG-1994;	94US-0289576.
PR	(IMMU-) IMMUNOMEDICS INC.	
XX		
PA	Hansen H, Leung S;	
XX		
DR	WPI: 1996-139454/14.	
DR	N-PSDB: AAT15802.	
XX		
XX	Chimeric and humanised LL2 antibodies - used to produce conjugates	
PT	for the therapy and diagnosis of B-cell lymphoma(s) and	
PT	leukaemia(s).	
XX		
PS	Claim 5; Page 35-36; 70pp; English.	
XX		
CC	The complementarity determining regions (CDRs) of mouse monoclonal	
CC	antibody (Mab) LL2 VK (AAR92215) and VH (AAR92216) regions were	
CC	recombinantly linked to the framework sequences of human VK and VH	
CC	regions, respectively, to give humanised LL2 VK (AAR92217) and VH	
CC	(AAR92218). These were subsequently linked, respectively, to human	
CC	kappa and IgG1 constant regions. A humanised Mab was obtd. that	
CC	retained the B-lymphoma and leukaemia cell targeting and	
CC	internalisation characteristics of the parental LL2 Mab, and which	
CC	exhibited a lowered HAMA reaction. It can be linked to e.g. a	
CC	cytostatic agent for therapeutic appln.	
XX		
SQ	Sequence 113 AA:	
Query Match	100.0%; Score 594; DB 17; Length 113;	
Best Local Similarity	100.0%; Pred. No. 3.3e-41;	
Matches 113; Conservative	0; Mismatches 0; Indels 0; Gaps 0	
OY	1 DIQLTQSSSLAVSAGENVMTWCKSSQSVLYSANHKNTLAWYQQRPGSPKILLIYMASTR 60	
Db	1 DIQLTQSSSLAVSAGENVMTWCKSSQSVLYSANHKNTLAWYQQRPGSPKILLIYMASTR 60	
OY	61 ESGVDRRTGSGSGTDFLTISRVOEDLAIYYCHQYLSWMFGGCTLEIKR 113	
Db	61 ESGVDRRTGSGSGTDFLTISRVOEDLAIYYCHQYLSWMFGGCTLEIKR 113	
RESULT 2		
AAW27695		
ID	AAW27695 standard; Protein: 113 AA.	
XX		
AC	AAW27695;	
XX		
DT	14-APR-1998 (first entry)	
XX		
DE	Variable kappa chain of Mab LL2.	
XX		
KW	Variable kappa chain; B cell; monoclonal antibody; Mab; LL2;	
KW	B cell lymphoma; lymphocytic leukaemia cell; murine;	
KW	diagnosis; treatment; B cell malignancy; non-Hodgkins lymphoma;	
KW	chronic lymphocytic leukaemia.	
XX		
OS	Mus sp.	
OS	Synthetic.	
XX		
Key	Location/Qualifiers	
FT	18..20	
FT	/note= "potential N-linked glycosylation site"	
FT	24..40	
FT	/note= "complementarity determining region 1"	
FT	56..62	
FT	/note= "complementarity determining region 2"	
FT	95..102	
FT	/note= "complementarity determining region 3"	
XX		
PN	W09734632-A1.	
XX		
DD	25-SEP-1997.	

```

XX      19-MAR-1997;          97WO-US04196.
XX
XX      20-MAR-1996;          96US-0013709.
XX
XX      (IMMUNO) IMMUNOMEDICS INC.
XX
XX      Hansen H, Leung S, Ou Z;
XX
XX      WPI: 1997-476995/44.
XX      N-PDSB: AAT88128.
XX
XX      Monoclonal antibody engineered to contain glycosylation site - In
XX      non-Fc constant heavy or light chain region, useful to diagnose or
XX      treat B cell malignancies, e.g. non-Hodgkins lymphoma
XX
XX      Example 3; Fig 4A; 88bp; English.
XX
XX      The present sequence is the variable kappa chain of the
XX      B cell specific monoclonal antibody (MAb) IL2, which contains an
XX      engineered tri-peptide N-glycan acceptor sequence. IL2 is a highly
XX      specific anti-B cell lymphoma and anti-lymphocytic leukaemia cell
XX      murine MAb. The MAb can be used to diagnose or treat B
XX      cell malignancies, e.g. non-Hodgkins lymphoma or chronic
XX      lymphocytic leukaemia. The glycosylation site allows a label or
XX      therapeutic agent of increased size to be conjugated to the
XX      carbohydrate moiety, without affecting the MAB's binding affinity
XX      or specificity.
XX
XX      Sequence      113 AA;
XX
XX      Query Match      100.0%; Score 594; DB 18; Length 113;
XX      Best Local Similarity 100.0%; Pred. No. 3,36-41;
XX      Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
YY      1 DIOLTQSSSLAVSAGENVYMSCKSGSVLSANHKNTLAWYOQRPGOSPKLLIYWASNR 60
YY      1 DIOLTQSSSLAVSAGENVYMSCKSGSVLSANHKNTLAWYOQRPGOSPKLLIYWASNR 60
DB      1 DIOLTQSSSLAVSAGENVYMSCKSGSVLSANHKNTLAWYOQRPGOSPKLLIYWASTR 60
YY      61 ESGVDPDRFTGSGSGDTFLLTSRVQVEDLAIIYCHQYLSSWTFGGGTKLEIKR 113
YY      |||||||
YY      61 ESGVDPDRFTGSGSGDTFLLTSRVQVEDLAIIYCHQYLSSWTFGGGTKLEIKR 113
DB      61 ESGVDPDRFTGSGSGDTFLLTSRVQVEDLAIIYCHQYLSSWTFGGGTKLEIKR 113

RESULT 3
AAW90226
ID      AAW90226 standard; Protein: 263 AA.
XX
XX      AAW90226;
XX
XX      10-MAY-1999 (first entry)
XX
XX      Anti-B7.2 monospecific triabody Ig10.
XX
XX      B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;
XX      CD86; T cell activation; inhibitor; graft versus host disease;
XX      transplant rejection; allograft rejection; autoimmune disease;
XX      allergy; therapy; human; triabody; antibody; Ig10.
XX
XX      Chimeric - Mus sp.
XX      OS Chimeric - synthetic.
XX
XX      Location/Qualifiers
XX      FT Key 1..24
XX      FT Peptide /note= "pe1b signal peptide"
XX      FT Region 25..144
XX      FT Peptide /note= "anti B7.2 MAB VH region"
XX      FT Peptide 145..257
XX      FT /note= "anti B7.2 MAB VL region"
XX      FT Peptide 258..263
XX      /note= "His6 tag"

MO9858965-A2
```

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XX 30-DEC-1998.
XX 22-JUN-1998; 98WO-EP03791.
XX 20-JUN-1997; 97EP-0870092.
XX (INNO-) INNOGENETICS NV.
XX Bosman A, Buyse M, Lorre K, Sablon E;
XX WPI: 1999-105615/09.
XX N-PSDB: AAX01660.
XX
XX New molecules which bind B7.1 and B7.2 - useful to prevent and treat
XX immune diseases including allograft rejection
XX
XX Example 7.3; Fig 34; 182pp; English.
XX
XX This polypeptide comprises a 1G10 monospecific triabody composed
XX of the VH region of anti-B7.2 monoclonal antibody (Mab) 1G10
XX joined to the VL region of 1G10. A triabody is a mono- a bi- or
XX a trispecific molecule recognising simultaneously e.g. two B7.2
XX and one B7.1 molecules. It has a rigid structure that prevents
XX simultaneous binding to the 3 targets. Each antigen-binding site
XX is formed by pairing of one VH and one VL domain from the same or
XX from two different polypeptides. The invention relates to novel
XX molecules, including triabodies, which can cross-link and/or
XX cross-react with the costimulatory molecules B7.1 and B7.2 expressed
XX on professional antigen-presenting cells, leading to the inhibition
XX of antigen-specific T cell activation. Methods are provided for
XX the production of such B7-binding molecules, and for their use in
XX the treatment or prevention of diseases of the immune system, in
XX particular graft rejection, graft versus host disease, allergy and
XX autoimmune diseases (claimed).
XX
XX Sequence 263 AA:
XX
XX Query Match 93.6%; Score 556; DB 20; Length 263;
XX Best Local Similarity 92.0%; Pred. No. 9e-38;
XX Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1 DIQLTQSSSLAVSAGEVNTWMSCKSSQSVLYSANHKNTLAWYQOKPGQSPKILLYMASTR 60
XX ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX DB 145 DIQLTQSSSLAVSAGEVNTWMSCKSSQSVLYSANHKNTLAWYQOKPGQSPKILLYMASTR 204
XX
XX QY 61 ESGVPRFTGSGSGTDFLTITSRVQVEDLAIYCHQYLSWTFGGGTLEIKR 113
XX ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX DB 205 ESGVPRFTGSGSGTDFLTITSRVQVEDLAIYCHQYLSWTFGGGTLEIKR 257
XX
XX RESULT 4
XX AAW90228
XX ID AAW90228 standard; Protein: 268 AA.
XX
XX AC AAW90228;
XX
XX 10-MAY-1999 (first entry)
XX
XX DE Anti-B7.1/anti-B7.2 bispecific triabody II.
XX
XX XX B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;
XX KM CD86; T cell activation; inhibitor; graft versus host disease;
XX KM transplant rejection; allograft rejection; autoimmune disease;
XX KM allergy; therapy; human; triabody; antibody; B7-24; 1G10.
XX
XX OS Chimeric - Mus sp.
XX OS Chimeric - synthetic.
XX
XX Key Location/Qualifiers
XX FT 1..39
XX FT Peptide /note= "g3p signal peptide"
XX FT Region 40..155

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FT Peptide /note= "anti B7.1 Mab VH region"
FT 156..268
FT FT /note= "anti B7.2 Mab VL region"
XX
XX WO958965-A2.
XX 30-DEC-1998.
XX 22-JUN-1998; 98WO-EP03791.
XX 20-JUN-1997; 97EP-0870092.
XX (INNO-) INNOGENETICS NV.
XX Bosman A, Buyse M, Lorre K, Sablon E;
XX WPI: 1999-105615/09.
XX N-PSDB: AAX01662.
XX
XX New molecules which bind B7.1 and B7.2 - useful to prevent and treat
XX immune diseases including allograft rejection
XX
XX Example 7.3; Fig 38; 182pp; English.
XX
XX This polypeptide comprises a bispecific triabody composed of the VH
XX region of anti-B7.1 monoclonal antibody (Mab) B7-24 joined to the
XX VL region of of anti-B7.2 Mab 1G10. A triabody is a mono- a bi- or
XX a trispecific molecule recognising simultaneously e.g. two B7.2
XX and one B7.1 molecules. It has a rigid structure that prevents
XX simultaneous binding to the 3 targets. Each antigen-binding site
XX is formed by pairing of one VH and one VL domain from the same or
XX from two different polypeptides. The invention relates to novel
XX molecules, including triabodies, which can cross-link and/or
XX cross-react with the costimulatory molecules B7.1 and B7.2 expressed
XX on professional antigen-presenting cells, leading to the inhibition
XX of antigen-specific T cell activation. Methods are provided for
XX the production of such B7-binding molecules, and for their use in
XX the treatment or prevention of diseases of the immune system, in
XX particular graft rejection, graft versus host disease, allergy and
XX autoimmune diseases (claimed).
XX
XX Sequence 268 AA:
XX
XX Query Match 93.6%; Score 556; DB 20; Length 268;
XX Best Local Similarity 92.0%; Pred. No. 9.1e-38;
XX Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1 DIQLTQSSSLAVSAGEVNTWMSCKSSQSVLYSANHKNTLAWYQOKPGQSPKILLYMASTR 60
XX ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX DB 156 DIQLTQSSSLAVSAGEVNTWMSCKSSQSVLYSANHKNTLAWYQOKPGQSPKILLYMASTR 215
XX
XX QY 61 ESGVPRFTGSGSGTDFLTITSRVQVEDLAIYCHQYLSWTFGGGTLEIKR 113
XX ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX DB 216 ESGVPRFTGSGSGTDFLTITSRVQVEDLAIYCHQYLSWTFGGGTLEIKR 268
XX
XX RESULT 5
XX AAW90222
XX ID AAW90222 standard; Protein: 268 AA.
XX
XX AC AAW90222;
XX
XX 10-MAY-1999 (first entry)
XX
XX DE Anti-B7.2 monospecific diabody 1G-10.
XX
XX XX B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;
XX KM CD86; T cell activation; inhibitor; graft versus host disease;
XX KM transplant rejection; allograft rejection; autoimmune disease;
XX KM allergy; therapy; human; diabody; antibody; 1G-10.
XX
XX OS Chimeric - Mus sp.
XX OS Chimeric - synthetic.

```

```

XX Key Location/Qualifiers
FH Peptide 1..24
FT /note="pe1b signal peptide"
FT 25..144
FT Region /note="anti B7.2 MAb VH region"
FT Peptide /note="anti B7.2 MAb VH region"
FT 145..149
FT /note="G4S flexible linker"
FT 150..262
FT Region /note="anti B7.2 MAb VL region"
FT 263..268
FT Peptide /note="His6 tag"
XX
XX WO9858965-A2.
XX
XX 30-DEC-1998.
XX
XX 22-JUN-1998; 98WO-EP03791.
XX
XX 20-JUN-1997; 97EP-0870092.
XX
XX (INNO-) INNOGENETICS NV.
XX
XX Bosman A, Buyse M, Lorre K, Sablon E;
XX
XX WPI; 1999-105615/09.
XX
XX N-PSDB; AAX01656.
XX
XX New molecules which bind B7.1 and B7.2 - useful to prevent and treat
XX immune diseases including allograft rejection
XX
XX Example 7.2; Fig 26; 182pp; English.
XX
XX This polypeptide comprises a 16-10 monospecific diabody composed
XX of the VH region of anti-B7.2 monoclonal antibody (MAb) 16-10
XX joined via a short, flexible linker to the VL region of 16-10.
XX Mono- or bispecific bivalent molecules are generated by shortening
XX the flexible linker sequence between the VH and VL of the anti-B7.1
XX scFv B7-24, the anti-B7.2 scFv 1610 and the scFv molecule with
XX dual specificity for B7.1 and B7.2 (B7.12) to 5-10 residues, and
XX for bispecific molecules by cross-pairing the VH and VL domains
XX from the 2 scFvs with different antigen recognition (B7.1/B7.2 and
XX B7.12/B7.12). The invention relates to novel molecules, including
XX diabodies, which can cross-link and/or cross-react with the
XX costimulatory molecules B7.1 and B7.2 expressed on professional
XX antigen-presenting cells, leading to the inhibition of antigen-
XX specific T cell activation. Methods are provided for the
XX production of such B7-binding molecules, and for their use in the
XX treatment or prevention of diseases of the immune system, in
XX particular graft rejection, graft versus host disease, allergy and
XX autoimmune diseases (claimed).
XX
XX Sequence 268 AA:
XX
XX Query Match 93.6%; Score 556; DB 20; Length 268;
XX Best Local Similarity 92.0%; Pred. No. 9.1e-38;
XX Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1 DIQLTQSPSSSLAVSAGEENTMCKSSQSVLYSANHKNYLAWYQKRGSPKLLIYWASTR 60
XX ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX DIELTQSPSSSLAVSAGEENTMCKSSQSVLYSANHKNYLAWYQKRGSPKLLIYWASTR 209
XX
XX QY 61 ESGVPRFTGSGSGTDETLISNVQVEDAIYYCHQYLSLWTFGGTKLEIKR 113
XX ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX ESGVPRFTGSGSGTDETLISNVQVEDAIYYCHQYLSLWTFGGTKLEIKR 262
XX
XX DB 210 ESGVPRFTGSGSGTDETLISNVQVEDAIYYCHQYLSLWTFGGTKLEIKR 262
XX
XX RESULT 6
XX ID AAW90224 standard; Protein: 273 AA.
XX AC AAW90224;
XX XX

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DT 10-MAY-1999 (first entry)
XX
XX Anti-B7.1/anti-B7.2 bispecific diabody II.
XX
XX B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;
XX CD86; T cell activation; inhibitor; graft versus host disease;
XX transplant rejection; allograft rejection; autoimmune disease;
XX allergy; therapy; human; diabody; antibody; B7-24; 1610.
XX
XX Chimeric - Mus sp.
XX
XX Chimeric - synthetic.
XX
XX
XX Key Location/Qualifiers
FH Peptide 1..39
FT /note="g3p signal peptide"
FT 40..155
FT Region /note="anti B7.1 MAb VH region"
FT Peptide /note="anti B7.1 MAb VH region"
FT 156..160
FT /note="G4S flexible linker"
FT 161..273
FT Region /note="anti B7.2 MAb VL region"
FT MISC-difference 21
FT /note="encoded by TCA"
XX
XX WO9858965-A2.
XX
XX 30-DEC-1998.
XX
XX 22-JUN-1998; 98WO-EP03791.
XX
XX 20-JUN-1997; 97EP-0870092.
XX
XX (INNO-) INNOGENETICS NV.
XX
XX Bosman A, Buyse M, Lorre K, Sablon E;
XX
XX WPI; 1999-105615/09.
XX
XX N-PSDB; AAX01658.
XX
XX New molecules which bind B7.1 and B7.2 - useful to prevent and treat
XX immune diseases including allograft rejection
XX
XX Example 7.2; Fig 30; 182pp; English.
XX
XX This polypeptide comprises a bispecific diabody composed of the VH
XX region of anti-B7.1 monoclonal antibody (MAb) B7-24 joined via a
XX short, flexible linker to the VL region of anti-B7.2 MAb 1610.
XX Mono- or bispecific bivalent molecules are generated by shortening
XX the flexible linker sequence between the VH and VL of the anti-B7.1
XX scFv B7-24, the anti-B7.2 scFv 1610 and the scFv molecule with
XX dual specificity for B7.1 and B7.2 (B7.12) to 5-10 residues, and
XX for bispecific molecules by cross-pairing the VH and VL domains
XX from the 2 scFvs with different antigen recognition (B7.1/B7.2 and
XX B7.12/B7.12). The invention relates to novel molecules, including
XX diabodies, which can cross-link and/or cross-react with the
XX costimulatory molecules B7.1 and B7.2 expressed on professional
XX antigen-presenting cells, leading to the inhibition of antigen-
XX specific T cell activation. Methods are provided for the
XX production of such B7-binding molecules, and for their use in the
XX treatment or prevention of diseases of the immune system, in
XX particular graft rejection, graft versus host disease, allergy and
XX autoimmune diseases (claimed).
XX
XX Sequence 273 AA:
XX
XX Query Match 93.6%; Score 556; DB 20; Length 273;
XX Best Local Similarity 92.0%; Pred. No. 9.3e-38;
XX Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1 DIQLTQSPSSSLAVSAGEENTMCKSSQSVLYSANHKNYLAWYQKRGSPKLLIYWASTR 60
XX ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX DIELTQSPSSSLAVSAGEENTMCKSSQSVLYSANHKNYLAWYQKRGSPKLLIYWASTR 220
XX
XX DB 161 DIELTQSPSSSLAVSAGEENTMCKSSQSVLYSANHKNYLAWYQKRGSPKLLIYWASTR 220
XX
XX

```

[illegible]

Query Match	93.6%	Score 556	DB 20	Length 556
Best Local Similarity	92.0%	Pred. 1.8e-37		
Matches 104	Conservative 5	Mismatches 4	Indels 0	Gaps 0
QY	1	DIGLTQSPSSSLAVSGAEVMTWSSCSRSSQSVLYISAHNKNTLAMYQKRPQSPKLLIYMASTR	60	
Db	136	DIELTQSPSSSLAVSGAEVMTWCKSSQSVLYSSNOKNTLAMYQKRPQSPKLLIYMASTR	195	
OY	61	ESGVDRRTGSGSGDTFTLTISRVQVEDLAYIYCHQYLSMTFFGGGTLEIKR	113	
Db	196	ESGVDRRTGSGSGDTFTLTISRVQVEDLAYIYCHQYLSMTFFGGGTLEIKR	248	
RESULT 8				
AAW90217				
ID	AAW90217	standard	Protein: 580 AA.	
XX	AAW90217			
AC				
XX				
DT	10-MAY-1999	(first entry)		
XX				
DE	Bispecific tetravalent antibody B1TAB7-24-IG10H6.			
KW	B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86; T cell activation; inhibitor; graft versus host disease; transplant rejection; allograft rejection; autoimmune disease; allergy; therapy; human; bispecific tetravalent antibody; B1TAB7; B1TAB7-24-IG10H6.			
XX				
OS	Chimeric - Mus sp.			
OS	Chimeric - Homo sapiens.			
OS	Chimeric - synthetic.			
XX				
FH	Key	Location/Qualifiers		
FT	Peptide	1..24		
FT		/note= "pe1b signal peptide"		
FT	Region	25..138		
FT		/note= "VH region anti B7.1 MAb"		
FT	Peptide	139..153		
FT		/note= "(G4S3) flexible linker"		
FT	Region	154..262		
FT		/note= "VL region anti B7.1 MAb"		
FT	Region	263..273		
FT		/note= "human IgG3 hinge region"		
FT	Domain	274..308		
FT		/note= "helix-turn-helix dimerisation domain"		
FT	Domain	309..319		
FT		/note= "human IgG3 hinge domain"		
FT	Region	320..446		
FT		/note= "VH region anti B7.2 MAb"		
FT	Peptide	447..461		
FT		/note= "(G4S3)flexible linker"		
FT	Region	462..574		
FT		/note= "VL region anti B7.2 MAb"		
FT	Peptide	575..580		
FT		/note= "His6 tag"		
FT	Misc-difference	261		
FT		/note= "encoded by C1G"		
FT	Misc-difference	322..327		

/note- "codons for these amino acids are not present in the DNA sequence for B71AB7-24-1G1-H6 provided in the specification"

MO9858965-AZ.
30-DEC-1998.
22-JUN-1998: 98WO-EP03791.
20-JUN-1997: 97EP-0870092.
(INNO-) INNOGENETICS NV.
Bosman A, Buyse M, Lorre K, Sablon E;
WPI: 1999-105615/09.
N-PSDB; AAX01651.
New molecules which bind B7.1 and B7.2 - useful to prevent and treat immune diseases including allograft rejection
Example 7.1; Fig 16; 182pp; English.

This polypeptide comprises the bispecific tetravalent antibody B71AB7-24-1G1H6. The molecule consists of 4 scfvs, i.e. 2 anti B7.1 scfvs and 2 anti B7.2 scfvs (tetravalency). One single B71AB is a homodimer of 2 identical molecules, each containing both an anti B7.1 and anti B7.2 scfv (bispecificity). An anti-B7.1 and an anti-B7.2 scfv are linked using a dimerisation domain (see AAM90219), which drives the homodimerisation of the molecule. DNA (see AAX01651) encoding the B71AB has been constructed to allow expression of the B71AB in transformed E. coli cells. The B71AB cross-links, and/or cross-reacts, with the costimulatory molecules B7.1 and B7.2 that are expressed on the membrane of professional antigen-presenting cells, leading to the inhibition of antigen-specific T cell activation. The invention relates to such B7-binding molecules, methods for their production, and their use for treating or preventing diseases of the immune system, in particular graft rejection, graft versus host disease, allergy and autoimmune diseases (claimed).

Sequence 580 AA:

Query Match 93.6%; Score 556; DB 20; Length 580;
Best Local Similarity 92.0%; Pred. No. 1.9e-37;
Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 1 DIOLTPSSSLAVSAGEVTMTSCSSQSVLYSANHNKNTLAWYQOKRGOSPKLLIYWA5TR 60
DB 462 DIELTQSPSSSLAVSAGEVTMTCKSSQSVLYSNQKNYLAWYQOKRGOSPKLLIYWA5TR 521

OY 61 ESGVPDRFTGSGSGTDFTLTISRVQEDAIYYCHQYLSWTFGGGCKLEIKR 113
DB 522 ESGVPDRFTGSGSGTDFTLTISRVQEDAIYYCHQYLSWTFGGGCKLEIKR 574

RESULT 9

AAR54933
ID AAR54933 standard; peptide; 112 AA.

AC AAR54933;

DT 25-MAR-2003 (updated)
DT 19-OCT-1994 (first entry)

DE MAb 022 VK chain.

KW Fc receptor; Fc; humanized antibody; hAb; IgG; cancer; allergy;
KW autoimmune diseases; heteroantibody; bifunctional antibody;
KW immunotoxin; CDR; complementarity determining region; VH;
KW heavy chain variable region; VK; kappa chain variable region;

KW mononuclear phagocyte; PCR; polymerase chain reaction; primer;
KW site-directed mutagenesis; monoclonal antibody; MAb.
OS Mus sp.

PN MO9410332-A1.

PD 11-MAY-1994.

PF 04-NOV-1993; 93WO-US10384.

PR 04-NOV-1992; 92GB-0023377.

PA (MEDA-) MEDAREX INC.

PI Carr FJ, Harris WJ, Tempest PR;

DR WPI: 1994-167486/20.

PT New humanised antibodies to Fc receptors - used for diagnosis or
PT for treatment of e.g. cancer, allergies and infectious and
PT auto-immune diseases

PS Disclosure; Page 23; 36pp; English.

XX Humanized antibodies (hAbs) for IgG Fc receptors on human phagocytes
XX comprise the CDR of mouse monoclonal antibody 22 (from hybridoma
CC 022WCL-1), VH chains from human IgG NEMM or KOL, and VK chains from
CC Ig REI. Sequences are provided for mouse 022 VH (AAR54931),
CC humanized NEMM-based VH (022 NMVH, AAR54929), humanized KOL-
CC based VH (022 KLVH, AAR54930), mouse 022 VK (AAR54933) and humanized
CC REI-based VK (022 HVVK, AAR54932). During hAb production, VH and VK
CC cDNAs were PCR amplified using primers given in AAO65378-87.
CC Mutagenesis of clone M13VHPCR2 KOL VH (L71R) was performed using
CC oligos AAO65388-89. The hAbs can be used in heteroantibody,
CC bifunctional antibody and immunotoxin production.
CC (Updated on 25-MAR-2003 to correct PN field.)

Sequence 112 AA:

Query Match 92.1%; Score 547; DB 15; Length 112;
Best Local Similarity 92.0%; Pred. No. 2.2e-37;
Matches 103; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 1 DIOLTPSSSLAVSAGEVTMTSCSSQSVLYSANHNKNTLAWYQOKRGOSPKLLIYWA5TR 60
DB 1 NIYMTQSPSSSLAVSAGEVTMTSCSSQSVLYSNQKNYLAWYQOKRGOSPKLLIYWA5TR 60

OY 61 ESGVPDRFTGSGSGTDFTLTISRVQEDAIYYCHQYLSWTFGGGCKLEIK 112
DB 61 ESGVPDRFTGSGSGTDFTLTISRVQEDAIYYCHQYLSWTFGGGCKLEIK 112

RESULT 10

AAE29266
ID AAE29266 standard; Protein; 112 AA.

AC AAE29266;

DT 27-JAN-2003 (first entry)

DE S. aureus ClfA specific monoclonal antibody 12-9VLA-1 protein.

XX Clumping factor A; ClfA; fibrinogen; fibrin; Clf40; Clf33; N3 protein;
KW immunological; staphylococcal infection; impetigo; pneumonia; furuncle;
KW septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.

OS Staphylococcus aureus.

XX Key Location/Qualifiers

FT Region 24..40 /note- "CDR1"

FT Region 56..62

FT Region /note="CDR2"
FT 95..102
FT /note="CDR3"
XX
PN MO200272600-A2.
XX
PD 19-SEP-2002.
XX
XX 28-JAN-2002; 2002MO-US02296.
XX
PF 26-JAN-2001; 2001US-264072P.
PR 12-MAR-2001; 2001US-274611P.
PR 18-JUN-2001; 2001US-298413P.
PR 30-JUL-2001; 2001US-308116P.
XX
XX (INHIT-) INHIBITEX INC.
XX
PI Patil JM, Hutchins JT, Domanski P, Patel P, Hall A;
XX
DR WPI; 2002-759834/82.
DR N-PSDB; AAD46865.
XX
XX New anti-clumping factor A (ClfA) monoclonal antibody, useful for
PT treating or preventing Staphylococcus aureus infection e.g. wound
PT infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis
PT in a human or animal
XX
XX Claim 11; Page 35; 80pp; English.
XX
XX The invention relates to monoclonal antibody which binds the clumping
CC factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA
CC monoclonal antibody is useful for treating or preventing S. aureus
CC infection in a human or animal, and for inhibiting the binding of
CC staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
CC S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3
CC protein is useful for inducing an immunological response in a human or
CC animal. These staphylococcal infections include wound infections, sepsis,
CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
CC present sequence is Staphylococcus aureus ClfA specific monoclonal
CC antibody 12-9VLA-1 (variable light sequence) protein.
XX
SQ Sequence 112 AA;
XX
XX Query Match 90.9%; Score 540; DB 23; Length 112;
XX Best Local Similarity 91.1%; Pred. No. 8e-37;
XX Matches 102; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
XX
OY 1 DIQLTQSPSSLAIVSAGEKNTVMSCKSSQSVLYSANHKNYLAWYQOKPGOSPRLTIYMASTR 60
DB 1 NIMMTQSPSSLAIVSAGEKNTVMSCKSSQSVLYSANHKNYLAWYQOKPGOSPRLTIYMASTR 60
OY 61 ESGVPRFTGSGSGDTFTLTISRQVEDLAIIYCHQYLSWTFEGGTRLEIK 112
DB 61 ESGVPRFTGSGSGDTFTLTISRQVEDLAIIYCHQYLSWTFEGGTRLEIK 112
XX
XX RESULT 11
XX AAE29264
XX ID AAE29264 standard; Protein; 112 AA.
XX
XX AAE29264;
XX
XX 27-JAN-2003 (first entry)
XX
XX S. aureus ClfA specific monoclonal antibody 13-2VLA-1 protein.
XX
XX Clumping factor A; ClfA; fibrinogen; fibrin; Clf40; Clf33; N3 protein;
KW immunological; staphylococcal infection; impetigo; pneumonia; furuncle;
KW septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.
XX
XX Staphylococcus aureus.
XX
XX Key Location/Qualifiers
FH

FT Region 24..40
FT /note="CDR1"
FT 56..62
FT /note="CDR2"
FT 95..102
FT /note="CDR3"
XX
PN MO200272600-A2.
XX
PD 19-SEP-2002.
XX
XX 28-JAN-2002; 2002MO-US02296.
XX
PF 26-JAN-2001; 2001US-264072P.
PR 12-MAR-2001; 2001US-274611P.
PR 18-JUN-2001; 2001US-298413P.
PR 30-JUL-2001; 2001US-308116P.
XX
XX (INHIT-) INHIBITEX INC.
XX
PI Patil JM, Hutchins JT, Domanski P, Patel P, Hall A;
XX
DR WPI; 2002-759834/82.
DR N-PSDB; AAD46863.
XX
XX New anti-clumping factor A (ClfA) monoclonal antibody, useful for
PT treating or preventing Staphylococcus aureus infection e.g. wound
PT infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis
PT in a human or animal
XX
XX Claim 11; Page 34; 80pp; English.
XX
XX The invention relates to monoclonal antibody which binds the clumping
CC factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA
CC monoclonal antibody is useful for treating or preventing S. aureus
CC infection in a human or animal, and for inhibiting the binding of
CC staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
CC S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3
CC protein is useful for inducing an immunological response in a human or
CC animal. These staphylococcal infections include wound infections, sepsis,
CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
CC present sequence is Staphylococcus aureus ClfA specific monoclonal
CC antibody 13-2VLA-1 (variable light sequence) protein.
XX
SQ Sequence 112 AA;
XX
XX Query Match 89.7%; Score 533; DB 23; Length 112;
XX Best Local Similarity 90.2%; Pred. No. 3e-36;
XX Matches 101; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
XX
OY 1 DIQLTQSPSSLAIVSAGEKNTVMSCKSSQSVLYSANHKNYLAWYQOKPGOSPRLTIYMASTR 60
DB 1 NIMMTQSPSSLAIVSAGEKNTVMSCKSSQSVLYSANHKNYLAWYQOKPGOSPRLTIYMASTR 60
OY 61 ESGVPRFTGSGSGDTFTLTISRQVEDLAIIYCHQYLSWTFEGGTRLEIK 112
DB 61 ESGVPRFTGSGSGDTFTLTISRQVEDLAIIYCHQYLSWTFEGGTRLEIK 112
XX
XX RESULT 12
XX AAE29268
XX ID AAE29268 standard; Protein; 112 AA.
XX
XX AAE29268;
XX
XX 27-JAN-2003 (first entry)
XX
XX S. aureus ClfA specific monoclonal antibody 35-220VLD-4 protein.
XX
XX Clumping factor A; ClfA; fibrinogen; fibrin; Clf40; Clf33; N3 protein;
KW immunological; staphylococcal infection; impetigo; pneumonia; furuncle;
KW septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.
XX

OS	Staphylococcus aureus.
XX	Key
XX	Location/Qualifiers
XX	Region
XX	24..40
XX	/note= "CDR1"
XX	Region
XX	56..62
XX	/note= "CDR2"
XX	95..102
XX	/note= "CDR3"
XX	WO200272600-A2.
XX	19-SEP-2002.
XX	28-JAN-2002; 2002MO-US02296.
XX	26-JAN-2001; 2001US-264072P.
XX	12-MAR-2001; 2001US-274611P.
XX	18-JUN-2001; 2001US-298413P.
XX	30-JUL-2001; 2001US-308116P.
XX	(INH1-) INHIBITEX INC.
XX	Patti JM, Hutchins JT, Domanski P, Patel P, Hall A;
XX	WPI; 2002-759634/82.
XX	N-PSDB; AAD46867.
XX	New anti-clumping factor A (ClfA) monoclonal antibody, useful for
XX	treating or preventing Staphylococcus aureus infection e.g. wound
XX	infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis
XX	in a human or animal
XX	Clam 11; Page 37; 80pp; English.
XX	The invention relates to monoclonal antibody which binds the clumping
XX	factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA
XX	monoclonal antibody is useful for treating or preventing S. aureus
XX	infection in a human or animal, and for inhibiting the binding of
XX	Staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
XX	S. aureus ClfA0 protein, S. aureus ClfA3 protein, or the S. aureus N3
XX	protein is useful for inducing an immunological response in a human or
XX	animal. These staphylococcal infections include wound infections, sepsis,
XX	impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
XX	present sequence is Staphylococcus aureus ClfA specific monoclonal
XX	antibody 35-220VND-4 (variable light sequence) protein.
XX	Sequence 112 AA:
XX	Query Match 89.4%; Score 531; DB 23; Length 112;
XX	Best Local Similarity 89.3%; Pred. No. 4.3e-36;
XX	Matches 100; Conservative 6; Mismatches 6; Indels 0; Gaps 0
XX	1 DIQLTQSFSSILAVSAGENVNTSCSSQSGVLSANHKNTLAWYQKPGSPKLLIYASTR 60
XX	1 NIMMTQSPSSILAVSAGEKVTMSCRSSQSVLSSNQKNLTAWYQKPGSPFTLLIYASTR 60
XX	61 ESGVDPDRFTSGSGGDFLTLLTSRNOVELATYYCHQYLSSTFFGGGTLEIK 112
XX	61 ESGVDPDRFTSGSGGDFLTLLTSRNOVELATYYCHQYLSSTFFGGGTLEIK 112
XX	RESULT 13
XX	AAR92217
XX	AAR92217 standard; Protein; 113 AA.
XX	AAR92217;
XX	28-MAY-1996 (first entry)
XX	Humanised LL2 Mab VK region.
XX	Humanised antibody; monoclonal antibody; Mab; LL2; B-cell lymphoma;

```

KW leukemia: therapy; diagnosis; complementarity determining region;
KM CDR; antibody engineering.
XX
OS Synthetic.
FH Key Location/Qualifiers
FT Region 24..40 /label= CDRI
FT Region 56..62 /label= CDR2
FT Region 95..103 /label= CDR3
FT
FT
FN MO9604925-A1.
PD
XX 22-FEB-1996.
XX
XX 11-AUG-1995; 95WO-USO9641.
XX PF
XX 12-AUG-1994; 94US-0289576.
XX PR
XX (IMMU-) IMMUNOMEDICS INC.
PA
XX Hansen H, Leung S;
XX PI
XX WIPI: 1996-139454/14.
XX DR
XX N-PSDB; AAT15803.
XX
XX Chimeric and humanised IL2 antibodies - used to produce conjugates
PT for the therapy and diagnosis of B-cell lymphoma(s) and
PT leukaemia(s).
XX
XX Claim 5; Page 38; 70pp; English.
XX PS
XX
CC The complementarity determining regions (CDRs) of mouse monoclonal
CC antibody (Mab) IL2 VK (AAR92215) and VH (AAR92216) regions were
CC recombinantly linked to the framework sequences of human VK and VH
CC regions, respectively, to give humanised IL2 VK (AAR92217) and VH
CC (AAR92218). These were subsequently linked, respectively, to human
CC kappa and IgG1 constant regions. A humanised Mab was obtd. that
CC retained the B-lymphoma and leukemia cell targeting and
CC internalisation characteristics of the parental IL2 Mab, and which
CC exhibited a lowered HAMA reaction. It can be linked to e.g. a
CC cytostatic agent for therapeutic appln.
XX
XX Sequence 113 AA;
SQ
Query Match 89.4%; Score 531; DB 17; Length 113;
Best Local Similarity 86.7%; Pred. No. 4,4e-36;
Matches 98; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
QY
1 DIQTGTSPSSLIASAGENVMTSCSSQSIVLYSANHKNYLAMYOOKPGOSPRLIYWASTR 60
Db 1 DIOITQSPSSISASVGDRTWMTSCSSQSIVLYSANHKNYLAMYOOKPKAKRLIIYWASTR 60
QY
61 ESGVPDDEFTSGSGTDFTLTIIRSYQVDALYYCHOVLLSWTGCGKLEIKR 113
Db 61 ESGVPSRFSGSGSTDFTLTIISLPADIAFYCHOLVLSWTGGKLEIKR 113
RESULT 14
ABG31024
ID ABG31024 standard; Protein; 272 AA.
XX
XX ABG31024;
XX
XX 05-NOV-2002 (first entry)
XX
XX Synthetic mouse fusion protein.
XX
XX Immunosuppressive; antirheumatic; antithyroid; antididiabetic; mouse;
KM neuroprotective; gene therapy; single chain antibody; variable fragment;
KW scFv; binding domain-immunoglobulin fusion protein; B-cell disorder;

```


KW malignant condition; rheumatoid arthritis; myasthenia gravis; psoriasis;
KW Grave's disease; Hashimoto's thyroiditis; type I diabetes mellitus;
KW multiple sclerosis; systemic lupus erythematosus; Sjogren's syndrome;
KW immune thrombocytopenic purpura; scleroderma; cancer; Chron's disease;
KW ulcerative colitis; inflammatory bowel disease; immunological effector;
KW cell mediated cytotoxicity; complement dependent cytotoxicity;
KW complement fixation; mouse.
XX Mus musculus.
OS Synthetic.
XX WO200256910-A1.
XX 25-JUL-2002.
XX 17-JAN-2002; 2002WO-US01487.
XX 17-JAN-2001; 2001US-0765208.
XX 17-JAN-2001; 2001US-0765208.
XX (GENE-) GENE-CRAFT INC.
XX Ledbetter JA, Hayden-Ledbetter M;
XX WPI: 2002-599691/64.
XX N-PSDB: ABR89856.
XX New human binding domain-immunoglobulin fusion protein useful for
XX treating a subject having or suspected of having a B-cell disorder or
XX malignant condition e.g. rheumatoid arthritis
XX Disclosure: Page 119; 136pp; English.
XX
XX The invention describes a binding domain-immunoglobulin fusion protein
XX that is capable of at least one immunological activity, comprising a
XX binding domain polypeptide fused to an immunoglobulin hinge region
XX polypeptide capable of specifically binding to an antigen, or an
XX immunoglobulin heavy chain CH2 or CH3 constant region polypeptide fused
XX to the hinge region polypeptide or to the CH2 constant region
XX polypeptide. The fusion protein is useful for treating a subject having
XX or suspected of having a B-cell disorder or malignant condition e.g.
XX rheumatoid arthritis, myasthenia gravis, Grave's disease, Hashimoto's
XX thyroiditis, type I diabetes mellitus, multiple sclerosis, systemic lupus
XX erythematosus, Sjogren's syndrome, immune thrombocytopenic purpura,
XX psoriasis, scleroderma, cancer and inflammatory bowel disease such as
XX Chron's disease and ulcerative colitis. The fusion protein retains the
XX ability to participate in well known immunological effector activities
XX including antibody dependent cell mediated cytotoxicity and/or complement
XX fixation in complement dependent cytotoxicity, despite having structures
XX that would not be expected to be capable of promoting the effector
XX activities. It can be produced in substantial quantities that are
XX typically greater than those routinely attained with single-chain
XX antibody constructs. This is the amino acid sequence of a synthetic
XX mouse immunoglobulin fusion protein.
XX
XX Sequence 272 AA;
SQ
Query Match 89.2%; Score 530; DB 23; Length 272;
Best Local Similarity 87.5%; Pred. No. 1.2e-35;
Matches 98; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLAIVSAGENVMTSKSSQSVLYSANHKNTLAWYQKPGSPKLLIYMASTR 60
DB 21 NIMTQSPSSLAIVSAGENVMTSKSSQSVLYSANHKNTLAWYQKPGSPKLLIYMASTR 80
QY 61 ESGVPDRFTGSGSGTDFLTITISRVQVEDLAIYCHQYLSWTFFGGGTLEIK 112
DB 81 ESGVPDRFTGSGSGTDFLTITISRVQVEDLAIYCHQYLSWTFFGGGTLEIK 132
RESULT 15
AAE29270
ID AAE29270 standard; Protein: 112 AA.
XX

AC AAE29270;
XX 27-JAN-2003 (first entry)
XX
XX S. aureus ClfA specific monoclonal antibody 12-9VL-Hu protein.
XX
XX Clumping factor A: ClfA; fibrinogen; fibrin; Clf40; Clf33; N3 protein;
XX immunological; staphylococcal infection; impetigo; pneumonia; furuncle;
XX septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.
XX
XX Staphylococcus aureus.
XX
XX Key Location/Qualifiers
XX Region 24..40
XX /note= "CDR1"
XX Region 56..62
XX /note= "CDR2"
XX Region 95..102
XX /note= "CDR3"
XX
XX WO200272600-A2.
XX 19-SEP-2002.
XX 28-JAN-2002; 2002WO-US02296.
XX
XX 26-JAN-2001; 2001US-264072P.
XX 12-MAR-2001; 2001US-274611P.
XX 18-JUN-2001; 2001US-298413P.
XX 30-JUL-2001; 2001US-308116P.
XX
XX (INH1-) INHIBITEX INC.
XX
XX Patti JM, Hutchins JT, Domanski P, Patel P, Hall A;
XX WPI: 2002-759834/82.
XX N-PSDB: AAD46869.
XX
XX New anti-clumping factor A (ClfA) monoclonal antibody, useful for
XX treating or preventing Staphylococcus aureus infection e.g. wound
XX infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis
XX in a human or animal
XX
XX Claim 11; Page 42; 80pp; English.
XX
XX The invention relates to monoclonal antibody which binds the clumping
XX factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA
XX monoclonal antibody is useful for treating or preventing S. aureus
XX infection in a human or animal, and for inhibiting the binding of
XX staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
XX S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3
XX protein is useful for inducing an immunological response in a human or
XX animal. These staphylococcal infections include wound infections, sepsis,
XX impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
XX present sequence is Staphylococcus aureus ClfA specific monoclonal
XX antibody 12-9VL-Hu (humanised variable light sequence) protein.
XX
XX Sequence 112 AA;
SQ
Query Match 88.7%; Score 527; DB 23; Length 112;
Best Local Similarity 88.4%; Pred. No. 9.2e-36;
Matches 99; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLAIVSAGENVMTSKSSQSVLYSANHKNTLAWYQKPGSPKLLIYMASTR 60
DB 1 DIWMTQSPDLSLAIVSAGENVMTSKSSQSVLYSANHKNTLAWYQKPGSPKLLIYMASTR 60
QY 61 ESGVPDRFTGSGSGTDFLTITISRVQVEDLAIYCHQYLSWTFFGGGTLEIK 112
DB 61 ESGVPDRFTGSGSGTDFLTITISRVQVEDLAIYCHQYLSWTFFGGGTLEIK 112
Search completed: October 7, 2003, 19:13:51

Wed Oct 8 09:40:34 2003

us-09-988-013a-2.rag

Page 10

Job time : 144.224 secs

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OM protein - protein search, using sw model

Run on: October 7, 2003, 19:07:41 ; Search time 58.4483 Seconds

(without alignments)
305.878 Million cell updates/sec

Title: US-09-988-013A-2

Perfect score: 594
Sequence: 1 DIQLOSPSSSLAVSAGENVW.....CHQYLSWTFGGTKLEIKR 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubppa/PCY_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubppa/PCYUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubppa/US09A_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	594	100.0	113	10	US-09-741-843-2
2	594	100.0	113	11	US-09-894-839-2
3	594	100.0	113	11	US-09-988-013A-2
4	547	92.1	112	12	US-10-229-335-28
5	540	90.9	112	15	US-10-229-335-28
6	533	89.7	112	15	US-10-056-052-10
7	531	89.4	112	15	US-10-056-052-14
8	530	89.2	272	12	US-10-053-530-14
9	527	89.2	272	15	US-10-207-655-14
10	527	88.7	112	15	US-10-056-052-18
11	525	88.4	113	10	US-09-741-843-6
12	525	88.4	113	11	US-09-894-839-6
13	525	88.4	113	11	US-09-988-013A-6
14	504	84.8	130	14	US-10-146-305-7
15	497	83.7	112	12	US-10-229-335-4

16	496	83.5	113	11	US-09-894-839-20	Sequence 20, App1
17	490.5	82.6	220	10	US-09-995-693-1	Sequence 1, App1
18	490.5	82.6	220	15	US-10-232-408-1	Sequence 1, App1
19	484	81.5	132	10	US-09-249-011A-4	Sequence 4, App1
20	479	80.6	141	12	US-10-390-986-16	Sequence 16, App1
21	478.5	80.6	113	12	US-10-160-506-71	Sequence 71, App1
22	478.5	80.6	113	12	US-10-160-506-91	Sequence 91, App1
23	474.5	79.9	113	12	US-09-215-163-42	Sequence 42, App1
24	473.5	79.7	155	12	US-10-345-618-11	Sequence 11, App1
25	473.5	79.7	142	12	US-10-345-618-6	Sequence 6, App1
26	473.5	79.7	495	12	US-10-345-618-4	Sequence 4, App1
27	471.5	79.4	134	12	US-10-255-478-58	Sequence 58, App1
28	469.5	79.0	114	10	US-09-274-163E-2	Sequence 2, App1
29	469.5	79.0	114	10	US-09-274-163E-16	Sequence 16, App1
30	468.5	78.9	113	10	US-09-274-163E-16	Sequence 16, App1
31	468.5	78.9	114	10	US-09-274-163E-4	Sequence 4, App1
32	468.5	78.9	284	12	US-10-255-478-70	Sequence 70, App1
33	467.5	78.7	113	10	US-09-956-206A-80	Sequence 80, App1
34	467.5	78.7	113	12	US-10-255-478-73	Sequence 73, App1
35	467.5	78.7	240	9	US-09-799-514-8	Sequence 8, App1
36	466.5	78.5	114	9	US-09-810-502-38	Sequence 38, App1
37	466.5	78.5	220	12	US-10-159-006-17	Sequence 17, App1
38	466.5	78.5	240	12	US-10-159-006-28	Sequence 28, App1
39	466.5	78.5	274	12	US-10-255-478-66	Sequence 66, App1
40	463.5	78.0	115	10	US-09-998-831-9	Sequence 9, App1
41	463.5	78.0	115	12	US-10-373-561-9	Sequence 9, App1
42	463.5	77.9	113	10	US-09-999-025-7	Sequence 7, App1
43	463.5	77.9	113	10	US-09-999-025-13	Sequence 13, App1
44	463.5	77.9	113	10	US-09-999-040-7	Sequence 7, App1
45	462.5	77.9	113	10	US-09-999-040-13	Sequence 13, App1

ALIGNMENTS

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RESULT 1
US-09-741-843-2
: Sequence 2, Application US/09741843
: Patent No. US20020102254A1
: GENERAL INFORMATION:
: APPLICANT: LEUNG, Shui-on
: APPLICANT: HANSEN, Hans
: TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL
: FILE REFERENCE: 018733/0996
: CURRENT APPLICATION NUMBER: US/09/741.843
: CURRENT FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: US 09/127,902
: PRIOR FILING DATE: 1998-08-03
: PRIOR APPLICATION NUMBER: US 08/690,102
: PRIOR FILING DATE: 1996-07-06
: PRIOR APPLICATION NUMBER: US 08/289,576
: PRIOR FILING DATE: 1994-08-12
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: Patentin version 3.1
: SEQ ID NO 2
: LENGTH: 113
: TYPE: PRT
: ORGANISM: Murinae gen. sp.
US-09-741-843-2
Query Match 100.0%; Score 594; DB 10; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.1e-47;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIQLOSPSSSLAVSAGENVWTCSSOSVYLSANHKNTLWYQOQPGQSPRLTIYMASTR 60
DB 1 DIQLOSPSSSLAVSAGENVWTCSSOSVYLSANHKNTLWYQOQPGQSPRLTIYMASTR 60
QY 61 ESGVPDFFTGSGSTDFLTISRQVEDLAIYVHQTLSWTFGGTKLEIKR 113
DB 61 ESGVPDFFTGSGSTDFLTISRQVEDLAIYVHQTLSWTFGGTKLEIKR 113
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RESULT 2
US-09-894-839-2
Sequence 2, Application US/09894839
Publication No. US20030035800A1
GENERAL INFORMATION:
APPLICANT: LEUNG, Shul-on
APPLICANT: HANSEN, Hans
APPLICANT: OU, Zhengxing
TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
FILE REFERENCE: 018733/1049
CURRENT APPLICATION NUMBER: US/09/894,839
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 09/155,107
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: US 60/013,709
PRIOR FILING DATE: 1996-03-20
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 113
TYPE: PRT
ORGANISM: Murinae gen. sp.
US-09-894-839-2

Query Match 100.0%; Score 594; DB 11; Length 113;
Best Local Similarity 100.0%; Pred. No. 2,1e-47;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DIQTGPSSTLAVSAGENVMTSCSSQSVLYSANHKNYLAWYQKPGQSPKLLITYASTR 60
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Db 1 DIQTGPSSTLAVSAGENVMTSCSSQSVLYSANHKNYLAWYQKPGQSPKLLITYASTR 60

OY 61 ESGVPDFFTSGSGSTDFTLTISRQVEDLAIYYCHQYLSWTFGGGKLEIKR 113
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Db 61 ESGVPDFFTSGSGSTDFTLTISRQVEDLAIYYCHQYLSWTFGGGKLEIKR 113

RESULT 3
US-09-988-013A-2
Sequence 2, Application US/09988013A
Publication No. US20030103979A1
GENERAL INFORMATION:
APPLICANT: LEUNG, Shul-on
APPLICANT: HANSEN, Hans
TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B
FILE REFERENCE: 18733/1082
CURRENT APPLICATION NUMBER: US/09/988,013A
CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: US 09/741,843
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/127,902
PRIOR FILING DATE: 1998-08-03
PRIOR APPLICATION NUMBER: US 08/690,102
PRIOR FILING DATE: 1996-07-06
PRIOR APPLICATION NUMBER: US 08/289,576
PRIOR FILING DATE: 1994-08-12
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 113
TYPE: PRT
ORGANISM: Murinae gen. sp.
US-09-988-013A-2

Query Match 100.0%; Score 594; DB 11; Length 113;
Best Local Similarity 100.0%; Pred. No. 2,1e-47;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DIQTGPSSTLAVSAGENVMTSCSSQSVLYSANHKNYLAWYQKPGQSPKLLITYASTR 60
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Db 1 DIQTGPSSTLAVSAGENVMTSCSSQSVLYSANHKNYLAWYQKPGQSPKLLITYASTR 60

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Oy      61  ESGVPDRFTGSGSGDTFTLTISRVOVEDLAIYYCHQYLSMTFGGCTLEIKR 113
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Db      61  ESGVPDRFTGSGSGDTFTLTISRVOVEDLAIYYCHQYLSMTFGGCTLEIKR 113

RESULT 4
US-10-229-335-28
: Sequence 28, Application US/10229335
: Publication No. US20030144483A1
: GENERAL INFORMATION:
: APPLICANT: MEDAREX, INC.
: TITLE OF INVENTION: HUMANIZED ANTIBODIES TO FC RECEPTORS FOR
: IMMUNOBLOBULIN G ON HUMAN MONONUCLEAR PHAGOCYTES
: NUMBER OF SEQUENCES: 28
: STREET: P.O. Box 953, 1545 Route 22 East
: CITY: Annandale
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 08801
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: ASCII text
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/10/229,335
: FILING DATE: 26-Aug-2002
: CLASSIFICATION: <unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/435,516
: FILING DATE: <unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Arnold, Beth E.
: REGISTRATION NUMBER: 35,430
: REFERENCE/DOCKET NUMBER: MXI-013
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 227-7400
: TELEFAX: (617) 227-5941
: INFORMATION FOR SEQ ID NO: 28:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 112 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FRAGMENT TYPE: Internal
: SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-229-335-28

Query Match      92.1%; Score 547; DB 12; Length 112;
Best Local Similarity 92.0%; Pred. No. 4.4e-43;
Matches 103; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

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Db      1  NIWVGSSSSILAVSAGENVMTSCRSSQSVLYLSNKNKTLAWYQQRGSPKILYYMASTR 60

Oy      61  ESGVPDRFTGSGSGDTFTLTISRVOVEDLAIYYCHQYLSMTFGGCTLEIKR 112
        |||||||
Db      61  ESGVPDRFTGSGSGDTFTLTISRVOVEDLAIYYCHQYLSMTFGGCTLEIKR 112

RESULT 5
US-10-056-052-10
: Sequence 10, Application US/10056052
: Publication No. US20030099656A1
: GENERAL INFORMATION:
: APPLICANT: PATTI, Joseph M
: APPLICANT: HUTCHINS, Jeff T
: APPLICANT: DOMANSKI, Paul
: APPLICANT: PATEL, Pratiksha
: APPLICANT: HALL, Andrea
: TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLPA PROTEIN . . .

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FILE REFERENCE: P07069US04/BAS
CURRENT APPLICATION NUMBER: US/10/056,052
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/308,116
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/298,413
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/274,611
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: 60/264,072
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 112
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-056-052-10

Query Match 90.9%; Score 540; DB 15; Length 112;
Best Local Similarity 91.1%; Pred. No. 1.9e-42;
Matches 102; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 1 DIOLTOSSSLAVAGENVMTSCSSOSVLSANKNTLAWYQOKPGSPKLLIYMASTR 60
DB 1 NIMMTOSSSLAVSAGEVMTSCSSOSVLSNKNLAWYQOKPGSPKLLIYMASTR 60
YQ 61 ESGVPRFTSGSGTDFLTITSRVOVEDLAIYCHQYLSWTFFGGTLEIK 112
DB 61 ESGVPRFTSGSGTDFLTITSRVOVEDLAIYCHQYLSWTFFGGTLEIK 112

RESULT 6
US-10-056-052-6
Sequence 6, Application US/10056052
Publication No. US20030099656A1
GENERAL INFORMATION:
APPLICANT: PATTI, Joseph M
APPLICANT: HUTCHINS, Jeff T
APPLICANT: DOMANSKI, Paul
APPLICANT: PATEL, Pratiksha
APPLICANT: HALL, Andrea
TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLPA PROTEIN . . .
FILE REFERENCE: P07069US04/BAS
CURRENT APPLICATION NUMBER: US/10/056,052
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/308,116
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/298,413
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/274,611
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: 60/264,072
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 112
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-056-052-6

Query Match 89.7%; Score 533; DB 15; Length 112;
Best Local Similarity 90.2%; Pred. No. 8.4e-42;
Matches 101; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 1 DIOLTOSSSLAVAGENVMTSCSSOSVLSANKNTLAWYQOKPGSPKLLIYMASTR 60
DB 1 NIMMTOSSSLAVSAGEVMTSCSSOSVLSNKNLAWYQOKPGSPKLLIYMASTR 60
YQ 61 ESGVPRFTSGSGTDFLTITSRVOVEDLAIYCHQYLSWTFFGGTLEIK 112
DB 61 ESGVPRFTSGSGTDFLTITSRVOVEDLAIYCHQYLSWTFFGGTLEIK 112

RESULT 7
US-10-056-052-14
Sequence 14, Application US/10056052
Publication No. US20030099656A1
GENERAL INFORMATION:
APPLICANT: PATTI, Joseph M
APPLICANT: HUTCHINS, Jeff T
APPLICANT: DOMANSKI, Paul
APPLICANT: PATEL, Pratiksha
APPLICANT: HALL, Andrea
TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLPA PROTEIN . . .
FILE REFERENCE: P07069US04/BAS
CURRENT APPLICATION NUMBER: US/10/056,052
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/308,116
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/298,413
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/274,611
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: 60/264,072
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 112
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-056-052-14

Query Match 89.4%; Score 531; DB 15; Length 112;
Best Local Similarity 89.3%; Pred. No. 1.3e-41;
Matches 100; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 1 DIOLTOSSSLAVAGENVMTSCSSOSVLSANKNTLAWYQOKPGSPKLLIYMASTR 60
DB 1 NIMMTOSSSLAVSAGEVMTSCSSOSVLSNKNLAWYQOKPGSPKLLIYMASTR 60
YQ 61 ESGVPRFTSGSGTDFLTITSRVOVEDLAIYCHQYLSWTFFGGTLEIK 112
DB 61 ESGVPRFTSGSGTDFLTITSRVOVEDLAIYCHQYLSWTFFGGTLEIK 112

RESULT 8
US-10-053-530-14
Sequence 14, Application US/10053530
Publication No. US20030133939A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey
APPLICANT: Hayden-Ledbetter, Martha
TITLE OF INVENTION: Binding Domain-Immunoglobulin Fusion Proteins
FILE REFERENCE: 390069,401
CURRENT APPLICATION NUMBER: US/10/053,530
CURRENT FILING DATE: 2002-01-17
PRIOR APPLICATION NUMBER: US 09/765,208
PRIOR FILING DATE: 2001-01-17
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.0
SEQ ID NO 14
LENGTH: 272
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: SITE
LOCATION: (1)..(272)
OTHER INFORMATION: MOOSE ANTI-HUMAN CD22 SCFV
US-10-053-530-14

Query Match 89.2%; Score 530; DB 12; Length 272;
Best Local Similarity 87.5%; Pred. No. 4e-41;
Matches 98; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Wed Oct 8 09:40:34 2003

us-09-988-013a-2.rapb

Page 6

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Job time : 59.4483 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 19:03:26 Search time 21.3966 Seconds

(without alignments)
126.112 Million cell updates/sec

Title: US-09-988-013a-2_COPY_24_40

Perfect score: 85
Sequence: 1 KSSQSVLYXSAHKNYLA 17

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	113	17	AA92215
2	85	100.0	113	18	AA92217
3	85	100.0	113	18	AAW27695
4	85	100.0	115	18	AAW27697
5	85	88.2	17	23	AAU70334
6	85	88.2	82	19	AAW62807
7	85	88.2	101	24	ABJ18696
8	85	88.2	113	21	ABJ18857
9	85	88.2	113	21	ABJ18861

10	75	88.2	113	21	ABJ18863	Amino acid sequenc
11	75	88.2	113	21	ABJ18865	Amino acid sequenc
12	75	88.2	113	21	ABJ18867	Amino acid sequenc
13	75	88.2	113	21	ABJ18869	Amino acid sequenc
14	75	88.2	113	21	ABJ18873	Amino acid sequenc
15	75	88.2	113	21	ABJ18881	Amino acid sequenc
16	75	88.2	113	22	ABJ62769	Amino acid sequenc
17	75	88.2	119	22	ABJ07172	Human HIV-1 monocl
18	75	88.2	120	22	AAJ65565	ebvH1dM MS119D10
19	75	88.2	124	20	AAJ57181	Amino acid sequenc
20	75	88.2	133	9	AAJ80894	Amino acid sequenc
21	75	88.2	133	15	AAJ48633	V-region of L chain
22	75	88.2	134	15	AAJ25158	Sequence of Hum4V
23	75	88.2	134	14	AAJ38317	V-region of L-chain
24	75	88.2	134	14	AAJ50690	Sequence encoded b
25	75	88.2	171	14	AAJ38320	Human Hum4 VL Clai
26	75	88.2	171	14	AAJ57184	Sequence of signal
27	75	88.2	171	20	AAJ50693	Amino acid sequenc
28	75	88.2	171	20	AAJ50697	Plasmid pATPFLAG F
29	75	88.2	239	21	AAJ03697	Immunoglobulin kap
30	75	88.2	260	20	AAJ57182	Amino acid sequenc
31	75	88.2	260	20	AAJ50691	Human SCFV1 protei
32	75	88.2	264	23	AAJ43142	Human ovarian anti
33	75	88.2	274	14	AAJ38319	Sequence of Hum4 V
34	75	88.2	274	20	AAJ57183	Amino acid sequenc
35	75	88.2	274	20	AAJ50692	Human Hum4L-CC49 V
36	75	88.2	284	14	AAJ38321	Sequence of pSC49F
37	75	88.2	284	20	AAJ57185	Amino acid sequenc
38	75	88.2	284	20	AAJ50694	Plasmid pSC49FLAG
39	74	87.1	112	23	AAJ29274	Anti-ClfA monoclon
40	74	87.1	112	15	AAJ54932	FC receptor human1
41	74	87.1	112	15	AAJ54933	MD 022 VR chain.
42	74	87.1	112	15	AAJ54934	S. aureus ClfA spe
43	74	87.1	112	23	AAJ29266	S. aureus ClfA spe
44	74	87.1	112	23	AAJ29270	S. aureus ClfA spe
45	74	87.1	263	20	AAJ90226	Anti-B7.2 monosp
			268	20	AAJ90228	Anti-B7.1/anti-B7.

ALIGNMENTS

RESULT 1	AA92215	standard; Protein; 113 AA.
ID	AA92215	standard; Protein; 113 AA.
XX	AA92215;	
AC	28-MAY-1996	(first entry)
XX		
DT	28-MAY-1996	(first entry)
XX		
DE	LL2 Mab VR region.	
XX		
KW	Humanized antibody; monoclonal antibody; Mab; LL2; B-cell lymphoma;	
KW	leukemia; therapy; diagnosis; complementarity determining region;	
KW	CDR; antibody engineering.	
XX		
OS	Mus musculus.	
XX		
FH	Key	Location/Qualifiers
FT	Region	24_40
FT		/label=CDR1
FT		/note="claim 6, page 44"
FT	Region	56_62
FT		/label=CDR2
FT		/note="claim 7, page 44"
FT	Region	95_103
FT		/label=CDR3
FT		/note="claim 8, page 44"
XX		
PN	WO9604925-A1.	
XX		
PD	22-FEB-1996.	
XX		
PF	11-AUG-1995;	95WO-US09641.

XX 12-AUG-1994; 94US-0289576.
 XX (IMMU-) IMMUNOMEDICS INC.
 XX
 XX Hansen H, Leung S;
 XX WPI: 1996-139454/14.
 XX N-PSDB; AAT15802.
 XX
 XX Chimeric and humanised LL2 antibodies - used to produce conjugates
 XX for the therapy and diagnosis of B-cell lymphoma(s) and
 XX leukaemia(s).
 XX
 XX Claim 5; Page 35-36; 70pp; English.
 XX
 XX The complementarity determining regions (CDRs) of mouse monoclonal
 XX antibody (Mab) LL2 VK (AAR92215) and VH (AAR92216) regions were
 XX recombinantly linked to the framework sequences of human VK and VH
 XX regions, respectively, to give humanised LL2 VK (AAR92217) and VH
 XX (AAR92218). These were subsequently linked, respectively, to human
 XX kappa and IgG1 constant regions. A humanised Mab was obtained that
 XX retained the B-lymphoma and leukaemia cell targeting and
 XX internalisation characteristics of the parental LL2 Mab, and which
 XX exhibited a lowered HAMA reaction. It can be linked to e.g. a
 XX cytostatic agent for therapeutic appln.
 XX
 XX Sequence 113 AA;
 XX
 XX Query Match 100.0%; Score 85; DB 17; Length 113;
 XX Best Local Similarity 100.0%; Pred. No. 6.7e-07;
 XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1 KSSQSVLYSANHNKNYLA 17
 XX ||||||||||||||||
 XX 24 KSSQSVLYSANHNKNYLA 40
 XX
 XX RESULT 2
 XX AAR92217 standard; Protein; 113 AA.
 XX
 XX AAR92217;
 XX
 XX 28-MAY-1996 (first entry)
 XX
 XX Humanised LL2 MAB VK region.
 XX
 XX Humanised antibody; monoclonal antibody; Mab; LL2; B-cell lymphoma;
 XX leukaemia; therapy; diagnosis; complementarity determining region;
 XX CDR; antibody engineering.
 XX
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 XX Region 24..40
 XX /label- CDRI
 XX Region 56..62
 XX /label- CDR2
 XX Region 95..103
 XX /label- CDR3
 XX
 XX W09604925-A1.
 XX
 XX 22-FEB-1996.
 XX
 XX 11-AUG-1995; 95MO-US09641.
 XX
 XX 12-AUG-1994; 94US-0289576.
 XX
 XX (IMMU-) IMMUNOMEDICS INC.
 XX Hansen H, Leung S;
 XX
 XX WPI: 1997-479995/44.

XX WPI: 1996-139454/14.
 XX N-PSDB; AAT15803.
 XX
 XX Chimeric and humanised LL2 antibodies - used to produce conjugates
 XX for the therapy and diagnosis of B-cell lymphoma(s) and
 XX leukaemia(s).
 XX
 XX Claim 5; Page 38; 70pp; English.
 XX
 XX The complementarity determining regions (CDRs) of mouse monoclonal
 XX antibody (Mab) LL2 VK (AAR92215) and VH (AAR92216) regions were
 XX recombinantly linked to the framework sequences of human VK and VH
 XX regions, respectively, to give humanised LL2 VK (AAR92217) and VH
 XX (AAR92218). These were subsequently linked, respectively, to human
 XX kappa and IgG1 constant regions. A humanised Mab was obtained that
 XX retained the B-lymphoma and leukaemia cell targeting and
 XX internalisation characteristics of the parental LL2 Mab, and which
 XX exhibited a lowered HAMA reaction. It can be linked to e.g. a
 XX cytostatic agent for therapeutic appln.
 XX
 XX Sequence 113 AA;
 XX
 XX Query Match 100.0%; Score 85; DB 17; Length 113;
 XX Best Local Similarity 100.0%; Pred. No. 6.7e-07;
 XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1 KSSQSVLYSANHNKNYLA 17
 XX ||||||||||||||||
 XX 24 KSSQSVLYSANHNKNYLA 40
 XX
 XX RESULT 3
 XX AAW27695
 XX AAW27695 standard; Protein; 113 AA.
 XX
 XX AAW27695;
 XX
 XX 14-APR-1998 (first entry)
 XX
 XX Variable kappa chain of Mab LL2.
 XX
 XX Variable kappa chain; B cell; monoclonal antibody; Mab; LL2;
 XX B cell lymphoma; lymphocytic leukaemia cell; murine;
 XX diagnosis; treatment; B cell malignancy; non-Hodgkins lymphoma;
 XX chronic lymphocytic leukaemia.
 XX
 XX Mus sp.
 XX
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 XX Region 18..20
 XX /note- "potential N-linked glycosylation site"
 XX Region 24..40
 XX /note- "complementarity determining region 1"
 XX Region 56..62
 XX /note- "complementarity determining region 2"
 XX Region 95..102
 XX /note- "complementarity determining region 3"
 XX
 XX W09734632-A1.
 XX
 XX 25-SEP-1997.
 XX
 XX 19-MAR-1997; 97MO-US04196.
 XX
 XX 20-MAR-1996; 96US-0013709.
 XX
 XX (IMMU-) IMMUNOMEDICS INC.
 XX Hansen H, Leung S, Qu Z;
 XX
 XX WPI: 1997-479995/44.

DR N-PSDB;AAT88128.
XX
PT Monoclonal antibody engineered to contain glycosylation site - in
PT non-Fc constant heavy or light chain region, useful to diagnose or
PT treat B cell malignancies, e.g. non-Hodgkins lymphoma
XX
PS
XX Example 3; Fig 4A; 88pp: English.
XX
CC The present sequence is the variable kappa chain of the
CC B cell specific monoclonal antibody (Mab) IL2, which contains an
CC engineered rti-peptide N-glycan acceptor sequence. IL2 is a highly
CC specific anti-B cell lymphoma and anti-lymphocytic leukaemia cell
CC murine Mab. The Mab can be used to diagnose or treat B
CC cell malignancies, e.g. non-Hodgkins lymphoma or chronic
CC lymphocytic leukaemia. The glycosylation site allows a label or
CC therapeutic agent of increased size to be conjugated to the
CC carbohydrate moiety, without affecting the Mab's binding affinity
CC or specificity.
XX
XX Sequence 113 AA;

	Query Match	Score	DB 18;	Length
	Best Local Similarity	100.0%;	Pred. No. 6,7e-07;	113;
Matches	Conservative	0;	Mismatches	0; Indels
Qy	1 KSSQSVLXSANHKNTYLA	17		
Db	24 KSSQSVLXSANHKNTYLA	40		

XX	AAW27697 standard; Protein: 115 AA.
XX	AAW27697
AC	AAW27697:
XX	14-APR-1998 (first entry)
DE	Variable kappa chain of Mab hLL2.
RW	Variable kappa chain; B cell; monoclonal antibody; Mab; hLL2;
KW	B cell lymphoma; lymphocytic leukaemia cell; murine; humanised;
RW	diagnosis; treatment; B cell malignancy; non-Hodgkins lymphoma;
XX	chronic lymphocytic leukaemia.
OS	Chimeric - Mus sp.
OS	Chimeric - Homo sapiens.
XX	
FH	Key
FT	Region
FT	Location/Qualifiers
FT	24..40
FT	/note= "complementarity determining region 1"
FT	Region
FT	56..62
FT	/note= "complementarity determining region 2"
FT	Region
FT	95..102
FT	/note= "complementarity determining region 3"
XX	
PN	MO9734632-A1.
PD	
PD	25-SEP-1997.
XX	
PP	19-MAR-1997; 97WC-USO4196.
PR	
PR	20-MAR-1996; 96US-0013709.
PA	(IMMU-)IMMUNOMEDICS=INC.
PT	Hansen H, Leung S, Ou Z;
XX	
DR	WPI; 1997-47995/44.
XX	N-PSDB; AAF86130.
PT	Monoclonal antibody engineered to contain glycosylation site - in non-Fc constant heavy or light chain region, useful to diagnose or

```

PT      treat B cell malignancies, e.g. non-Hodgkins lymphoma
PS
XX
XX      Example 3; Fig 5A; 88pp; English.
CC
CC      The present sequence is the variable kappa chain of the
CC      B cell specific monoclonal antibody (Mab) hu12. hu12 is a highly
CC      specific anti-B cell lymphoma and anti-lymphocytic leukaemia cell
CC      humanised murine Mab. The Mab can be used to diagnose or treat B
CC      cell malignancies, e.g. non-Hodgkins lymphoma or Chronic
CC      lymphocytic leukaemia.
XX
XX
SQ      Sequence      115 AA;

Query Match      100.0%; Score 85; DB 18; Length 115;
Best Local Similarity 100.0%; Pred. No. 6.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KSSQSVLYSANHKNTLA 17
      |||
DB      24 KSSQSVLYSANHKNTLA 40

```

RESULT 5	
AAU70334	
ID	AAU70334 standard; Peptide; 17 AA
vv	

DT 14-FEB-2002 (first entry)

DE Human Kappa IV light chain CDRI

KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR
 KW Complementarily determining region; framework region; IgBP;
 KW transgenic plant; immunoglobulin binding protein array;
 KW IgM; IgG; IgA; IgD; IgE; IgY; IgM; kappa; lambda; CHBP.

OS Homo sapiens.

PN WO200183806-A1

PD 08-NOV-2001.

PF 02-MAY-2001; 2001WO-US14349.

PR 02-MAY-2000; 2000US-0563222.

PA (EPIC-) EPICYTE PHARM INC.

PI Hlatt AC, Hein MB;

WPI: 2002-055482/07

PT Preparing immunoglobulin binding protein array in plant cells by
PT transforming the cells with different polynucleotides encoding binding
PT protein polypeptides specific to ligand, selecting plant cells for
PT preparing array -

PS Disclosure; page 14; 129pp; English

CC The invention relates to transforming a population of cells (e.g. plant
CC cells), comprising using a library of two different polynucleotides
CC encoding different immunoglobulin binding protein (IgBP) polypeptides
CC that specifically bind to a ligand or form one or more disulphide bonds
CC with polypeptides in transfected cells, to generate an IgBP that
CC binds to a ligand, and transformed plant cells are selected, and
CC preparing an IgBP array in plant cells. At least one peptide sequence has
CC at least 75% sequence identity to a framework region (FR) of a native
CC IgM, IgG, IgA, IgD, IgE, IgY, kappa or lambda immunoglobulin molecule.
CC The method is useful for preparing an immunoglobulin binding protein
CC array, preferably heavy chain binding protein (CHBP) array in eukaryotic
CC cells especially plant cells (e.g. *Agrobacterium tumefaciens* or maize)
CC or other eukaryotic cells (e.g. insect cells or mammalian cells). The

CC CHBP is useful for discovery of e.g. screening assays of IgBPs having
CC desired characteristics. The present sequence is a mammalian
CC immunoglobulin derived peptide that may be incorporated into an IgBP of
CC the invention.

SO Sequence 17 AA;

Query Match 88.2%; Score 75; DB 23; Length 17;
Best Local Similarity 88.2%; Pred. No. 4e-06;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSSQSVLYSANHKNTLYA 17
|||||||:|:|:|:|:|:|
DB 1 KSSQSVLYSSNNKNTLYA 17

RESULT 6
AAM62807
ID AAM62807 standard; Peptide; 82 AA.

AC AAM62807;

DT 23-SEP-1998 (first entry)

DE Amino acid sequence of a human antibody fragment.

OS Human; immunoglobulin; Ig; transgenic; non-human mammal;

KW inactivated endogenous Ig locus; B-cell development;

KW human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene;

KW kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa;

XX production; antibody.

OS Homo sapiens.

XX WO9824893-A2.

PD 11-JUN-1998.

PF 03-DEC-1997; 97WO-US23091.

PR 03-DEC-1996; 96US-0759620.

PA (ABGE-) ABGENIX INC.

PI Green L, Jakobovits A, Klapholz S, Kucherlapati R;

PI Mendez M;

XX WPI; 1998-33314/29.

DR WPI; 1998-33314/29.

XX New transgenic non-human mammals - having an inactivated

PT immunoglobulin locus and a near complete human immunoglobulin locus,

PT used for production of human antibodies

XX Disclosure; Page 78; 128pp; English.

PS AAM62793-822 represent fragments of human antibodies produced by

CC transgenic Xenomice, created using the method of the invention. The

CC specification describes a transgenic non-human mammal which has genome

CC modifications that comprise an inactivated endogenous immunoglobulin (Ig)

CC locus, so that the mammal does not display normal B-cell development. The

CC modified genome also has an inserted human heavy chain Ig locus in

CC germ-line configuration, the human heavy chain Ig locus comprising a human

CC micro constant region and regulatory and switch sequences, human J-H

CC genes, human D-H genes, and human V-H genes and an inserted human kappa

CC light chain Ig locus in germ-line configuration, the human kappa light

CC chain Ig locus comprising a human kappa constant region, J-kappa genes,

CC and V-kappa genes, where the number of V-H and V-kappa genes inserted

CC are selected to restore normal B-cell development in the mammal. The

CC transgenic animals have a near complete human Ig locus, including both a

CC human heavy chain locus and a human kappa light chain locus. They can

CC be used for the production of human antibodies when exposed to

CC particular antigens e.g. when exposed to human IL-8, EGFR or TNF- alpha

CC the mice will produce antibodies to IL-8, EGFR or TNF- alpha

CC respectively.

XX Sequence 82 AA;

Query Match 88.2%; Score 75; DB 19; Length 82;
Best Local Similarity 88.2%; Pred. No. 2.4e-05;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSSQSVLYSANHKNTLYA 17
|||||||:|:|:|:|:|:|
DB 5 KSSQSVLYSSNNKNTLYA 21

RESULT 7
ABJ18696
ID ABJ18696 standard; Protein; 101 AA.

AC ABJ18696;

DT 06-MAR-2003 (first entry)

DE Antibody library related human protein sequence SEQ ID No 25.

KW Library; recombinant antibody; clustering variable region; in silico;

KW immunogenicity; antibody therapeutic; human.

OS Homo sapiens.

XX WO200284277-A1.

PD 24-OCT-2002.

PF 17-APR-2002; 2002WO-US12202.

PR 17-APR-2001; 2001US-284407P.

PA (ABMA-) ABMAXIS INC.

PI Luo P;

PI WPI; 2003-093043/08.

DR WPI; 2003-093043/08.

XX Constructing a library of recombinant antibodies useful as source of

PT antibody candidates for screening antigens comprises clustering

PT variable regions of antibodies having known 3-dimensional structures

PT into structural ensembles

XX Disclosure; Page 115; 119pp; English.

PS The invention relates to a novel method for the construction of a library

CC of recombinant antibodies. The novel method comprises clustering variable

CC regions of a collection of antibodies having known 3D structures into at

CC least two families of structural ensembles, each comprising at least two

CC different antibody sequences but with substantially identical main chain

CC conformations. The method is useful for constructing a library of

CC artificial antibodies in silico which provides a structurally diverse and

CC yet functionally more relevant source of antibody candidates which can

CC then be screened for binding a wide variety of target molecules,

CC including small molecules, and biomacromolecules such as proteins,

CC peptides and nucleic acids. The libraries constructed are useful as a

CC source of antibody candidates for further screening for novel antibodies

CC with high affinity against a wide range of antigens and having no or

CC minimum immunogenicity to human subjects treated with antibody

CC therapeutics. This sequence represents a human peptide region of an

CC antibody relating to the novel antibody library construction method of

CC the invention.

SO Sequence 101 AA;

Query Match 88.2%; Score 75; DB 24; Length 101;
Best Local Similarity 88.2%; Pred. No. 3.1e-05;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSVLYSANHKNYLA 17
 DB 24 KSSQSVLYSSNNKNYLA 40

RESULT 8

ID AAB18857 standard; Protein; 113 AA.

AC AAB18857;

DE 08-FEB-2001 (first entry)

XX Amino acid sequence of anti-p53 antibody light chain clone 163.2.

KW p53; antibody; immune response; vaccine; gene therapy; cancer;

OS rheumatoid arthritis; coronary heart disease.

XX Homo sapiens.

PN WO200056770-A1.

PD 28-SEP-2000.

PF 15-MAR-2000; 2000MO-AU00189.

PR 19-MAR-1999; 99AU-0009321.

PA (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.

PI Ward RL, Coomber DMJ;

DR WPI; 2000-638249/61.

XX N-PSDB; AAA96134.

PT Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide

XX fragments, useful in treatment and diagnosis of cancer, rheumatoid

XX arthritis and coronary heart disease

XX Claim 30; Page 132; 163pp; English.

XX The present sequence represents the light chain of an antibody reactive

CC against p53. The antibody is obtained from a vertebrate host expressing

CC an immune response against a naturally occurring disease. The antibodies

CC are useful in pharmaceutical compositions, which additionally contain

CC chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes

CC or gadolinium. The polypeptide components of the antibodies are useful in

CC vaccines, for inducing an immune response against a disease in a

CC vertebrate, for treatment and/or prophylaxis of disease and for detection

CC purposes. The nucleic acid sequences can be used to detect a disease as

CC well as for gene therapy and recombinant production of the polypeptides.

CC In particular, the following can be treated cancer, rheumatoid arthritis

CC and coronary heart disease. Cancers include carcinogenic tumours, tumours

CC of epithelial origin, e.g. colorectal cancer, breast cancer lung cancer,

CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,

CC gastric cancer, brain cancer, bladder cancer, prostate cancer and

CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,

CC e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.

XX Sequence 113 AA;

XX Query Match 88.2%; Score 75; DB 21; Length 113;

XX Best Local Similarity 88.2%; Pred. No. 3.5e-05;

XX Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSVLYSANHKNYLA 17

DB 24 KSSQSVLYSSNNKNYLA 40

RESULT 9

AAB18861

ID AAB18861 standard; Protein; 113 AA.

XX AAB18861;

DE 08-FEB-2001 (first entry).

XX Amino acid sequence of anti-p53 antibody light chain clone 163.6.

KW p53; antibody; immune response; vaccine; gene therapy; cancer;

OS rheumatoid arthritis; coronary heart disease.

XX Homo sapiens.

PN WO200056770-A1.

PD 28-SEP-2000.

PF 15-MAR-2000; 2000MO-AU00189.

PR 19-MAR-1999; 99AU-0009321.

PA (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.

PI Ward RL, Coomber DMJ;

DR WPI; 2000-638249/61.

XX N-PSDB; AAA96138.

PT Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide

XX fragments, useful in treatment and diagnosis of cancer, rheumatoid

XX arthritis and coronary heart disease

XX Claim 30; Page 136; 163pp; English.

XX The present sequence represents the light chain of an antibody reactive

CC against p53. The antibody is obtained from a vertebrate host expressing

CC an immune response against a naturally occurring disease. The antibodies

CC are useful in pharmaceutical compositions, which additionally contain

CC chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes

CC or gadolinium. The polypeptide components of the antibodies are useful in

CC vaccines, for inducing an immune response against a disease in a

CC vertebrate, for treatment and/or prophylaxis of disease and for detection

CC purposes. The nucleic acid sequences can be used to detect a disease as

CC well as for gene therapy and recombinant production of the polypeptides.

CC In particular, the following can be treated cancer, rheumatoid arthritis

CC and coronary heart disease. Cancers include carcinogenic tumours, tumours

CC of epithelial origin, e.g. colorectal cancer, breast cancer lung cancer,

CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,

CC gastric cancer, brain cancer, bladder cancer, prostate cancer and

CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,

CC e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.

XX Sequence 113 AA;

XX Query Match 88.2%; Score 75; DB 21; Length 113;

XX Best Local Similarity 88.2%; Pred. No. 3.5e-05;

XX Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSVLYSANHKNYLA 17

DB 24 KSSQSVLYSSNNKNYLA 40

RESULT 10

AAB18863

ID AAB18863 standard; Protein; 113 AA.

AC AAB18863;

DE 08-FEB-2001 (first entry)

XX Amino acid sequence of anti-p53 antibody light chain clone 163.7.

KW p53; antibody; immune response; vaccine; gene therapy; cancer;

KW	rheumatoid arthritis; coronary heart disease.
XV	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Misc-difference 101
ET	/note= "Arg encoded by CCA"
XX	
PN	MO200056770-A1.
PD	
PD	28-SEP-2000.
XX	
XX	
PF	15-MAR-2000; 2000WO-AU00189.
PR	
PR	19-MAR-1999; 99AU-0009321.
PA	(SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.
P1	
P1	Ward RL, Coomber DMJ;
XX	
DR	WPI: 2000-638249/61.
DR	N-PSDB; AAA96140.
XX	
PT	Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide fragments, useful in treatment and diagnosis of cancer, rheumatoid arthritis and coronary heart disease
XX	
PS	Claim 30; Page 138; 163pp; English.
XX	
CC	The present sequence represents the light chain of an antibody reactive against p53. The antibody is obtained from a vertebrate host expressing an immune response against a naturally occurring disease. The antibodies are useful in pharmaceutical compositions, which additionally contain chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes or gadolinium. The polypeptide components of the antibodies are useful in vaccines, for inducing an immune response against a disease in a vertebrate, for treatment and/or prophylaxis of disease and for detection purposes. The nucleic acid sequences can be used to detect a disease as well as for gene therapy and recombinant production of the polypeptides. In particular, the following can be treated cancer, rheumatoid arthritis and coronary heart disease. Cancers include carcinogenic tumours, tumours of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer, head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer, gastric cancer, brain cancer, bladder cancer, prostate cancer and urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours, e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.
SQ	Sequence 113 AA:
	Query Match 88.2%; Score 75; DB 21; Length 113; Best Local Similarity 88.2%; Pred. No. 3.5e-05;
	Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0
OY	I KSSQSIVLYSANHKNYLA 17 ::: Db 24 KSSQSIVLYSSNNKXYLA 40
RESULT 11	
AAB18865	
ID	AAB18865 standard; Protein: 113 AA.
XX	
AC	AAB18865;
XX	
DT	08-FEB-2001 (first entry)
DE	
XX	Amino acid sequence of anti-p53 antibody light chain clone 163.9.
XX	p53; antibody; Immune response; Vaccine; gene therapy; cancer;
KW	rheumatoid arthritis; coronary heart disease.
XX	
XS	Homo sapiens
XX	

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PN WO2000056770-AI.  
XX  
PD 28-SEP-2000.  
XX  
PF 15-MAR-2000; 200OWO-AU00189.  
XX  
PR 19-MAR-1999; 99AU-000932L.  
PA (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.  
PI Ward RL, Coomber DMJ;  
DR WPI: 2000-638249/61.  
NR N-PSTB: AAA96142.  
XX Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide fragments, useful in treatment and diagnosis of cancer, rheumatoid arthritis and coronary heart disease -  
PT  
PP  
PS Claim 30; Page 140; 163pp; English.  
XX  
XX The present sequence represents the light chain of an antibody reactive against p53. The antibody is obtained from a vertebrate host expressing an immune response against a naturally occurring disease. The antibodies are useful in pharmaceutical compositions, which additionally contain chelators, drugs, produgs, toxins and imaging markers e.g. radiolabelled or gadolinium. The polypeptide components of the antibodies are useful in vaccines, for inducing an immune response against a disease in a vertebrate, for treatment and/or prophylaxis of disease and for detection purposes. The nucleic acid sequences can be used to detect a disease as well as for gene therapy and recombinant production of the polypeptides. In particular, the following can be treated cancer, rheumatoid arthritis and coronary heart disease. Cancers include carcinogenic tumours, tumours of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer, head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer, gastric cancer, brain cancer, bladder cancer, prostate cancer and urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours, e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.  
SQ Sequence 113 AA:  
  
Query Match 88.2%; Score 75; DB 21; Length 113;  
Best Local Similarity 88.2%; Pred. No. 3.5e-05;  
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0.  
QY 1 KSSOSVLYSANHKNYLA 17  
IIIIIIIII:::IIIIII  
DB 24 KSSOSVLYSSNNKNXYLA 40  
  
RESULT 12  
AAB18867  
ID AAB18867 standard; Protein; 113 AA.  
XX  
AA18867:  
AC  
AD  
AE 08-FEB-2001. (first entry)  
AF  
AG  
AH  
AI Amino acid sequence of anti-p53 antibody light chain clone 163.14.  
AJ  
AK  
AL P53: antibody; Immune response; Vaccine; gene therapy; cancer;  
AM Rheumatoid arthritis; coronary heart disease.  
AN  
AO Homo sapiens.  
AP  
AQ WO2000056770-A1.  
AR  
AS  
AT 28-SEP-2000.  
AW  
AX 15-MAR-2000; 200OWO-AU00189.  
AY  
AZ 19-MAR-1999; 99AU-000932L.
```

PA (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.
 XX Ward RL, Coomber DMJ;
 PI
 DR WPI: 2000-638249/61.
 DR N-PSDB; AAA96144.
 XX
 PT Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide
 PT fragments, useful in treatment and diagnosis of cancer, rheumatoid
 PT arthritis and coronary heart disease
 XX
 PS Claim 30; Page 142; 163pp; English.
 XX
 CC The present sequence represents the light chain of an antibody reactive
 CC against p53. The antibody is obtained from a vertebrate host expressing
 CC an immune response against a naturally occurring disease. The antibodies
 CC are useful in pharmaceutical compositions, which additionally contain
 CC chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes
 CC or gadolinium. The polypeptide components of the antibodies are useful in
 CC vaccines, for inducing an immune response against a disease in a
 CC vertebrate, for treatment and/or prophylaxis of disease and for detection
 CC purposes. The nucleic acid sequences can be used to detect a disease as
 CC well as for gene therapy and recombinant production of the polypeptides.
 CC In particular, the following can be treated cancer, rheumatoid arthritis
 CC and coronary heart disease. Cancers include carcinogenic tumours, tumours
 CC of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer,
 CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,
 CC gastric cancer, brain cancer, bladder cancer, prostate cancer and
 CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,
 CC e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.
 CC
 SO Sequence 113 AA;
 XX
 Query Match 88.2%; Score 75; DB 21; Length 113;
 Best Local Similarity 88.2%; Pred. No. 3.5e-05;
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KSSQSVLYSANHKNYLA 17
 IIIIIIIIIIIIIIIIIIII
 Db 24 KSSQSVLYSSNNKNYLA 40
 IIIIIIIIIIIIIIIIIIII
 RESULT 13
 AAB18869
 ID AAB18869 standard; Protein; 113 AA.
 AC
 XX AAB18869;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Amino acid sequence of anti-p53 antibody light chain clone 163.15.
 XX
 KW p53; antibody; immune response; vaccine; gene therapy; cancer;
 KW rheumatoid arthritis; coronary heart disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200056770-A1.
 XX
 PD 28-SEP-2000.
 XX
 PF 15-MAR-2000; 2000MO-AU00189.
 XX
 PR 19-MAR-1999; 99AU-0009321.
 XX
 PA (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.
 XX
 PI Ward RL, Coomber DMJ;
 XX
 DR WPI: 2000-638249/61.
 DR N-PSDB; AAA96144.
 XX
 PT Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide

PT fragments, useful in treatment and diagnosis of cancer, rheumatoid
 PT arthritis and coronary heart disease
 XX
 PS Claim 30; Page 144; 163pp; English.
 XX
 CC The present sequence represents the light chain of an antibody reactive
 CC against p53. The antibody is obtained from a vertebrate host expressing
 CC an immune response against a naturally occurring disease. The antibodies
 CC are useful in pharmaceutical compositions, which additionally contain
 CC chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes
 CC or gadolinium. The polypeptide components of the antibodies are useful in
 CC vaccines, for inducing an immune response against a disease in a
 CC vertebrate, for treatment and/or prophylaxis of disease and for detection
 CC purposes. The nucleic acid sequences can be used to detect a disease as
 CC well as for gene therapy and recombinant production of the polypeptides.
 CC In particular, the following can be treated cancer, rheumatoid arthritis
 CC and coronary heart disease. Cancers include carcinogenic tumours, tumours
 CC of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer,
 CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,
 CC gastric cancer, brain cancer, bladder cancer, prostate cancer and
 CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,
 CC e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.
 CC
 SO Sequence 113 AA;
 XX
 Query Match 88.2%; Score 75; DB 21; Length 113;
 Best Local Similarity 88.2%; Pred. No. 3.5e-05;
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KSSQSVLYSANHKNYLA 17
 IIIIIIIIIIIIIIIIIIII
 Db 24 KSSQSVLYSSNNKNYLA 40
 IIIIIIIIIIIIIIIIIIII
 RESULT 14
 AAB18873
 ID AAB18873 standard; Protein; 113 AA.
 AC
 XX AAB18873;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Amino acid sequence of anti-p53 antibody light chain clone 163.17.
 XX
 KW p53; antibody; immune response; vaccine; gene therapy; cancer;
 KW rheumatoid arthritis; coronary heart disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200056770-A1.
 XX
 PD 28-SEP-2000.
 XX
 PF 15-MAR-2000; 2000MO-AU00189.
 XX
 PR 19-MAR-1999; 99AU-0009321.
 XX
 PA (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.
 XX
 PI Ward RL, Coomber DMJ;
 XX
 DR WPI: 2000-638249/61.
 DR N-PSDB; AAA96150.
 XX
 PT Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide
 PT fragments, useful in treatment and diagnosis of cancer, rheumatoid
 PT arthritis and coronary heart disease
 XX
 PS Claim 30; Page 148; 163pp; English.
 XX
 CC The present sequence represents the light chain of an antibody reactive
 CC against p53. The antibody is obtained from a vertebrate host expressing
 CC an immune response against a naturally occurring disease. The antibodies

are useful in pharmaceutical compositions, which additionally contain chelators, drugs, prodrugs, toxins and imaging markers e.g. radioisotopes or gadolinium. The polypeptide components of the antibodies are useful in vaccines, for inducing an immune response against a disease in a vertebrate, for treatment and/or prophylaxis of disease and for detection purposes. The nucleic acid sequences can be used to detect a disease as well as for gene therapy and recombinant production of the polypeptides. In particular, the following can be treated cancer: rheumatoid arthritis and coronary heart disease. Cancers include carcinogenic tumours, tumours of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer, head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer, gastric cancer, brain cancer, bladder cancer, prostate cancer and urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours, e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.

Sequence 113 AA:

Query Match 88.2%; Score 75; DB 21; Length 113;
Best Local Similarity 88.2%; Pred. No. 3.5e-05;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSVLYSANHKNYLA 17
|||||||:|:|:|
DB 24 KSSQSVLYSSNNKNYLA 40

RESULT 15

AAB18881

ID AAB18881 standard: Protein; 113 AA.

AC AAB18881;

DT 08-FEB-2001 (first entry)

DE Amino acid sequence of anti-p53 antibody light chain clone 163.24.

KM p53; antibody; immune response; vaccine; gene therapy; cancer;

OS Rheumatoid arthritis; coronary heart disease.

PN Homo sapiens.

PD WO200056770-A1.

PF 28-SEP-2000.

PR 15-MAR-2000; 2000WO-AU00189.

PA 19-MAR-1999; 99AU-0009321.

PI (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.

PT Ward RL, Coomber DWJ;

DR WPI: 2000-638249/61.

PS N-PSDB; AAA96158.

PT Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide

fragments, useful in treatment and diagnosis of cancer, Rheumatoid

arthritis and coronary heart disease

Claim 30; Page 156; 163pp; English.

The present sequence represents the light chain of an antibody reactive against p53. The antibody is obtained from a vertebrate host expressing an immune response against a naturally occurring disease. The antibodies are useful in pharmaceutical compositions, which additionally contain chelators, drugs, prodrugs, toxins and imaging markers e.g. radioisotopes or gadolinium. The polypeptide components of the antibodies are useful in vaccines, for inducing an immune response against a disease in a vertebrate, for treatment and/or prophylaxis of disease and for detection purposes. The nucleic acid sequences can be used to detect a disease as well as for gene therapy and recombinant production of the polypeptides. In particular, the following can be treated cancer, rheumatoid arthritis

and coronary heart disease. Cancers include carcinogenic tumours, tumours of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer, head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer, gastric cancer, brain cancer, bladder cancer, prostate cancer and urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours, e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.

Sequence 113 AA:

Query Match 88.2%; Score 75; DB 21; Length 113;
Best Local Similarity 88.2%; Pred. No. 3.5e-05;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSVLYSANHKNYLA 17
|||||||:|:|:|
DB 24 KSSQSVLYSSNNKNYLA 40

Search completed: October 7, 2003, 19:13:52
Job time : 22.3966 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 19:07:41 ; Search time 8.7931 Seconds
(without alignments) 305.878 Million cell updates/sec

Title: US-09-988-013a-2_COPY_24_40
Perfect score: 85
Sequence: 1 KSSQSVLYXSNHKNYLA 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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18: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
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2	85	100.0	113	10	US-09-741-843-6
3	85	100.0	113	11	US-09-894-839-2
4	85	100.0	113	11	US-09-894-839-6
5	85	100.0	113	11	US-09-894-839-20
6	85	100.0	113	11	US-09-988-013A-2
7	85	100.0	113	11	US-09-988-013A-6
8	85	100.0	113	11	US-09-563-222-14
9	85	100.0	113	11	US-09-563-222-14
10	85	100.0	113	11	US-09-563-222-14
11	85	100.0	113	11	US-09-563-222-14
12	85	100.0	113	11	US-09-563-222-14
13	85	100.0	113	11	US-09-563-222-14
14	85	100.0	113	11	US-09-563-222-14
15	85	100.0	113	11	US-09-563-222-14

16	75	88.2	260	12	US-10-255-478-64	Sequence 64, Appl
17	75	88.2	274	12	US-10-255-478-66	Sequence 66, Appl
18	75	88.2	284	12	US-10-255-478-70	Sequence 70, Appl
19	74	87.1	112	12	US-10-229-335-4	Sequence 4, Appl
20	74	87.1	112	12	US-10-229-335-28	Sequence 28, Appl
21	74	87.1	112	15	US-10-056-052-6	Sequence 6, Appl
22	74	87.1	112	15	US-10-056-052-10	Sequence 10, Appl
23	74	87.1	112	15	US-10-056-052-18	Sequence 18, Appl
24	73	85.9	113	10	US-09-274-163E-16	Sequence 16, Appl
25	73	85.9	114	9	US-09-810-502-38	Sequence 38, Appl
26	73	85.9	114	10	US-09-274-163E-2	Sequence 2, Appl
27	73	85.9	114	10	US-09-274-163E-4	Sequence 4, Appl
28	73	85.9	114	10	US-09-274-163E-6	Sequence 6, Appl
29	73	85.9	114	10	US-09-274-163E-11	Sequence 11, Appl
30	73	85.9	114	10	US-09-274-163E-16	Sequence 16, Appl
31	73	85.9	114	10	US-09-274-163E-21	Sequence 21, Appl
32	72	84.7	114	14	US-10-025-687-11	Sequence 11, Appl
33	72	84.7	114	14	US-10-025-687-11	Sequence 11, Appl
34	72	84.7	114	15	US-10-125-687-11	Sequence 11, Appl
35	72	84.7	114	15	US-10-125-687-11	Sequence 11, Appl
36	72	84.7	114	15	US-10-171-452A-1	Sequence 1, Appl
37	72	84.7	114	15	US-10-390-986-16	Sequence 16, Appl
38	71	83.5	114	15	US-10-056-052-14	Sequence 14, Appl
39	71	83.5	114	9	US-09-925-299-1226	Sequence 1226, Ap
40	70	82.4	114	11	US-09-925-299-1226	Sequence 1226, Ap
41	70	82.4	114	14	US-10-146-305-9	Sequence 9, Appl
42	70	82.4	113	10	US-09-999-025-7	Sequence 7, Appl
43	70	82.4	113	10	US-09-999-025-9	Sequence 9, Appl
44	70	82.4	113	10	US-09-999-025-13	Sequence 13, Appl
45	70	82.4	113	10	US-09-999-025-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-741-843-2
Sequence 2, Application US/09741843
Patent No. US20020102254A1
GENERAL INFORMATION:
APPLICANT: LEUNG, Shul-on
TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL
FILE REFERENCE: 018733/0996
CURRENT APPLICATION NUMBER: US/09/741,843
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/127,902
PRIOR FILING DATE: 1998-08-03
PRIOR APPLICATION NUMBER: US 08/690,102
PRIOR FILING DATE: 1996-07-06
PRIOR APPLICATION NUMBER: US 08/289,576
PRIOR FILING DATE: 1994-08-12
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patent version 3.1
SEQ ID NO 2
LENGTH: 113
TYPE: PRT
ORGANISM: Murinae gen. sp.
US-09-741-843-2
Query Match 100.0%; Score 85; DB 10; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KSSQSVLYXSNHKNYLA 17
DB 24 KSSQSVLYXSNHKNYLA 40
RESULT 2
US-09-741-843-6
Sequence 6, Application US/09741843

Patent No. US20020102254A1
GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA
FILE REFERENCE: 018733/0996
CURRENT APPLICATION NUMBER: US/09/741,843
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/127,902
PRIOR FILING DATE: 1998-08-03
PRIOR APPLICATION NUMBER: US 08/690,102
PRIOR FILING DATE: 1996-07-06
PRIOR APPLICATION NUMBER: US 08/289,576
PRIOR FILING DATE: 1994-08-12
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 113
TYPE: PRT
ORGANISM: Homo sapiens
US-09-741-843-6

Query Match 100.0%; Score 85; DB 11; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSSQSVLYSANHKNTLA 17
DB 24 KSSQSVLYSANHKNTLA 40

RESULT 3
US-09-894-839-2
Sequence 2, Application US/09894839
Publication No. US20030035800A1
GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
APPLICANT: HANSEN, Hans
APPLICANT: OU, Zhengxing
TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
FILE REFERENCE: 018733/1049
CURRENT APPLICATION NUMBER: US/09/894,839
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 09/155,107
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: US 60/013,709
PRIOR FILING DATE: 1996-03-20
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 113
TYPE: PRT
ORGANISM: Murinae gen. sp.
US-09-894-839-2

Query Match 100.0%; Score 85; DB 11; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSSQSVLYSANHKNTLA 17
DB 24 KSSQSVLYSANHKNTLA 40

RESULT 4
US-09-894-839-6
Sequence 6, Application US/09894839
Publication No. US20030035800A1
GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
APPLICANT: HANSEN, Hans
APPLICANT: OU, Zhengxing

TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
FILE REFERENCE: 018733/1049
CURRENT APPLICATION NUMBER: US/09/894,839
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 09/155,107
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: US 60/013,709
PRIOR FILING DATE: 1996-03-20
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 113
TYPE: PRT
ORGANISM: Homo sapiens
US-09-894-839-6

Query Match 100.0%; Score 85; DB 11; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSSQSVLYSANHKNTLA 17
DB 24 KSSQSVLYSANHKNTLA 40

RESULT 5
US-09-894-839-20
Sequence 20, Application US/09894839
Publication No. US20030035800A1
GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
APPLICANT: HANSEN, Hans
APPLICANT: OU, Zhengxing
TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
FILE REFERENCE: 018733/1049
CURRENT APPLICATION NUMBER: US/09/894,839
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 09/155,107
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: US 60/013,709
PRIOR FILING DATE: 1996-03-20
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 113
TYPE: PRT
ORGANISM: Homo sapiens
US-09-894-839-20

Query Match 100.0%; Score 85; DB 11; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSSQSVLYSANHKNTLA 17
DB 24 KSSQSVLYSANHKNTLA 40

RESULT 6
US-09-988-013a-2
Sequence 2, Application US/09988013A
Publication No. US20030103979A1
GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
APPLICANT: HANSEN, Hans
APPLICANT: OU, Zhengxing
TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
FILE REFERENCE: 18733/1082
CURRENT APPLICATION NUMBER: US/09/988,013A
CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: US 09/741,843
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/127,902

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; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/690,102
; PRIOR FILING DATE: 1996-07-06
; PRIOR APPLICATION NUMBER: US 08/289,576
; PRIOR FILING DATE: 1994-08-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 113
; TYPE: PRF
; ORGANISM: Murinae gen. sp.
US-09-988-013a-2

Query Match      100.0%; Score 85; DB 11; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 KSSQSVLYSANHKNYLA 17
Db      24 KSSQSVLYSANHKNYLA 40

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; Sequence 6, Application US/09988013A
; Publication No. US20030103979A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shu-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-
; TITLE OF INVENTION: CELL LYMPHOMA AND LEUKEMIA CELLS
; FILE REFERENCE: 18733/1082
; CURRENT APPLICATION NUMBER: US/09/988,013A
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 09/741,843
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/127,902
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/690,102
; PRIOR FILING DATE: 1996-07-06
; PRIOR APPLICATION NUMBER: US 08/289,576
; PRIOR FILING DATE: 1994-08-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 113
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-988-013a-6

Query Match      100.0%; Score 85; DB 11; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 KSSQSVLYSANHKNYLA 17
Db      24 KSSQSVLYSANHKNYLA 40

RESULT 8
US-09-563-222-14
; Sequence 14, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Heit, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; TITLE OF INVENTION: EUKARYOTIC CELLS
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
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; TYPE: PRF
; ORGANISM: Homo sapien
US-09-563-222-14

Query Match      88.2%; Score 75; DB 11; Length 17;
Best Local Similarity 88.2%; Pred. No. 9.5e-06;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY      1 KSSQSVLYSANHKNYLA 17
Db      1 KSSQSVLYSSNNKNYLA 17

RESULT 9
US-10-078-958-15
; Sequence 15, Application US/10078958
; Publication No. US20030070185A1
; GENERAL INFORMATION:
; APPLICANT: JAKOBOVITS, AYA
; APPLICANT: KUCHERLAPAT, RAJU
; APPLICANT: KLAPHOLT, SUSAN
; APPLICANT: MENDEZ, MICHAEL J.
; APPLICANT: GREEN, LARRY
; TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOCI INCLUDING
; TITLE OF INVENTION: PLURAL VH AND VK REGIONS AND ANTIBODIES PRODUCED
; FILE REFERENCE: CELL 4.18 CON
; CURRENT APPLICATION NUMBER: US/10/078,958
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 08/759,620
; PRIOR FILING DATE: 1996-12-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 82
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-078-958-15

Query Match      88.2%; Score 75; DB 15; Length 82;
Best Local Similarity 88.2%; Pred. No. 5e-05;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY      1 KSSQSVLYSANHKNYLA 17
Db      5 KSSQSVLYSSNNKNYLA 21

RESULT 10
US-10-025-687-25
; Sequence 25, Application US/10025687
; Publication No. US20020142255A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
; FILE REFERENCE: 26050-705
; CURRENT APPLICATION NUMBER: US/10/025,687
; CURRENT FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 101
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-025-687-25

Query Match      88.2%; Score 75; DB 14; Length 101;
Best Local Similarity 88.2%; Pred. No. 6.3e-05;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY      1 KSSQSVLYSANHKNYLA 17
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Db 24 KSSQSVLYSSNNKNYLA 40

RESULT 11
US-10-194-975-89
Sequence 89, Application US/10194975
Publication No. US20030039649A1
GENERAL INFORMATION:
APPLICANT: Foote, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.01
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn version 3.1
SEQ ID NO 89
LENGTH: 101
TYPE: PRT
ORGANISM: Homo sapiens
US-10-194-975-89

Query Match 88.2%; Score 75; DB 15; Length 101;
Best Local Similarity 88.2%; Pred. No. 6.3e-05;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSSQSVLYSSNNKNYLA 17
Db 24 KSSQSVLYSSNNKNYLA 40

RESULT 12
US-10-125-687-25
Sequence 25, Application US/10125687
Publication No. US20030054407A1
GENERAL INFORMATION:
APPLICANT: Luo, Peter
TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
FILE REFERENCE: 26050-705
CURRENT APPLICATION NUMBER: US/10/125,687
CURRENT FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 25
LENGTH: 101
TYPE: PRT
ORGANISM: Homo sapiens
US-10-125-687-25

Query Match 88.2%; Score 75; DB 15; Length 101;
Best Local Similarity 88.2%; Pred. No. 6.3e-05;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSSQSVLYSSNNKNYLA 17
Db 24 KSSQSVLYSSNNKNYLA 40

RESULT 13
US-09-956-206A-80
Sequence 80, Application US/09956206A
Patent No. US20020164339A1
GENERAL INFORMATION:
APPLICANT: DO COUJO, FERNANDO J.R.
CERIANI, ROBERTO L.
PETERSON, JERRY A.
TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
MC3 ANTI-BA6 ANTIBODY, METHODS OF USE THEREOF, AND
METHODS OF HUMANIZING ANTIBODY PEPTIDES
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/956,206A

FILING DATE: 19-APR-2002

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/525,539

FILING DATE: 14-SEP-1995

APPLICATION NUMBER: PCT/US95/11683

FILING DATE: 14-SEP-1995

APPLICATION NUMBER: 08/487,598

FILING DATE: 7-JUNE-1995

APPLICATION NUMBER: 08/307,868

FILING DATE: 16-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: WITT, ERIC

REGISTRATION NUMBER: 44,408

REFERENCE/DOCKET NUMBER: 276332000101

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 813-5600

TELEFAX: (650) 494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 80:

SEQUENCE CHARACTERISTICS:

LENGTH: 113 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 80:

Query Match 88.2%; Score 75; DB 10; Length 113;
Best Local Similarity 88.2%; Pred. No. 7.1e-05;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSSQSVLYSSNNKNYLA 17
Db 24 KSSQSVLYSSNNKNYLA 40

RESULT 14
US-09-995-529-6
Sequence 6, Application US/09995529
Publication No. US2003009655A1
GENERAL INFORMATION:
APPLICANT: Watkins, Jeffrey D.
Huse, William D.
TITLE OF INVENTION: Humanized Collagen Antibodies and
FILE REFERENCE: P-TX 4976
CURRENT APPLICATION NUMBER: US/09/995,529
CURRENT FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 113
TYPE: PRT
ORGANISM: Homo sapiens
US-09-995-529-6

Query Match 88.2%; Score 75; DB 11; Length 113;
Best Local Similarity 88.2%; Pred. No. 7.1e-05;

Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSSQSVLYSANHKNTLA 17
|||||||:|||||
DB 24 KSSQSVLYSSNNKNTLA 40

RESULT 15
US-10-255-478-58

; Sequence 58, Application US/10255478
; Publication No. US20030165498A1

; GENERAL INFORMATION:

; APPLICANT: Mezes, Peter S.

; APPLICANT: Richard, Ruth A.

; APPLICANT: Johnson, Kimberly S.

; APPLICANT: Schiom, Jeffrey

; APPLICANT: Kashmiri, Syed V.S.

; APPLICANT: Shu, Liming

; APPLICANT: Padian, Eduardo A.

; TITLE OF INVENTION: Composite Antibodies of Humanized Human Subgroup IV Light Chain

; FILE REFERENCE: 37777E

; CURRENT APPLICATION NUMBER: US/10/255,478

; PRIOR APPLICATION NUMBER: US/08/961,309

; PRIOR FILING DATE: 1997-10-30

; PRIOR APPLICATION NUMBER: US 60/030,173

; PRIOR FILING DATE: 1996-10-31

; PRIOR APPLICATION NUMBER: US 08/261,354

; PRIOR FILING DATE: 1994-06-16

; PRIOR APPLICATION NUMBER: US 07/964,536

; PRIOR FILING DATE: 1992-10-20

; PRIOR APPLICATION NUMBER: US 07/510,697

; PRIOR FILING DATE: 1990-07-17

; NUMBER OF SEQ ID NOS: 78

; SOFTWARE: Microsoft Word 97 SR-2

; SEQ ID NO: 58

; LENGTH: 134

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: Hum4 VL

; LOCATION: 1..134

; US-10-255-478-58

Query Match 88.2%; Score 75; DB 12; Length 134;

Best Local Similarity 88.2%; Pred. No. 8.5e-05;

Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSSQSVLYSANHKNTLA 17
|||||||:|||||

DB 44 KSSQSVLYSSNNKNTLA 60

Search completed: October 7, 2003, 19:24:24

Job time : 9.7931 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 19:07:11 ; Search time 6.33103 Seconds

(without alignments)
258.231 million cell updates/sec

Title: US-09-988-013a-2_COPY_24_40

Perfect score: 85

Sequence: 1 KSSOSVLYSANHNKNTLA 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	88.2	92	2	Ig kappa chain V r
2	75	88.2	92	2	Ig kappa chain V r
3	75	88.2	92	2	Ig kappa chain V r
4	75	88.2	92	2	Ig kappa chain V r
5	75	88.2	92	2	Ig kappa chain V r
6	75	88.2	92	2	Ig kappa chain V r
7	75	88.2	92	2	Ig kappa chain V r
8	75	88.2	106	2	Ig kappa chain V r
9	75	88.2	113	2	Ig kappa chain V r
10	75	88.2	113	2	Ig kappa chain V r
11	75	88.2	120	2	Ig kappa chain V r
12	75	88.2	121	1	antibody light cha
13	75	88.2	133	1	Ig kappa chain pre
14	75	88.2	134	1	Ig kappa chain pre
15	75	88.2	134	1	anti-sm antibody V
16	74	87.1	103	2	Ig light chain V r
17	74	87.1	103	2	Ig light chain V r
18	73	85.9	114	1	Ig kappa chain V r
19	72	84.7	114	1	Ig kappa chain V-I
20	72	84.7	129	2	Ig kappa chain V-I
21	71	83.5	101	2	Ig kappa chain - h
22	71	83.5	101	2	Ig kappa chain V r
23	71	83.5	112	2	Ig kappa chain V r
24	70	82.4	113	2	Ig kappa chain V r
25	69	81.2	92	2	antitumor monoclon
26	69	81.2	92	2	Ig kappa chain V r
27	68	80.0	134	1	Ig kappa chain pre
28	68	80.0	96	2	Ig kappa chain V r
29	68	80.0	112	2	Ig kappa chain V r
			113	2	Ig kappa chain V r

30	68	80.0	138	2	S26040	Ig kappa chain pre
31	67	78.8	124	2	S40364	Ig kappa chain - h
32	66	77.6	114	2	S44116	Ig kappa chain V-J
33	66	77.6	132	2	S46373	Ig kappa chain V-J
34	66	77.6	240	2	S06084	Ig kappa chain pre
35	65	76.5	102	2	A34153	Ig kappa chain V-I
36	62	72.9	104	2	PH1053	Ig kappa chain V r
37	62	72.9	113	2	JC2270	Ig light chain V r
38	62	72.9	134	2	PC1214	Ig kappa chain pre
39	61	71.8	105	2	C30535	Ig kappa chain V r
40	61	71.8	107	2	G30535	Ig kappa chain V r
41	61	71.8	107	2	D30535	Ig kappa chain V r
42	61	71.8	107	2	F30535	Ig kappa chain V r
43	61	71.8	108	2	E30535	Ig kappa chain V r
44	61	71.8	112	2	E30538	Ig kappa chain V r
45	61	71.8	112	2	F30538	Ig kappa chain V r

ALIGNMENTS

RESULT 1

S37533

Ig kappa chain V region (V-kappa 4) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S37533

R:Klein, U.; Kuipers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993

A:Description: Human IGM(+) IgD(+) cells, the major B cell subset in the peripheral bl

A:Reference number: S37501

A:Accession: S37533

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-92 <KLE>

A:Cross-references: EMBL:226627; NID:g405708; PIDN:CA81380.1; PID:g405709

A:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotrimer; Immunoglobulin

Query Match

88.2%; Score 75; DB 2; Length 92;

Best Local Similarity 88.2%; Pred. No. 1.3e-05;

Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSSOSVLYSANHNKNTLA 17

DB 2 KSSOSVLYSSNNKNTLA 18

RESULT 2

S37530

Ig kappa chain V region (V-kappa 4) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S37530

R:Klein, U.; Kuipers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993

A:Description: Human IGM(+) IgD(+) cells, the major B cell subset in the peripheral bl

A:Reference number: S37501

A:Accession: S37530

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-92 <KLE>

A:Cross-references: EMBL:226630; NID:g405702; PIDN:CA81383.1; PID:g405703

A:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotrimer; Immunoglobulin

Query Match

88.2%; Score 75; DB 2; Length 92;

Best Local Similarity 88.2%; Pred. No. 1.3e-05;

Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSSOSVLYSANHNKNTLA 17

DB 2 KSSOSVLYSSNNKNTLA 18

RESULT 3
S37529
Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37529
R:Klein, U.; Kupepers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human Igm(+) Igd(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37529
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:Z26631; NID:9405700; PIDN:CAA81384.1; PID:9405701
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 88.2%; Score 75; DB 2; Length 92;
Best Local Similarity 88.2%; Pred. No. 1.3e-05;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSSOSVLYSANHKNYLA 17
|||||||:|||||
Db 2 KSSOSVLYSSNNKNYLA 18

RESULT 4
S37535
Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37535
R:Klein, U.; Kupepers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human Igm(+) Igd(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37535
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:Z26625; NID:9405712; PIDN:CAA81378.1; PID:9405713
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 88.2%; Score 75; DB 2; Length 92;
Best Local Similarity 88.2%; Pred. No. 1.3e-05;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSSOSVLYSANHKNYLA 17
|||||||:|||||
Db 2 KSSOSVLYSSNNKNYLA 18

RESULT 5
S37534
Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37534
R:Klein, U.; Kupepers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human Igm(+) Igd(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37534
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:Z26626; NID:9405710; PIDN:CAA81379.1; PID:9405711
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 88.2%; Score 75; DB 2; Length 92;
Best Local Similarity 88.2%; Pred. No. 1.3e-05;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSSOSVLYSANHKNYLA 17
|||||||:|||||
Db 2 KSSOSVLYSSNNKNYLA 18

RESULT 6
S37532
Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37532
R:Klein, U.; Kupepers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human Igm(+) Igd(+) cells, the major B cell subset in the peripheral bl
A:Reference number: S37501
A:Accession: S37532
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:Z26628; NID:9405706; PIDN:CAA81381.1; PID:9405707
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 88.2%; Score 75; DB 2; Length 92;
Best Local Similarity 88.2%; Pred. No. 1.3e-05;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSSOSVLYSANHKNYLA 17
|||||||:|||||
Db 2 KSSOSVLYSSNNKNYLA 18

RESULT 7
A49138
IGA kappa rheumatoid factor variable - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A49138
R:Gause, A.; Kupepers, R.; Mierau, R.
Clin. Exp. Immunol. 88, 430-434, 1992
A:Title: A somatically mutated V kappa IV gene encoding a human rheumatoid factor 11g
A:Reference number: A49138; MUID:92298590; PMID:1606727
A:Accession: A49138
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-106 <GAU>
A:Cross-references: GB:S37926; NID:9298207; PIDN:AAB22366.1; PID:9298208
A:Note: sequence inconsistent with the nucleotide translation
C:Note: sequence extracted from NCI backbone (NCBI:106633, NCBI:P106637)
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
F:20-99/Domain: Immunoglobulin homology <IM>

Query Match 88.2%; Score 75; DB 2; Length 106;
Best Local Similarity 88.2%; Pred. No. 1.5e-05;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSSOSVLYSANHKNYLA 17
|||||||:|||||
Db 28 KSSOSVLYSSNNKNYLA 44

RESULT 8
S30523
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S30523
R:Marlette, X.

submitted to the EMBL Data Library, October 1992
A:Reference number: S30520

A:Accession: S30523

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 <MAR>

A:Cross-references: EMBL:Z18329

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-96/Domain: immunoglobulin homology <IMM>

Query Match

88.2%; Score 75; DB 2; Length 113;

Best Local Similarity 88.2%; Pred. No. 1.6e-05;

Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSSOSVLYSANHKNTLA 17

|||||||:|:|||||

DB 24 KSSOSVLYSSNNKNTLA 40

RESULT 9

S34003

Ig kappa chain V region - human

C:Species: Homo sapiens (man)

C>Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: S34003

R:Marlette, X.; Tsapis, A.; Brouet, J.C.

Eur. J. Immunol. 23, 846-851, 1993

A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal

A:Reference number: S34001; MUID:93209281; PMID:7681398

A:Accession: S34003

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 <MAR>

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-96/Domain: immunoglobulin homology <IMM>

Query Match

88.2%; Score 75; DB 2; Length 113;

Best Local Similarity 88.2%; Pred. No. 1.6e-05;

Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSSOSVLYSANHKNTLA 17

|||||||:|:|||||

DB 24 KSSOSVLYSSNNKNTLA 40

RESULT 10

S34002

Ig kappa chain V region - human

C:Species: Homo sapiens (man)

C>Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: S34002; S30522

R:Marlette, X.; Tsapis, A.; Brouet, J.C.

Eur. J. Immunol. 23, 846-851, 1993

A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal

A:Reference number: S34001; MUID:93209281; PMID:7681398

A:Accession: S34002

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 <MAR>

A:Cross-references: EMBL:Z18328

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-96/Domain: immunoglobulin homology <IMM>

Query Match

88.2%; Score 75; DB 2; Length 113;

Best Local Similarity 88.2%; Pred. No. 1.6e-05;

Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSSOSVLYSANHKNTLA 17

|||||||:|:|||||

DB 24 KSSOSVLYSSNNKNTLA 40

RESULT 11

S51147

antibody light chain V region - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000

C:Accession: S51147

R:de Kruijf, J.; Boel, E.; Logtenberg, T.

submitted to the EMBL Data Library, January 1995

A:Description: Selection and application of human SCFV antibody fragments from a semi

A:Reference number: S51147

A:Accession: S51147

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-120 <DEK>

A:Cross-references: EMBL:X83714; NID:9633227; PIDN:CAA56689.1; PID:9633228

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

F:16-96/Domain: immunoglobulin homology <IMM>

Query Match

88.2%; Score 75; DB 2; Length 120;

Best Local Similarity 88.2%; Pred. No. 1.7e-05;

Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSSOSVLYSANHKNTLA 17

|||||||:|:|||||

DB 24 KSSOSVLYSSNNKNTLA 40

RESULT 12

K4H0

Ig kappa chain precursor V-IV region - human

C:Species: Homo sapiens (man)

C>Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Aug-1996

C:Accession: A01902

R:Klobeck, H.G.; Bornkamm, G.W.; Combrato, G.; Mocikat, R.; Pohlenz, H.D.; Zachau, H

Nucleic Acids Res. 13, 6515-6529, 1985

A:Title: Subgroup IV of human immunoglobulin K light chains is encoded by a single ge

A:Reference number: A93589; MUID:86041853; PMID:2997712

A:Accession: A01902

A:Molecule type: DNA

A:Residues: 1-121 <KLO>

A:Note: the sequence was determined from the germline gene

A:Note: there is only one Ig kappa V-IV gene

C:Genetics:

A:introns: 17/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-121/Product: Ig kappa chain precursor V-IV region #status predicted <MAT>

F:21-43/Region: framework 1

F:36-116/Domain: immunoglobulin homology <IMM>

F:44-60/Region: complementarity-determining 1

F:61-75/Region: framework 2

F:76-82/Region: complementarity-determining 2

F:83-114/Region: framework 3

F:115-121/Region: complementarity-determining 3

F:43-114/Disulfide bonds: #status predicted

Query Match

88.2%; Score 75; DB 1; Length 121;

Best Local Similarity 88.2%; Pred. No. 1.7e-05;

Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSSOSVLYSANHKNTLA 17

|||||||:|:|||||

DB 44 KSSOSVLYSSNNKNTLA 60

RESULT 13

K4H0U1

Ig kappa chain precursor V-IV region (J1) - human

C/Species: Homo sapiens (man)
 C/Date: 30-Jun-1987 #sequence-revision 30-Jun-1987 #text-change 21-Jan-2000
 C/Accession: A01904
 R:Klobeck, H.G.; Bornkamm, G.W.; Combrlato, G.; Moolkat, R.; Pohlentz, H.D.; Zachau, H.G.
 Nucleic Acids Res. 13, 6515-6529, 1985
 A/Title: Subgroup IV of human immunoglobulin K light chains is encoded by a single gene
 A/Reference number: A93589; MID:86041853; PMID:297712
 A/Accession: A01904
 A/Molecule type: DNA
 A/Residues: 1-133 <RIO>
 A/Cross-references: GB:200022; GB:X51570; NID:933158; PIDN:CA477317.1; PID:9296554
 A/Note: the sequence was determined from the differentiated gene
 C/Genetics:
 A/Gene: GDB:IGKV
 A/Cross-references: GDB:119341; OMIM:146980
 A/Map position: 2p12-2p12
 A/Intons: 17/1
 C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16 C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C/Keywords: heterotetramer; Immunoglobulin
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-133/Product: Ig kappa chain V-IV region (JI) #status predicted <MAT>
 F:21-43/Region: framework 1
 F:36-116/Domain: immunoglobulin homology <IMM>
 F:44-60/Region: complementarity-determining 1
 F:61-75/Region: framework 2
 F:76-82/Region: complementarity-determining 2
 F:83-114/Region: framework 3
 F:115-122/Region: complementarity-determining 3
 F:123-133/Region: framework 4
 F:43-114/Disulfide bonds: #status predicted

Query Match 88.2%; Score 75; DB 1; Length 133;
 Best Local Similarity 88.2%; Pred. No. 1.9e-05;
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSSOSVLYSSNNKNYLA 17
 DB 44 KSSOSVLYSSNNKNYLA 60

RESULT 14
 S49531
 anti-Sm antibody VL chain (V kappa 4/J kappa 3) - human
 C/Species: Homo sapiens (man)
 C/Date: 01-Feb-1995 #sequence-revision 12-May-1995 #text-change 21-Jan-2000
 C/Accession: S49531
 R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
 submitted to the EMBL Data Library, October 1994
 A/Description: Molecular characterization of natural human anti-Sm autoantibodies.
 A/Reference number: S48797
 A/Accession: S49531
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-134 <MAH>
 A/Cross-references: EMBL:S46347; NID:9560841; PIDN:CA486466.1; PID:9560842
 C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
 F:36-116/Domain: immunoglobulin homology <IMM>

Query Match 88.2%; Score 75; DB 2; Length 134;
 Best Local Similarity 88.2%; Pred. No. 1.9e-05;
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSSOSVLYSSNNKNYLA 17
 DB 44 KSSOSVLYSSNNKNYLA 60

RESULT 15
 S26337
 Ig light chain V region - mouse (fragment)
 C/Species: Mus musculus (house mouse)

C/Date: 19-Mar-1998 #sequence-revision 19-Mar-1998 #text-change 20-Jun-2000
 C/Accession: S26337; S78449
 R:Stark, S.E.; Caton, A.J.
 J. Exp. Med. 174, 613-624, 1991
 A/Title: Antibodies that are specific for a single amino acid interchange in a protein
 A/Reference number: S26309; MID:91341421; PMID:1908510
 A/Accession: S26337
 A/Molecule type: mRNA
 A/Residues: 1-101 <STA>
 A/Cross-references: EMBL:X59193
 R:Caton, A.J.
 submitted to the EMBL Data Library, April 1991
 A/Reference number: S78447
 A/Accession: S78449
 A/Molecule type: mRNA
 A/Residues: 1-60, 'T', 'G', 'S', '93-101 <CAT>
 A/Cross-references: EMBL:X59193; NID:952323; PIDN:CA441903.1; PID:91334067
 C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C/Keywords: heterotetramer; Immunoglobulin
 F:8-88/Domain: immunoglobulin homology <IMM>

Query Match 87.1%; Score 74; DB 2; Length 101;
 Best Local Similarity 88.2%; Pred. No. 2.1e-05;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSSOSVLYSSNNKNYLA 17
 DB 16 KSSOSVLYSSNNKNYLA 32

Search completed: October 7, 2003, 19:21:47
 Job time: 6.33103 secs

Query Match 88.2%; Score 75; DB 1; Length 121;
 Best Local Similarity 88.2%; Pred. No. 2.7e-06;
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSSOSVLYSANHKNYLA 17
 |||||||:|||||
 DB 44 KSSOSVLYSSNNKNYLA 60

RESULT 2

KV4B_HUMAN STANDARD; PRT; 133 AA.
 ID KV4B_HUMAN
 AC P06313;
 DT 01-JAN-1988 (rel. 06, Created)
 DT 01-JAN-1988 (rel. 06, Last sequence update)
 DT 15-JUL-1999 (rel. 38, Last annotation update)
 DE Ig kappa chain V-IV region JI precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-86041653; PubMed-2997712;
 RA Klobbeck H.G., Borikamm G.W., Combrato G., Mocklat R., Pohlenz H.D.,
 RA Zachau H.G.;
 RT Supergroup IV of human immunoglobulin K light chains is encoded by a
 RT single germline gene.
 RL Nucleic Acids Res. 13:6515-6529(1985).

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CC EMBL: 200022; CAA77317.1; -
 CC PIR: A01904; K4H0J1.
 DR HSSP; P80362; 1MTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; P:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 DR Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 1 133 IG KAPPA CHAIN V-IV REGION JI.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 61 75 FRAMEWORK-2.
 FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 83 114 FRAMEWORK-3.
 FT DOMAIN 115 122 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 123 132 FRAMEWORK-4.
 FT DISULFID 43 114 BY SIMILARITY.
 FT NON_TER 133 133
 SQ SEQUENCE 133 AA; 14632 MW; 5FB3953066744AF4 CRC64;

Query Match 88.2%; Score 75; DB 1; Length 133;
 Best Local Similarity 88.2%; Pred. No. 3e-06;
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSSOSVLYSANHKNYLA 17
 |||||||:|||||
 DB 44 KSSOSVLYSSNNKNYLA 60

RESULT 3
 KV4A_HUMAN STANDARD; PRT; 114 AA.
 ID KV4A_HUMAN
 AC P01625;
 DT 21-JUL-1986 (rel. 01, Created)
 DT 01-OCT-1996 (rel. 34, Last sequence update)
 DT 15-SEP-2003 (rel. 42, Last annotation update)
 DE Ig kappa chain V-IV region Len.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE-76004342; PubMed-50995;
 RA Schneider M., Hilemann N.;
 RT "The primary structure of a monoclonic immunoglobulin-L-chain of
 RT subgroup IV of the kappa type (Bence-Jones protein Len).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
 RN [2]
 RP REVISION TO 9.
 RA Salomon A.;
 RL Submitted (Aug-1996) to the SWISS-PROT data bank.

CC -1 MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1 MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PDB; 1EEQ; 01-FEB-01.
 DR PDB; 1EEU; 03-FEB-01.
 DR PDB; 1EFQ; 09-FEB-01.
 DR PDB; 1EK3; 06-MAR-01.
 DR PDB; 1LVE; 21-JAN-98.
 DR PDB; 3LVE; 18-MAY-99.
 DR PDB; 5LVE; 28-MAR-01.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; P:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 DR Immunoglobulin V region; Bence-Jones protein; 3D-structure.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 40 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 41 55 FRAMEWORK-2.
 FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 63 94 FRAMEWORK-3.
 FT DOMAIN 95 101 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 102 113 FRAMEWORK-4.
 FT DISULFID 23 94 BY SIMILARITY.
 FT NON_TER 114 114
 SQ SEQUENCE 114 AA; 12640 MW; 0647FD17E236485 CRC64;

Query Match 85.9%; Score 73; DB 1; Length 114;
 Best Local Similarity 88.2%; Pred. No. 5.6e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSSOSVLYSANHKNYLA 17
 |||||||:|||||
 DB 24 KSSOSVLYSSNNKNYLA 40

RESULT 4

KV4D_HUMAN STANDARD; PRT; 109 AA.
 ID KV4D_HUMAN
 AC P83593;
 DT 15-SEP-2003 (rel. 42, Created)
 DT 15-SEP-2003 (rel. 42, Last sequence update)
 DT 15-SEP-2003 (rel. 42, Last annotation update)
 DE Ig kappa chain V-IV region 5TH (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Abdominal adipose tissue;
RX PubMed=9588180;
RA Olsen K.E., Sletten K., Westermarck P.;
RT "Extended analysis of AL-amyloid protein from abdominal wall
  subcutaneous fat biopsy: kappa IV immunoglobulin light chain.";
RL Biochem. Biophys. Res. Commun. 245:713-716(1998).
CC -1- FUNCTION: May play an important role in fibrillogenesis.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG_1.
DR PROSITE: PS50835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 40 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 41 55 FRAMEWORK-2.
FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 63 94 FRAMEWORK-3.
FT DOMAIN 95 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 109 FRAMEWORK-4.
FT DISULFD 23 94 BY SIMILARITY.
FT UNSURE 23 23
FT UNSURE 94 94
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 12060 MW; 0C4F31EA11E12A0B CRC64;

Query Match 84.7%; Score 72; DB 1; Length 109;
Best Local Similarity 82.4%; Pred. No. 8.1e-06;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSSOSVLXSNHKNYLA 17
Db 24 KSSOSVLXSNHKNYLA 40
:|||||:|||||

RESULT 5
KV4C_HUMAN STANDARD; PRT; 134 AA.
ID P06314;
DC 01-JAN-1988 (Rel. 05, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region B17 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041854; PubMed=2997713;
RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned
  cDNA probe.";
RL Nucleic Acids Res. 13:6531-6544(1985).
RN [2]
RP REVISION TO 76.
RA Marsh P.;
RL Submitted (OCT-1986) to the EMBL/Genbank/DBJ databases.
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CC EMBL: X02990; CAA26733.1; -.
DR HSSP: P80362; IWTI.

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DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 134 IG KAPPA CHAIN V-IV REGION B17.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 122 133 FRAMEWORK-4.
FT DISULFD 43 114 BY SIMILARITY.
FT NON_TER 134 134
SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD0738832 CRC64;

Query Match 81.2%; Score 69; DB 1; Length 134;
Best Local Similarity 76.5%; Pred. No. 3.4e-05;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSSOSVLXSNHKNYLA 17
Db 44 KSSOSVLXSNHKNYLA 60
:|||||:|||||

RESULT 6
PDRF_YEAST STANDARD; PRT; 1529 AA.
ID PDRF_YEAST
AC 004182;
DC 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ATP-dependent permease PDR15.
GN PDR15 OR YDR406W OR D9509.24.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
  Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Dietrich F.S., Milligan J., Allen E., Araujo R., Aviles E., Beino A.,
  Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M.,
  Hunkeler-Smith S., Hyman R., Kamp C., Laskhari D., Lew H., Lin D.,
  Muscedale D., Nakahara K., Namath A., Oefner P., Oh C., Patel F.X.,
  Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N.,
  Winant A., Yellon M., Botstein D., Davis R.W.;
RL Submitted (AUG-1995) to the EMBL/Genbank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. PDR5 SUBFAMILY.
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  or send an email to license@isb-sib.ch).
CC EMBL: U32274; AAB64846.1; -.
DR PIR: S69686; S69688.
DR SGD: S0002814; PDR15.
DR InterPro: IPR003593; AAA_Artpase.
DR InterPro: IPR003439; ABC_transporter.
DR InterPro: IPR005285; PDR.
DR Pfam: PF00005; ABC_tran; 2.
DR ProDom: PD000006; ABC_transporter; 2.

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DR SMART: SM00382; AAA; 2.
 DR TIGR00956; ABC_TRANSPORTER_1; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER_2; 2.
 DR KATP-binding; Transmembrane; Glycoprotein; Transport.
 FT DOMAIN 1 531 POTENTIAL.
 FT TRANSMEM 532 552 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 566 588 POTENTIAL.
 FT TRANSMEM 618 638 POTENTIAL.
 FT TRANSMEM 643 663 POTENTIAL.
 FT TRANSMEM 700 720 POTENTIAL.
 FT TRANSMEM 784 804 POTENTIAL.
 FT DOMAIN 805 1219 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1220 1240 POTENTIAL.
 FT TRANSMEM 1313 1333 POTENTIAL.
 FT TRANSMEM 1341 1361 POTENTIAL.
 FT TRANSMEM 1369 1389 POTENTIAL.
 FT TRANSMEM 1397 1417 POTENTIAL.
 FT TRANSMEM 1493 1513 POTENTIAL.
 FT DOMAIN 1514 1529 CYTOPLASMIC (POTENTIAL).
 FT NP_BIND 920 927 ATP (POTENTIAL).
 FT DOMAIN 13 24 POLY-SER.
 FT DOMAIN 66 69 POLY-SER.
 FT DOMAIN 794 797 POLY-PHE.
 FT CARBOHYD 558 558 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 744 744 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 1529 AA; 172255 MW; DB58FB2E0534974 CRC64;

Query Match 49.4%; Score 42; DB 1; Length 1529;
 Best Local Similarity 61.5%; Pred. No. 31;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 SSOVSYSANHNK 14
 DB 53 TSOSLYTANSNN 65

RESULT 7
 YG2L_YEAST STANDARD; PRT; 1237 AA.
 AC P53254;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Hypothetical 140.5 kDa protein in CTR1-PRP31 intergenic region.
 GN YG000W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_Taxid=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wedler H., Scharfe M., Wedler E., Wambutt R.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Hernandez K., Weber N., Wipfl P., Schmidheini T.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY TO S.POMBE SPBC776.08C.
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 CC -----
 CC EMBL: 272875; CA97093.1; -
 CC FIR: S64385; S64385.
 CC SGD: S0003322; YG0090W.
 CC InterPro: IPR005554; Nrap.
 CC Pfam: PF03813; Nrap; 1.

KW Hypothetical protein.
 SQ SEQUENCE 1237 AA; 140484 MW; 9A2B5C885493D7D3 CRC64;
 Query Match 48.2%; Score 41; DB 1; Length 1237;
 Best Local Similarity 66.7%; Pred. No. 37;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 SYLYSANHNKYL 16
 DB 335 SYLSSTHENYL 346

RESULT 8
 PICE_MOUSE STANDARD; PRT; 365 AA.
 ID PICE_MOUSE
 AC Q9DLE8; Q8BG61; Q8CGN6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 1-acyl-sn-glycerol-3-phosphate acyltransferase epsilon (EC 2.3.1.51)
 DE (1-AGP acyltransferase 5) (1-AGPAT 5) (Lygophosphatidic acid
 DE acyltransferase-epsilon) (LPAAT-epsilon) (1-acylglycerol-3-phosphate
 DE O-acyltransferase 5).
 GN AGPAT5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NMRI;
 RA Lu B., Jiang Y.J., Chan M., Choy P.C.;
 RT Identification and characterization of 1-acylglycerolphosphate
 RT acyltransferase-epsilon.
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J, and NOD; TISSUE=Cerebellum, Embryo, and Spleen;
 RX MEDLINE=22354683; PubMed=12466851;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamana H., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Balderelli R., Hill D.P., Bolt C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chochua C., Cordani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Perle G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempé C.A., Seton M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wysshaw-Boris A., Yanagisawa M., Yang L., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume T., Fukuda S.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arikawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.
 RL Nature 420:563-573(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Czech II; TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Lauber J, Duesterhoeft A, Beyer A, Koehrer K, Strack N,
 RA Mewe H, W, Ottenwaelder B, Obermaier B, Tampe J, Heubner D.,
 RA Wambutt R, Korn B, Klein M, Pouska A.;
 RA "Towards a catalog of human genes and proteins: sequencing and
 RA analysis of 500 novel complete protein coding human cDNAs.";
 RA Genome Res. 11:422-435(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Placenta;
 RA Isogai T, Ota T, Hayashi K, Sugiyama T, Otsuki T, Suzuki Y.,
 RA Nishikawa T, Nagai K, Sugano S, Shiratori A, Sudo H.,
 RA Magatsuna M, Hosogi T, Faku Y, Kodaira H, Kondo H, Sugawara M.,
 RA Takahashi M, Chiba Y, Ishida S, Murakawa K, Ono Y, Takiguchi S.,
 RA Watanabe S, Kimura K, Murakami K, Ishii S, Kawai Y, Saito K.,
 RA Yamamoto J, Wakamatsu A, Nakamura Y, Nagahara K, Masuno Y.,
 RA Ninomiya K, Iwayanagi T.;
 RA "NEO human cDNA sequencing project.";
 RA Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RA MEDLINE=2238257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B, Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H, Moore T, Max S.I., Wang J., Hsieh F.,
 RA Ditschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo W.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uscid T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millhys S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RA and mouse cDNA sequences.";
 RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: CONVERTS LYSCOPHOSPHATIDIC ACID (LPA) INTO PHOSPHATIDIC
 CC ACID BY INCORPORATING ACYL MOIETY AT THE 2 POSITION (BY
 CC SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Acyl-CoA + 1-acyl-sn-glycerol 3-phosphate =
 CC CoA + 1,2-diacyl-sn-glycerol 3-phosphate.
 CC -1- PATHWAY: De novo phospholipid biosynthesis; second step.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: BELONGS TO THE 1-ACYL-SN-GLYCEROL-3-PHOSPHATE
 CC ACYLTRANSFERASE FAMILY.
 CC -1- CAUTION: It is uncertain whether Met-1 or Met-12 is the initiator.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AF375789; AK54809.1; -;
 CC EMBL: AL136587; CAB66522.1; -;
 CC EMBL: AK002072; BAA92069.1; ALT_INIT.
 CC EMBL: BC023550; AA823550.1; -;
 CC InterPro: IPR002123; Acyltransferase.
 CC Pfam: PF01553; Acyltransferase; 1.
 CC SMART: SM00563; PISC; 1.
 CC Phospholipid biosynthesis; Transferase; Acyltransferase;
 CC Transmembrane.
 KM TRANSMEM 15 35 POTENTIAL.
 FT TRANSMEM 61 81 POTENTIAL.
 FT TRANSMEM 344 364 POTENTIAL.

FT CONFLICT 156 156 L -> V (IN REF. 2 AND 4).
 SQ SEQUENCE 364 AA; 42072 MW; 90A0F87FC7C78081 CRC64;
 Query Match 45.9%; Score 39; DB 1; Length 364;
 Best Local Similarity 35.7%; Pred. NO. 22;
 Matches 5; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KSSQSVLYSANRKN 14
 Db 82 KKNENITVLANHQS 95
 : : : : :
 ID SYG_BOMMO STANDARD; PRT; 680 AA.
 AC 004451;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Glycyl-tRNA synthetase (EC 6.1.1.14) (Glycine-tRNA ligase) (GLYRS).
 OS Bombyx mori (Silk moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
 OC Bombycidae; Bombyx.
 OC NCBI_TaxID=7091;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RA MEDLINE=93216727; PubMed=8463296;
 RA Nada S., Chang P.K., Dignam J.D.;
 RT "Primary structure of the gene for glycyl-tRNA synthetase from Bombyx
 RT mori";
 RT J. Biol. Chem. 268:7660-7667(1993).
 CC -1- CATALYTIC ACTIVITY: ATP + glycine + tRNA(Gly) = AMP + diphosphate
 CC + glycyl-tRNA(Gly).
 CC -1- SUBUNIT: Homodimer.
 CC -1- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
 CC -1- SIMILARITY: Contains 1 WHEP-TRS domain.
 CC
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 CC
 CC EMBL: L08106; AA62231.1; -;
 CC HSSP: P56206; IAT1.
 CC InterPro: IPR004154; HGRP_antlicodon.
 CC InterPro: IPR002314; tRNA-synt_2b.
 CC InterPro: IPR002315; tRNA-synt_gly.
 CC InterPro: IPR006195; tRNA_ligase_II.
 CC InterPro: IPR000738; WHEP-TRS.
 CC Pfam: PF03129; HGRP_antlicodon; 1.
 CC Pfam: PF00587; tRNA-synt_2b; 1.
 CC Pfam: PF00458; WHEP-TRS; 1.
 CC PRINTS: PR01043; TRNASYNTGLY.
 CC TIGRPFAM: TIGR00389; glys_dimeric; 1.
 CC PROSITE: PS00862; AA_tRNA_LIGASE_II; 1.
 CC PROSITE: PS00762; WHEP-TRS; 1.
 KM Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
 FT DOMAIN 20 65 WHEP-TRS.
 SQ SEQUENCE 680 AA; 76920 MW; 59118DA04922672F CRC64;
 QY 1 KSSQSVLYSANRKN 13
 Db 313 KNTQSLVLSADNQ 325
 : : : : :
 Query Match 45.9%; Score 39; DB 1; Length 680;
 Best Local Similarity 53.8%; Pred. NO. 43;
 Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

RESULT 12
 SM4F_HUMAN STANDARD; PRT; 770 AA.
 ID SM4F_HUMAN
 AC 095754; 09NS35; 39, Created
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Semaphorin 4F precursor (Semaphorin W) (Sema W) (Semaphorin M) (Sema M).
 GN SEMA4F OR SEMA4F OR SEMA4F
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A. (ISOFORM SMALL).
 RP TISSUE-Brain.
 RX MEDLINE=99162633; PubMed=10051670;
 RA Eclins J.A., Kikuchi K., Chedotal A., de Castro F., Goodman C.S., Kimura T.;
 RT "Cloning, expression, and genetic mapping of Sema W, a member of the semaphorin family.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:2491-2496(1999).
 [2]
 RP SEQUENCE FROM N.A. (ISOFORM LONG).
 RA Chen F., Do A., Do T., Weisler M., Roe B.A.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 [3]
 RP SEQUENCE FROM N.A. (ISOFORM LONG).
 RC TISSUE-Amygdala;
 RX MEDLINE=21154917; PubMed=11230166;
 RA Wiemann S., Well B., Wellenreuther R., Gassenhuber J., Giesel S., Ansgor W., Boecker M., Bloeker H., Bauersachs S., Blum H., Lauber J., Duesterhoeft A., Beyer A., Koehler K., Strack N., Mewes H.-W., Ottenwelder B., Oberwiler B., Tampe J., Heubner D., Wambut R., Korn B., Klein M., Poustka A.;
 RT "Towards a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs.";
 RL Genome Res. 11:422-435(2001).
 [4]
 RP SEQUENCE OF 347-770 FROM N.A.
 RA Jang W., Spilson S.V., Hua A., Roe B., Weisler M.H.;
 RT "Large-scale comparative sequence analysis of human and mouse genomic DNA in the mm2 region of mouse chromosome 6 reveals coding regions of three new genes.";
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: HAS GROWTH CONE COLLAPSE ACTIVITY AGAINST RETINAL GANGLION-CELL AXONS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms-2;
 CC Name-Long;
 CC IsoId=095754-1; Sequence=Displayed;
 CC Name-Short;
 CC IsoId=095754-2; Sequence=VSP_006043;
 CC -1- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
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 CC -----
 DR EMBL; AB022317; BAA75631.1; -
 DR EMBL; AC006544; -; NOT_ANNOTATED_CDS.
 DR EMBL; AL136552; CAB66487.1; -
 DR EMBL; AF053369; AAF80660.1; -
 DR Gene; HGNC:10734; SEMA4F.
 DR MIM; 603706; -

DR GO; GO:0005887; C:Integral to plasma membrane; TAS.
 DR GO; GO:0005624; C:membrane fraction; TAS.
 DR GO; GO:0007411; P:axon guidance; TAS.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR GO; GO:0007399; P:neurogenesis; TAS.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 KW Signal; Transmembrane; Immunoglobulin domain; Multigene family;
 KW Neurogenesis; Developmental protein; Glycoprotein;
 KW Alternative splicing.
 FT SIGNAL 1 34 POTENTIAL.
 FT CHAIN 35 770 SEMAPHORIN 4F.
 FT DOMAIN 35 659 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 660 680 POTENTIAL.
 FT DOMAIN 681 770 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 65 496 SEMA.
 FT DOMAIN 512 563 PSI.
 FT DOMAIN 580 635 IG-LIKE C2-TYPE.
 FT DISULFD 587 628 BY SIMILARITY.
 FT CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 509 509 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPIC 120 274 Missing (in isoform short).
 FT FTID=VSP_006043.
 FT S -> N (IN REF. 1).
 FT CONFLICT 533 533 S -> N (IN REF. 1).
 FT SEQUENCE 770 AA; 83511 MW; CFB974B41DF09C8 CRC64;
 Query Match 45.9%; Score 39; DB 1; Length 770;
 Best Local Similarity 72.7%; Pred. No. 50;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Oy 6 VLYSANRKNYL 16
 |||:| |||
 Db 186 VLYAATVKNYL 196
 RESULT 13
 CDH_PHACH STANDARD; PRT; 773 AA.
 ID CDH_PHACH
 AC 001738; 000047;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Cellulose dehydrogenase precursor (EC 1.1.99.18) (CDH) (Cellulose-dehydrogenase)
 GN CDH-1 AND CDH-2.
 OS Phanerochaete chrysosporium.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes; Aphyllophorales; Corticiaceae; Phanerochaete.
 NC NCBL_TaxID=5306;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-OGC101;
 RX MEDLINE=97077226; PubMed=8919793;
 RA Li B., Nagalla S.R., Renganathan V.;
 RT "Cloning of a cDNA encoding cellulose dehydrogenase, a hemoflavoenzyme from Phanerochaete chrysosporium.";
 RL Appl. Environ. Microbiol. 62:1329-1335(1996).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-OGC101;
 RX MEDLINE=97176414; PubMed=9023960;
 RA Li B., Nagalla S.R., Renganathan V.;
 RT "Cellulose dehydrogenase from Phanerochaete chrysosporium is encoded by two allelic variants.";
 RL Appl. Environ. Microbiol. 63:796-799(1997).
 [3]
 RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 19-208.

RA MEDLINE-20139694; PubMed-10673428;
RA Halberg B.M., Bergfors T., Boeckro K., Petersson G., Henriksson G.,
RA Dine C.;
RT "A new scaffold for binding haem in the cytochrome domain of the
RT extracellular flavocytochrome cellobiose dehydrogenase.";
RL Structure 8:79-88(2000).
CC -1- FUNCTION: Degrades both lignin and cellobiose. Oxidizes cellobiose
CC to cellobionolactone.
CC -1- CATALYTIC ACTIVITY: cellobiose + acceptor = cellobiono-1,5-lactone
CC + reduced acceptor.
CC -1- COFACTOR: Binds 1 FAD, 1 HEME and 1 Iron ion per subunit.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: IN THE C-TERMINAL SECTION, BELONGS TO THE GMC
CC OXIDOREDUCTASES FAMILY.
CC -----
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CC -----
CC EMBL: U46081; AAC49277.1; -
CC EMBL: U65888; AAB61455.1; -
CC EMBL: U50409; AAB92262.1; -
CC PDB: 1D7B; 18-OCT-99.
CC PDB: 1D7C; 18-OCT-99.
CC PDB: 1D7D; 18-OCT-99.
CC PDB: 1KDG; 13-NOV-02.
CC PDB: 1NAA; 14-JAN-03.
CC InterPro: IPR000172; GMC_oxred.
CC InterPro: IPR001100; Pyr_redox.
CC Pfam: PF05199; GMC_oxred_C; 1.
CC Pfam: PF00732; GMC_oxred_N; 1.
CC PRINTS: PR00411; PNDRTASE1.
CC PROSITE: PS00623; GMC_OXRED_1; 1.
CC PROSITE: PS00624; GMC_OXRED_2; 1.
CC Cellulose degradation; Oxidoreductase; FAD; Flavoprotein; Heme;
CC Multigene family; Signal; 3D-structure.
CC SIGNAL 1 18
CC CHAIN 19 773 CELLOBIOSE DEHYDROGENASE.
CC DOMAIN 19 208 HEME DOMAIN.
CC METAL 235 773 OXIDOREDUCTASE.
CC METAL 83 83 IRON (HEME AXIAL LIGAND).
CC METAL 181 181 IRON (HEME AXIAL LIGAND).
CC NE_BIND 236 265 FAD (ADP PART) (POTENTIAL).
CC STRAND 20 20
CC STRAND 22 22
CC TURN 27 29
CC STRAND 32 38
CC STRAND 39 42
CC STRAND 43 49
CC STRAND 62 69
CC TURN 70 71
CC STRAND 74 78
CC TURN 79 80
CC STRAND 88 94
CC TURN 95 96
CC STRAND 97 104
CC STRAND 112 113
CC STRAND 119 122
CC TURN 124 125
CC STRAND 127 128
CC STRAND 132 140
CC TURN 141 141
CC STRAND 144 144
CC TURN 146 147
CC STRAND 150 150
CC TURN 153 154
CC STRAND 156 164
CC TURN 171 172
CC TURN 174 175

FT STRAND 183 190
FT HELIX 191 193
FT STRAND 195 195
FT TURN 197 198
FT HELIX 199 203
FT TURN 204 205
SQ SEQUENCE 773 AA; 82007 MW; 54F721E779AA4D7B CRC64;
Query Match 45.9%; Score 39; DB 1; Length 773;
Best Local Similarity 58.3%; Pred. No. 50;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 5 SVLYSANHNYL 16
DB 192 STAHSAANYNYL 203
RESULT 14
KV2E_HUMAN STANDARD; PRT; 117 AA.
ID KV2E_HUMAN
AC P06309;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 19 kappa chain V-II region G607 precursor (fragment).
OS Homo sapiens (Human).
OC Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-84191506; PubMed-6325927;
RA Klobbeck H.G., Solomon A., Zachau H.G.;
RT "Contribution of human V kappa II germ-line genes to light-chain
RT diversity.";
RL Nature 309:73-76(1984).
CC -----
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CC -----
CC EMBL: Z00009; -; NOT_ANNOTATED_CDS.
CC PIR: A01889; K2HDGM.
CC HSSP: P80362; 1MTL.
CC GO: GO:0005576; C:extracellular; NAS.
CC GO: GO:0003823; F:antigen binding activity; NAS.
CC GO: GO:0006955; P:immune response; NAS.
CC InterPro: IPR007110; Ig_Like.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003596; Ig_V.
CC Pfam: PF00047; Ig_1.
CC SMART: SM00406; IGV_1.
CC PROSITE: PS0835; IG_Like; 1.
CC Immunoglobulin V region; Signal.
CC KW NON_TER 1
CC FT SIGNAL 1 4
CC FT CHAIN 5 117 IG KAPPA CHAIN V-II REGION G607.
CC FT DOMAIN 5 27 COMPLEMENTARITY-DETERMINING-1.
CC FT DOMAIN 28 43 COMPLEMENTARITY-DETERMINING-2.
CC FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING-3.
CC FT DOMAIN 59 65 COMPLEMENTARITY-DETERMINING-4.
CC FT DOMAIN 66 97 FRAMEWORK-2.
CC FT DOMAIN 98 106 FRAMEWORK-3.
CC FT DOMAIN 107 116 FRAMEWORK-4.
CC FT DISULFID 27 97 BY SIMILARITY.
CC FT NON_TER 117
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;
Query Match 45.3%; Score 38.5; DB 1; Length 117;

Best Local Similarity 62.5%; Pred. No. 7.5;
Matches 10; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 KSSQSVLYSANHKNYL 16
:||||:| | | |
Db 28 RSSQSLHNS-NGNYL 42

RESULT 15

RECX_CLOAB

ID RCX_CLOAB STANDARD; PRT; 214 AA.

AC 097GF7;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Regulatory protein reex.

GN RCX OR CAC2410.

OS Clostridium acetobutylicum.

OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;

OC Clostridium.

OX NCBI_TaxID=1488;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;

RA MEDLINE-21359325; PubMed-11466286;

RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,

RA Gibson R., Lee H.M., Dubois J., Qiu D., Hill J., Wolf Y.I.,

RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

RA Bennett G.N., Koonin E.V., Smith D.R.;

RT Genome sequence and comparative analysis of the solvent-producing

RT bacterium Clostridium acetobutylicum.

RL J. Bacteriol. 183:4823-4838(2001).

CC - FUNCTION: Modulates reca activity (By similarity).

CC - SUBCELLULAR LOCATION: Cytoplasmic (Potential).

CC - SIMILARITY: BELONGS TO THE RCX FAMILY.

CC -----

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CC -----

CC EMBL: AE007741; AAK80365.1; -

DR PIR: B97197; B97197.

DR HAMAP: MF_01114; -; 1.

DR InterPro: IPR003783; RCX.

DR Pfam: PF02631; RCX; 1.

KW Complete proteome.

SQ SEQUENCE 214 AA; 25501 MW; 3957D81B7FE9B4AB CRC64;

QY 8 YSANHKNYL 16

Db 152 YSANHKNYL 160

Search completed: October 7, 2003, 19:14:57
Job time: 5.45862 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 19:04:06 ; Search time 16.9414 Seconds

(without alignments)
258.946 Million cell updates/sec

Title: US-09-988-013a-2_COPY_24_40

Perfect score: 85

Sequence: 1 KSSQSVLYSANHKNTYIA 17

Scoring table: BLOSUM62

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	65.9	107	11	Q9ERZ9
2	50	58.8	130	4	Q9NP29
3	45	52.9	146	8	Q8MOE1
4	44	51.8	378	16	Q8U1X2
5	43	50.6	306	5	Q9BK13
6	43	50.6	1360	4	Q9HCK2
7	43	50.6	1746	4	Q8NHE1
8	43	50.6	1833	4	Q9NR92
9	43	50.6	2012	5	Q8IDC5
10	43	50.6	2316	4	Q8WXA6
11	43	50.6	2362	4	Q8NG31
12	42	49.4	90	12	Q4Z047
13	42	49.4	160	9	Q8SDC2
14	42	49.4	291	16	Q94467
15	42	49.4	291	16	Q8XNP9
16	42	49.4	330	16	Q25502

17	42	49.4	415	10	Q9SCW7	Q9SIW7 arabidopsis
18	42	49.4	708	5	Q9W0D8	Q9W0D8 drosophila
19	42	49.4	779	10	Q9LNU0	Q9LNU0 arabidopsis
20	42	49.4	2672	5	Q8IEE4	Q8IEE4 plasmid
21	41	48.2	207	2	Q46674	Q46674 escherichia
22	41	48.2	444	11	Q9D2Q3	Q9D2Q3 mus musculus
23	41	48.2	480	5	Q8IND4	Q8IND4 drosophila
24	41	48.2	518	5	Q8I3Q2	Q8I3Q2 plasmid
25	41	48.2	1351	5	Q8T6H3	Q8T6H3 dictyostell
26	40.5	47.6	119	2	Q9EV97	Q9EV97 streptococ
27	40.5	47.6	297	16	Q8R6A4	Q8R6A4 fusobacteri
28	40	47.1	365	11	Q8CGN6	Q8CGN6 mus musculu
29	40	47.1	365	11	Q8BG61	Q8BG61 mus musculu
30	40	47.1	406	16	Q8K8Q8	Q8K8Q8 streptococ
31	40	47.1	410	16	Q9A1L2	Q9A1L2 streptococ
32	40	47.1	410	16	Q8P2R6	Q8P2R6 streptococ
33	40	47.1	425	5	Q8MYE8	Q8MYE8 dictyostell
34	40	47.1	469	16	Q8NPY5	Q8NPY5 corynebacte
35	40	47.1	488	17	Q979J5	Q979J5 thermoplas
36	40	47.1	506	10	Q4O140	Q4O140 lycopersico
37	40	47.1	510	8	Q92Y12	Q92Y12 papilio ind
38	40	47.1	542	4	Q9NSG4	Q9NSG4 homo sapien
39	40	47.1	543	5	Q8I345	Q8I345 plasmid
40	40	47.1	564	5	Q8IS03	Q8IS03 babesia bov
41	40	47.1	673	4	Q9NSG3	Q9NSG3 homo sapien
42	40	47.1	674	4	Q9NW27	Q9NW27 homo sapien
43	40	47.1	674	4	Q9BTX1	Q9BTX1 homo sapien
44	40	47.1	702	5	Q9SP17	Q9SP17 tenebrio mo
45	40	47.1	797	10	Q9SK37	Q9SK37 arabidopsis

ALIGNMENTS

RESULT 1

ID	Q9ERZ9	PRELIMINARY:	PRT:	107 AA.
AC	Q9ERZ9	01-MAR-2001 (TREMBLrel. 16, Created)		
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Anti human TNF-alpha light chain variable region (Fragment).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;			
RT	"Cloning and sequencing of the light chain fragment of variable region genes of an anti-hTNF-a monoclonal antibody."			
RL	J. Cell. Mol. Immunol. 12:21-26(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;			
RT	"Construction and sequencing of the single-chain antibody gene of a human TNF-alpha specific monoclonal antibody."			
RL	Ti 4 Chun i Ta Hsueh Hsueh Pao 19:373-376(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;			
RT	Submitted (May-2000) to the EMBL/GenBank/DBJ databases.			
RL	EMBL: AF262753; AAC23804.1; -			
DR	HSSP: P80362; IWTI.			
DR	InterPro: IPR007110; Ig-1like.			
DR	InterPro: IPR003066; Ig_MHC.			
DR	InterPro: IPR003596; Ig_V.			
DR	Pfam: PF00047; Ig_1.			
DR	SMART: SM00406; IGV_1.			
DR	PROSITE: PSS0835; IG_LIKE; 1.			
FT	NON_TER			
FT	SEQUENCE	107 AA;	11784 MW;	2B15FEA6604A26C3 CRC64;

Query Match 65.9%; Score 56; DB 11; Length 107;
 Best Local Similarity 76.5%; Pred. No. 0.1;
 Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 KSSOSVLYSANHKNYLA 17
 ||||| | |||||
 DB 21 KSSOSVLYSANHKNYLA 37

RESULT 2

O9NP29 PRELIMINARY; PRT; 130 AA.
 AC O9NP29;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Microfibrillar protein 2 (Fragment).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RA MEDLINE=96354815; PubMed=8753791;
 RA Ozaevath K.J., Xia S., Hirose H., Tilson M.D.;
 RT "Two hypothetical proteins of human aortic adventitia, with Ig kappa,
 RT collagenous, and aromatic-rich motifs."
 RL Biochem. Biophys. Res. Commun. 225:500-504(1996).
 RN [2]
 RP SEQUENCE FROM N.A.

RA MEDLINE=97367690; PubMed=9224393;
 RA Ozaevath K.J., Hirose H., Xia S., Chew D., Knoetgen J. III,
 RA Tilson M.D.;
 RT "Expression of two novel recombinant proteins from aortic adventitia
 RT (kappaIb) sharing amino acid sequences with cytomegalovirus."
 RL J. Surg. Res. 69:277-282(1997).
 RN [3]
 RP SEQUENCE FROM N.A.

RA Ozaevath K.J., Xia S., Hirose H., Tilson M.D.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF206020; AAF62402.1; -
 DR HSSP; P80362; 1MTL.

FT NON_TER 130
 SQ SEQUENCE 130 AA; 14128 MW; 51275185AOC6FAIE CRC64;

Query Match 58.8%; Score 50; DB 4; Length 130;
 Best Local Similarity 52.9%; Pred. No. 1.3;
 Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 KSSOSVLYSANHKNYLA 17
 :||| : : : |||||
 DB 44 RSSOHLFGSNSKNYLA 60

RESULT 3

O8MOE1 PRELIMINARY; PRT; 146 AA.
 AC O8MOE1;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE NADH dehydrogenase subunit 2 (Fragment).
 GN NAD2.
 OS Cryptococcus neoformans var. neoformans.
 OG Mitochondrion.
 CC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
 CC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
 OX NCBI_TaxID=40410;
 RN [1]
 RP SEQUENCE FROM N.A.

RA STRAIN-IFM 5844;
 RA Litter J., Kucsera J.;
 RT "Partial sequence of the NADH dehydrogenase subunit 2 gene and the

RT NADH dehydrogenase subunit 3 gene of Cryptococcus neoformans var.
 RT neoformans IFM 5844."
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF534567; AAN01219.1; -
 DR InterPro; IPR001750; Oxidored_q1.
 DR Pfam; PF00361; Oxidored_q1.1.
 FT NAD; Oxidoreductase; Ubiquinone; Mitochondrion.
 FT NON_TER 1
 SQ SEQUENCE 146 AA; 15835 MW; 83782F70D64DC4E8 CRC64;

Query Match 52.9%; Score 45; DB 8; Length 146;
 Best Local Similarity 57.1%; Pred. No. 9.6;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 SSOSVLYSANHKNY 15
 :||| | |
 DB 52 AKQVLYSATHSYG 65

RESULT 4

O8UIX2 PRELIMINARY; PRT; 378 AA.
 AC O8UIX2;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hypothetical protein phm.
 GN PHM OR ATU0169 OR AGR_C_279.
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 CC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 CC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=176299;
 RN [1]
 RP SEQUENCE FROM N.A.

RA MEDLINE=21608550; PubMed=11743193;
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr., Woo L.,
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boyce D. St.,
 RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
 RA Kuyavina T., Levy R., Li M.-J., McClelland E., Palmeri A.,
 RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Nester E.W.;
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 RT C58."
 RL Science 294:2317-2323(2001).
 RN [2]
 RP SEQUENCE FROM N.A.

RA MEDLINE=21608551; PubMed=11743194;
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
 RA Quicillo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
 RA Houniel K., Gordon J., Vaudin M., Iarchouk O., Epp A., Liu F.,
 RA Wollam C., Allinger M., Doughy D., Scott C., Lapps C., Markelz B.,
 RA Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
 RA Cleio C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 RT Agrobacterium tumefaciens C58."
 RL Science 294:2323-2328(2001).
 DR EMBL; AE008991; AAL41193.1; -
 DR EMBL; AE007958; AAK65988.1; -
 DR InterPro; IPR006680; Amidohydro_1.
 DR Pfam; PF01979; Amidohydro_1.
 KW Hypothetical protein; Complete proteome.

SO SEQUENCE 378 AA; 41200 MW; 81EB8B837A75EB45 CRC64;

Query Match 51.8%; Score 44; DB 16; Length 378;
 Best Local Similarity 47.1%; Pred. No. 37;
 Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 1 KSSOSVLYSANHKNYLA 17
 : : | ||| | : |||||

DB 201 RQASAEYSAKHDVLA 217

RESULT 5
09BK13
ID 09BK13 PRELIMINARY; PRT; 306 AA.

AC 09BK13; 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, last annotation update)
DE Glyceraldehyde-3-phosphate dehydrogenase (Fragment).
GN GAPC.
OS Parametium tetraurelia.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Penicillida;
OC Parametium.
OX NCBI_TaxID=5888;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21143069; PubMed-11230543;
RA Fast N.M., Kissinger J.C., Roos D.S., Keeling P.J.;
RT "Nuclear-Encoded, Plastid-Targeted Genes Suggest a Single Common
Origin for Alpicomplexan and Dinoflagellate Plastids."
RL Mol. Biol. Evol. 18:418-426(2001).
CC -1 SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
DERIVATION: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
CC DEHYDROGENASE FAMILY.
DR EMBL; AF319452; AAK20731.1; -.
DR HSSP; P56649; IDS.
DR InterPro; IPR000173; GAP_dhhydrogenase.
DR Pfam; PF00044; gpdh_1.
DR Pfam; PR002800; gpdh_C_1.
DR PRINTS; PR00078; G3PDHGNASE.
DR PROSITE; PS00071; GAPDH; 1.
KW Oxidoreductase.
FT NON_TER 1
FT 306
SQ SEQUENCE 306 AA; 32657 MW; 680D7EC6EDA527C CRC64;

Query Match 50.6%; Score 43; DB 5; Length 306;
Best Local Similarity 41.2%; Pred. No. 44;
Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 KSSOSVLYSANHNKNTYA 17
DB 117 KGTPTFYGVNHNENYNA 133

RESULT 6
09HCK2
ID 09HCK2 PRELIMINARY; PRT; 1360 AA.

AC 09HCK2; 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, last annotation update)
DE Hypothetical protein KIAA1570 (Fragment).
GN KIAA1570.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20450683; PubMed-10997877;
RA Nagase T., Kikuno R., Nakayama M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes.
XVIII. The complete sequences of 100 new cDNA clones from brain which
code for large proteins in vitro."
RL DNA Res. 7:273-281(2000).
DR EMBL; AB046790; BAB13396.1; -.
KW Hypothetical protein.
FT NON_TER 1
FT 1360
SQ SEQUENCE 1360 AA; 154971 MW; 7834D7E626D212B8 CRC64;

Query Match 50.6%; Score 43; DB 4; Length 1360;

Best Local Similarity 42.9%; Pred. No. 1.9e+02;
Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 1 KSSOSVLYSANHNK 14
DB 115 KNDKTIVFSENHNK 128

RESULT 7
08NHE1
ID 08NHE1 PRELIMINARY; PRT; 1746 AA.

AC 08NHE1; 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, last annotation update)
DE D40 protein.
GN D40.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-Testis;
RX MEDLINE-22081483; PubMed-12087463;
RA Takimoto M., Wei G., Dosaka-Akita H., Mao P., Kondo S., Sakuregi N.,
RA Chiba I., Miura T., Itoh N., Sasao T., Koya R.C., Tsukamoto T.,
RA Fujimoto S., Kato H., Kuzumaki N.;
RT "Frequent expression of new cancer/testis gene D40/AF15q14 in lung
cancer of smokers."
RL Br. J. Cancer 86:1757-1762(2002);
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE-Testis;
RX MEDLINE-20241296; PubMed-10780384;
RA Wei G., Takimoto M., Yoshida I., Mao P., Koya R.C., Miura T.,
RA Kuzumaki N.;
RT "Chromosomal assignment of a novel huma gene D40."
RL Nucleic Acids Symp. Ser. 42:71-72(1999).
DR EMBL; AB022190; BAC05691.1; -.
SQ SEQUENCE 1746 AA; 195451 MW; 8183D802B8CE0991 CRC64;

Query Match 50.6%; Score 43; DB 4; Length 1746;
Best Local Similarity 42.9%; Pred. No. 2.5e+02;
Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 1 KSSOSVLYSANHNK 14
DB 1071 KNDKTIVFSENHNK 1084

RESULT 8
09NR92
ID 09NR92 PRELIMINARY; PRT; 1833 AA.

AC 09NR92; 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)
DE AF15q14 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20438193; PubMed-10980622;
RA Hayette S., Tigaud I., Vanier A., Martel S., Corbo L., Charlin C.,
RA Bellard E., Deleage G., Magaud J.P., Rimokh R.;
RT "AF15q14, a novel partner gene fused to the MLL gene in an acute
myeloid leukaemia with a t(11;15)(q23;q14)."
RL Oncogene 19:4446-4450(2000).
DR EMBL; AF248041; AAF97513.1; -.
SQ SEQUENCE 1833 AA; 205683 MW; D13BBE8784B78369 CRC64;

Query Match 50.6%; Score 43; DB 4; Length 1833;
 Best Local Similarity 42.9%; Pred. No. 2.6e+02;
 Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 1 KSSOSVLYSANHKN 14
 DB 1071 KNDKTIVESENHKN 1084

RESULT 9

OBIDC5 PRELIMINARY; PRT: 2012 AA.
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN MAL13p1.285.
 OS Plasmodium falciparum (isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_Taxid=36329;
 RP SEQUENCE FROM N.A.
 RA Harris B., Lennard N., Clark L., Line A., Barron A., Corton C.,
 RA Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett J.,
 RA Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrett B.,
 RL Submitted (Sep-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL844509; CAD52700.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 2012 AA; 238205 MW; 7A3C897267EAE718 CRC64;

Query Match 50.6%; Score 43; DB 5; Length 2012;
 Best Local Similarity 35.3%; Pred. No. 2.9e+02;
 Matches 6; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

OY 1 KSSOSVLYSANHKN 17
 DB 1092 KENRTVYLNHKN 1108

RESULT 10

OBWXA6 PRELIMINARY; PRT: 2316 AA.
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE AF15q14 Isoform 2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20438193; PubMed=10980622;
 RA Hayette S., Tliguid I., Vanter A., Martel S., Corbo L., Charrin C.,
 RA Belliard E., Deleage G., Magaud J.P., Rimokh R.,
 RT "AF15q14, a novel partner gene fused to the MLL gene in an acute
 myeloid leukemia with a t(11;15)(q23;q14).";
 RL Oncogene 19:4446-4450(2000).
 GN [2]
 RP SEQUENCE FROM N.A.
 RA Hayette S., Rimokh R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF461041; AAL67803.1; -
 SQ SEQUENCE 2316 AA; 262517 MW; AD77046BFCB8321C CRC64;

Query Match 50.6%; Score 43; DB 4; Length 2316;
 Best Local Similarity 42.9%; Pred. No. 3.3e+02;
 Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 1 KSSOSVLYSANHKN 14

DB 1071 KNDKTIVESENHKN 1084

RESULT 11

OBNG31 PRELIMINARY; PRT: 2342 AA.
 AC OBNG31.
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE AF15q14.
 GN AF15Q14.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RP SEQUENCE FROM N.A.
 RA Kuefer M.U., Chinwalla V., Zelenyk-Le N.J., Behm F.G., Naewe C.W.,
 RA Rakestraw K.M., Rainoldi S.C., Morris S.W.,
 RT "Characterization of the MLL partner gene, AF15q14, involved in the
 t(11;15)(q23;q14-15).";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF173994; AAM45143.1; -
 SQ SEQUENCE 2342 AA; 265284 MW; 6844183244CCB86B CRC64;

Query Match 50.6%; Score 43; DB 4; Length 2342;
 Best Local Similarity 42.9%; Pred. No. 3.4e+02;
 Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 1 KSSOSVLYSANHKN 14
 DB 1097 KNDKTIVESENHKN 1110

RESULT 12

O42047 PRELIMINARY; PRT: 90 AA.
 AC O42047;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE Matrix protein 2.
 GN M2.
 OS Human respiratory syncytial virus (strain B1).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
 OX NCBI_Taxid=79692;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-B1;
 RA Karron R.A., Buongiorno D.A., Georgiu A.F., Whitehead S.S.,
 RA Adamus J.E., Clements-Mann M.L., Harris D.O., Randolph V.B.,
 RA Uden S.A., Murphy B.R., Sidhu M.S.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 GN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-B1;
 RA Sidhu M.S., Uden S.A., Murphy B.R.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF013255; AAB82448.1; -
 DR EMBL; AF013255; AAB82448.1; -
 KW Matrix protein.
 SQ SEQUENCE 90 AA; 10587 MW; 16D886E983DE3994 CRC64;

Query Match 49.4%; Score 42; DB 12; Length 90;
 Best Local Similarity 53.3%; Pred. No. 19;
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 2 SSOSVLYSANHKN 16
 DB 23 SSESMTATFNHKN 37

RESULT 13

08SDC2
ID 08SDC2 PRELIMINARY; PRT; 160 AA.
AC 08SDC2;
DT 01-JUN-2002 (TRENBLREL. 21, Created)
DT 01-JUN-2002 (TRENBLREL. 21, Last sequence update)
DT 01-OCT-2002 (TRENBLREL. 22, Last annotation update)
DE PHIK2040.
OS Pseudomonas phage phik2.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=169683;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21914557; PubMed=11916376;
RA Mesyanzhinov V.V., Robben J., Grymonprez B., Kostynchenko V.A.,
Bourkatsseva M.V., Sykylinda N.N., Kiylov V.V., Volckaert G.,
"The genome of bacteriophage phik2 of Pseudomonas aeruginosa.",
J. Mol. Biol. 317:1-19(2002).
RL [2]
RN SEQUENCE FROM N.A.
RA Mesyanzhinov V.V., Robben J., Grymonprez B., Kostynchenko V.A.,
Bourkatsseva M.V., Sykylinda N.N., Kiylov V.V., Volckaert G.,
Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF399011; AAL82941.1; -
DR InterPro: IPR000387; TYR_phosphatase.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
KW Hydrolase.
SQ SEQUENCE 160 AA; 18179 MW; 189BDD24A3992106 CRC64;

Query Match 49.4%; Score 42; DB 9; Length 160;
Best Local Similarity 80.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 LYSANHKNTYL 16
DB 35 LYSANHKNTYL 44

RESULT 14

094467
ID 094467 PRELIMINARY; PRT; 291 AA.
AC 094467;
DT 01-FEB-1997 (TRENBLREL. 02, Created)
DT 01-FEB-1997 (TRENBLREL. 02, Last sequence update)
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
DE SRNA-binding protein.
OS Dictyostelium discoideum (slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-AA2;
RX MEDLINE=98086164; PubMed=9426195;
RA Oberosler P., Nellen W.,
"Functional activity and developmental regulation of DdRBP1, a RNA
binding protein in Dictyostelium discoideum.",
Biol. Chem. 378:1353-1360(1997).
RL EMBL; Y07952; CAA69250.1; -
DR HSSP; P09651; IHAL.
DR InterPro: IPR000504; RNA_rec_mot.
DR Pfam: PF00076; rrm; 1.
DR SMART: SM00360; RRM; 1.
DR PROSITE: PS50102; RRM; 1.
DR PROSITE: PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 291 AA; 31767 MW; D8B717C82AE0C2D5 CRC64;

Query Match 49.4%; Score 42; DB 5; Length 291;
Best Local Similarity 62.5%; Pred. No. 61;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 SSQSIVLYSANHKNTYL 17
DB 125 SSRATVTSANTINMLA 140

RESULT 15

08XNP9
ID 08XNP9 PRELIMINARY; PRT; 291 AA.
AC 08XNP9;
DT 01-MAR-2002 (TRENBLREL. 20, Created)
DT 01-MAR-2002 (TRENBLREL. 20, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE Hypothetical protein CPE0283.
GN CPE0283.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-13 / Type A;
RX PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.,
"Complete genome sequence of Clostridium perfringens, an anaerobic
flesh-eater.",
Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
RL EMBL; AP003186; BAB79989.1; -
DR InterPro: IPR001823; Aldol-epimerase.
DR Pfam: PF01263; Aldose_epim; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 291 AA; 34015 MW; E2B6D485064CFE38 CRC64;

Query Match 49.4%; Score 42; DB 16; Length 291;
Best Local Similarity 56.2%; Pred. No. 61;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 KSSQSVLYSANHKNTYL 16
DB 211 KSNKISLKSNNHKNTYL 226

Search completed: October 7, 2003, 19:19:55
Job time: 18.9414 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 19:03:26 ; Search time 8.81034 Seconds
(without alignments) 126.112 Million cell updates/sec

Title: US-09-988-013a-2_COPY_56_62
Perfect score: 38
Sequence: 1 WASTRES 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: A_Geneseq_19Jun03: *
2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT: *
3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT: *
4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT: *
5: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT: *
6: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1984.DAT: *
7: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1985.DAT: *
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9: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1987.DAT: *
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11: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1989.DAT: *
12: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1990.DAT: *
13: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1991.DAT: *
14: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1992.DAT: *
15: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1993.DAT: *
16: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1994.DAT: *
17: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1995.DAT: *
18: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1996.DAT: *
19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1997.DAT: *
20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT: *
21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT: *
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT: *
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT: *
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	7	14	AA30157
2	38	100.0	7	15	AA57964
3	38	100.0	7	15	AA57966
4	38	100.0	7	15	AA57967
5	38	100.0	7	20	AA50317
6	38	100.0	7	21	AA50713
7	38	100.0	7	21	AA50752
8	38	100.0	7	21	AA5234
9	38	100.0	7	23	AA32227
					AA529275

10	38	100.0	7	23	ABP2361	Human immunopeptid
11	38	100.0	7	23	ABG6854	CD2 VL peptide.
12	38	100.0	7	23	AAU81257	Human trkC antibod
13	38	100.0	7	23	AAU70335	Human Kappa IV lig
14	38	100.0	7	23	AAU70347	Mouse Kappa I lig
15	38	100.0	7	24	ABP98681	Human GAH antibody
16	38	100.0	7	24	ABP98689	Human GAH antibody
17	38	100.0	7	24	ABG34369	Escherichia coli I
18	38	100.0	7	24	ABG34369	CD2 of HMEG-1 lig
19	38	100.0	15	23	ABG68859	CD2 sequence remo
20	38	100.0	82	17	AA62807	Amino acid sequenc
21	38	100.0	84	17	AAU1491	Monoclonal antibod
22	38	100.0	84	17	AAU9878	Monoclonal antibod
23	38	100.0	94	21	AAU5669	Partial peptide fr
24	38	100.0	101	24	AAU18696	Antibody library r
25	38	100.0	105	23	ABR07184	MS11955 light chai
26	38	100.0	107	19	AAU80817	Amino acid sequenc
27	38	100.0	107	19	AAU80814	Amino acid sequenc
28	38	100.0	107	20	AAU17955	Human kappa 8 ligh
29	38	100.0	110	13	AAU30012	Light chain variab
30	38	100.0	110	19	AAU56520	Anti-DNA IL/IM (R2
31	38	100.0	110	19	AAU56517	H221 antibody VL r
32	38	100.0	111	15	AAU52059	Light chain variab
33	38	100.0	112	13	AAU28807	5A8 VL. Synthetic
34	38	100.0	112	15	AAU54932	Fc receptor humant
35	38	100.0	112	15	AAU54933	MAB 022 VR chain.
36	38	100.0	112	23	AAU29264	S. aureus ClfA spe
37	38	100.0	112	23	AAU29266	S. aureus ClfA spe
38	38	100.0	112	23	AAU29268	S. aureus ClfA spe
39	38	100.0	112	23	AAU29270	S. aureus ClfA spe
40	38	100.0	112	23	ABG76514	HCV EI antigen mon
41	38	100.0	112	23	ABG76524	HCV EI antigen mon
42	38	100.0	112	23	ABG76548	HCV EI antigen mon
43	38	100.0	113	13	AAU25407	Light chain variab
44	38	100.0	113	15	AAU50313	Humanised light ch
45	38	100.0	113	15	AAU50314	Humanised light ch

ALIGNMENTS

RESULT 1	AA30157	standard; Protein; 7 AA.
ID	AA30157	
XX	AA30157	
AC	AA30157	
DT	25-MAR-2003	(updated)
DT	06-MAY-1993	(first entry)
XX		
DE	Mab GAH variable region of light chain.	
XX		
KW	Monoclonal antibody; hybridoma; PCR; variable region;	
KW	constant region; heavy chain; light chain.	
XX		
OS	Synthetic.	
PN	EP520499-A1.	
XX		
PD	30-DEC-1992.	
XX		
PF	26-JUN-1992;	92EP-0110841.
XX		
PR	28-JUN-1991;	91JP-0158859.
PR	28-JUN-1991;	91JP-0158860.
PR	28-JUN-1991;	91JP-0158861.
XX		
PA	(MITU) MITSUBISHI KASEI CORP.	
XX		
PI	Hirakawa Y, Hosokawa S, Ito N, Nagaike K, Tagawa T;	
XX		
DR	WPI, 1993-001328/01.	
DR	N-PSDB; AA033044.	

```

XX Human monoclonal antibody specific for a cancer cell membrane
PT surface antigen - prepd. from a hybridoma obtd. by cell fusion
PT between human lymphocytes derived from cancer patients and mouse
PT myeloma cells
PS
PS Claim 3; Page 30 + 23; 37pp; English.
XX
CC The sequence is described below as the specification as having 27 bases.
CC A human mAb specifically binding to a surface antigen of cancer
CC cell membrane comprises variable regions of the heavy and light
CC chains having the amino acid sequences of AAR30153-55 and AAR30156-58
CC respectively, encoded by DNA sequences AAQ3040-42 and AAQ3043-45
CC respectively. The antibody is obtained from a hybridoma producing
CC human antibody GmH.
CC (Updated on 25-MAR-2003 to correct PN field.)
SQ Sequence 7 AA:
SQ
Query Match 100.0%; Score 38; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. NO. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY 1 WASTRES 7
Db 1 WASTRES 7
| | | | |
| | | | |
DE MAB NFS2 light chain variable region CDR2.
XX
XX Monoclonal antibody; Plasmodium falci-parum; CDR;
KW complementarity determining region; fusion protein;
RW murine; variable; light; heavy; chain; malaria.
XX
XX Plasmodium falci-parum.
OS
XX WO9405690-A1.
PN 17-MAR-1994.
PD
XX 08-SEP-1993; 93WO-US08435;
PF
XX 09-SEP-1992; 92US-0941654.
PR
XX (SMIK ) SMITHKLINE BEECHAM CORP.
PA (USSA ) US SEC OF ARMY.
PA (USNA ) US SEC OF NAVY.
XX
XX Charoenyit Y, Hoffman S, Hurle M, Rosenberg M;
PI Saioff JC, Sylvestre DR, Gross MS;
XX
XX MPI: 1994-101115/12.
DR N-PSTDB: ANO44837.
DR
XX New engineered antibodies and fusion proteins for preventing
PT Plasmodium infection - contg. murine antibody CDR sequences, and
PT corresp. nucleic acid, vectors and transformed cells
XX
XX Disclosure: Page 68; 98pp; English.
XX
XX Naturally-occurring (AAQ44841-42) and synthetic (AAQ44825-28)
CC variable light chain and variable heavy chain sequences
CC derived from murine mAb NFS2 are provided. Murine mAb NFS2,
CC its variable chain peptides, CDRs, functional fragments,

```

Query Match	Similarity	Score	DB	Length	7;
Best Local	7;	Conservative	100.0%;	Pred. No. 9.3e+05;	Matches 7; Indels 0; Gaps 0;
Matches	7;	Conservative	0;	Mismatches 0;	Indels 0; Gaps 0;
Sequence	7 AA;				
Query Match	Similarity	Score	DB	Length	7;
Best Local	7;	Conservative	100.0%;	Pred. No. 9.3e+05;	Matches 7; Indels 0; Gaps 0;
Matches	7;	Conservative	0;	Mismatches 0;	Indels 0; Gaps 0;
Sequence	7 AA;				

```

Db          |||||
            1 WASTRES 7

RESULT 4
AAR50317
ID AAR50317 standard; Protein; 7 AA.
XX
XX AAR50317;
AC
XX
XX 25-MAR-2003 (updated)
DT 05-OCT-1994 (first entry)
XX
XX MAb NFS2 light chain variable region CDR2 (modified).
DE
XX
XX Monoclonal antibody; Plasmodium falciparum; CDR;
KM complementarity determining region; fusion protein;
KM murine; variable; light; heavy; chain; malaria.
XX
XX Synthetic.
OS
XX W09405690-A1.
XX
XX 17-MAR-1994.
PD
XX
XX 08-SEP-1993; 93WO-US08435.
PF
XX
XX 09-SEP-1992; 92US-0941654.
PR
XX
XX (SMR ) SMITHKLINE BEECHAM CORP.
PA (USNA ) US SEC OF ARMY.
XX (USNA ) US SEC OF NAVY.
XX
XX Charenylt Y, Hoffman S, Hurle M, Rosenberg M;
PI Sadoff JC, Sylvestre DR, Gross MS;
XX
XX WPI; 1994-101115/12.
DR
XX N-PSDB; AAO44833.
XX
XX New engineered antibodies and fusion proteins for preventing
PT Plasmodium infection - contg. murine antibody CDR sequences, and
XX
XX corresp. nucleic acid, vectors and transformed cells
XX
XX Claim 16; Page 83; 98pp; English.
XX
XX Naturally-occurring (AAQ44841-42) and synthetic (AAQ44825-28)
XX variable light chain and variable heavy chain sequences
XX derived from murine mAb NFS2 are provided. Murine mAb NFS2,
XX its variable chain peptides, CDRs, functional fragments,
XX CDR fragments, and analogs are useful in prodn. of fusion
XX proteins, esp. engineered antibodies. These prods. are
XX used to protect humans against Plasmodium infections.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
XX Sequence 7 AA:
SQ
XX
XX Query Match 100.0%; Score 38; DB 15; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX 1 WASTRES 7
DB 1 WASTRES 7
XX
XX
XX RESULT 5
XX AAY08713
XX ID AAY08713 standard; protein; 7 AA.
XX
XX AAY08713;
XX
XX 10-AUG-1999 (first entry)
XX

```

```

DE Human milk fat globule antigen binding fragment 5.
XX
XX Immunoglobulin; immunospecific; variable domain; CDR; cancer antigen;
KM complementarity determining region; infectious disease agent antigen;
KM cellular receptor; infectious agent; chemotherapeutic agent; vaccine;
KM cancer; infectious disease; autoimmune disease; rheumatoid arthritis;
KM ulcerative colitis; psoriasis; allergy; immunosay reagent; diagnosis;
KM veterinary medicine; antibody; immunisation; antibody; immune tolerance;
KM human milk fat globule antigen; cryptic expression;
XX anti-idiotypic immune response.
XX
XX Homo sapiens.
OS
XX W0925378-A1.
XX
XX 27-MAY-1999.
PD
XX
XX 13-NOV-1998; 98WO-US24302.
PF
XX
XX 10-APR-1998; 98US-0081403.
PR 14-NOV-1997; 97US-0065716.
XX
XX (EURO-) EUROCELTIQUE SA.
PA
XX Burch RM;
XX
XX WPI; 1999-357555/30.
XX
XX Modified immunoglobulins including engineered binding site
XX
XX Claim 9; Page 76; 123pp; English.
XX
XX This invention describes a novel modified immunoglobulin (mig), or its
XX fragment, that binds immunospecifically to one member (M1) of a binding
XX pair comprises a variable domain (V) having at least one CDR of the
XX (complementarity determining region) that contains a portion of the
XX second member (M2) of the pair. This portion is not present in the
XX natural CDR and M1 is a cancer antigen, infectious disease agent antigen,
XX a cellular receptor for an infectious agent (provided the binding site is
XX not NAMP or NMDP) or a member of a receptor-ligand pair. mig (also
XX related molecules containing the same V region), optionally coupled to a
XX chemotherapeutic agent, are used in therapeutic and/or prophylactic
XX compositions, or vaccines, against cancers, infectious or autoimmune
XX diseases (rheumatoid arthritis, ulcerative colitis or psoriasis) or
XX allergies. They can also be used as immunosay reagents for diagnosing
XX these conditions. mig can be used in human or veterinary medicine. mig
XX have higher affinity or specificity than native antibodies. Manipulation
XX of CDR ensures binding specificity and avoids the unpredictable
XX immunization and screening procedures currently used. It is now possible
XX to generate antibodies against antigens that are inaccessible, by virtue
XX of immune tolerance or cryptic expression. mig neutralize antigens
XX directly or they induce an anti-idiotypic immune response. This sequence
XX represents a fragment of modified immunoglobulin that immunospecifically
XX binds to a binding pair in which the first member is the human milk fat
XX globule antigen.
XX
XX
XX Sequence 7 AA:
SQ
XX
XX Query Match 100.0%; Score 38; DB 20; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX 1 WASTRES 7
DB 1 WASTRES 7
XX
XX
XX RESULT 6
XX AAB07952
XX ID AAB07952 standard; peptide; 7 AA.
XX
XX AAB07952;
XX
XX

```

DE 14-NOV-2000 (first entry)

XX CDR2 sequence from an antibody with affinity for B7 molecules.

XX

KM Complementarity determining region; CDR; antibody; B7 molecule; B7-1;

KM B7-2; humanised immunoglobulin; autoimmune disease; infectious disease;

KM inflammatory disorder; systemic lupus erythematosus; diabetes mellitus;

KM Insults; asthma; arthritis; inflammatory bowel disease; cancer;

KM inflammatory dermatitis; multiple sclerosis; transplant rejection;

KM proliferative disease; leukemia; lymphoma; anaemia; sickle-cell anaemia;

KM thalassemia; aplastic anaemia; myeloid dysplasia syndrome.

XX

OS Mus sp.

XX

PN WO200047625-A2.

PD 17-AUG-2000.

XX

PF 09-FEB-2000; 2000WO-US03303.

XX

PR 12-FEB-1999; 99US-0249011.

PR 24-JUN-1999; 99US-0339596.

XX

PA (GENY) GENETICS INST INC.

XX

PI Co MS, Vasquez M, Carreno B, Gelinker AC, Collins M, Goldman S;

PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;

XX

DR WPI; 2000-524532/47.

XX

PT Humanised immunoglobulin having a binding specificity to B7-1 (derived

PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-1524) molecules,

PT modulates immune responses and can therefore treat e.g. autoimmune

PT diseases, infectious diseases -

XX

PS Disclosure: Page 28; 162pp: English.

XX

CC The present sequence represents a complementarity determining region

CC (CDR) 2 from the light chains of an murine antibody with having a

CC binding specificity to B7-2 molecules. The sequence is used to construct

CC humanised immunoglobulins, which comprise an antigen binding region of

CC non-human origin and a portion of a human immunoglobulin. The humanized

CC immunoglobulins are useful for treating autoimmune diseases, infectious

CC diseases, inflammatory disorders, systemic lupus erythematosus, diabetes

CC mellitus, Insults; asthma, arthritis, inflammatory bowel disease,

CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are

CC also useful for treating a transplant recipient or preventing transplant

CC rejection in a transplant recipient, and treating proliferative disease

CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,

CC thalassemia and aplastic anaemia). Inborn errors of metabolism,

CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.

XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 21; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7

DB 1 WASTRES 7

RESULT 7

AAV95234

ID AAV95234 standard; Peptide: 7 AA.

XX

AC AAV95234;

XX

DT 29-AUG-2000 (first entry)

XX

DE Human monoclonal antibody LEN VL CDR2.

KM Human; monoclonal antibody; LEN; humanised antibody; CC49; HuCC49;

KM CDR; complementarity determining region; colon cancer;

KM tumor associated glycoprotein-72; TAG-72; tumour marker; carcinoma;

KM diagnosis; therapy.

XX

OS Homo sapiens.

XX

EH Key Location/Qualifiers

FT Region 1..6

FT /note= "specificity determining region"

XX

PN WO200026394-A1.

XX

PD 11-MAY-2000.

XX

PF 29-OCT-1999; 99WO-US25552.

XX

PR 31-OCT-1998; 98US-0106534.

PR 02-NOV-1998; 98US-0106757.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Kashmiri SVS, Padlan EA, Schlom J;

XX

DR WPI; 2000-365637/31.

XX

PT Chimeric variants of CC49 monoclonal antibodies useful for detecting

PT and treating cancers associated with the expression of the pancarcinoma

PT tumor-associated antigen TAG-72 -

XX

PS Disclosure: Fig 2; 76pp: English.

XX

CC The present sequence is that of complementarity determining region

CC 2 (L-CDR2) of the light chain variable region (VL) of human

CC monoclonal antibody LEN. The invention is directed toward

CC mouse-human chimeric variants of CC49 Mabs with minimal murine

CC content, to methods of making such variants, and to their

CC therapeutic application. Variants are provided of huCC49, a

CC humanised Mab formed by grafting hypervariable regions from murine

CC CC49 into VL and VH frameworks of human MAb5 LEN and 21/28' CL,

CC respectively, while retaining murine framework residues required

CC for integrity of the antigen combining site structure. HuCC49

CC binds to the human pancarcinoma tumor associated glycoprotein-72

CC (TAG-72), which is found on the surface of certain human tumors.

CC Novel variants of huCC49 of the invention have fewer than all 6

CC CDRs of CC49 present. Also provided are specifically determining

CC region (SDR) variants of huCC49 in which only SDRs of at least 1

CC CDR from CC49 are present. Particular variants of HuCC49 have

CC either L-CDR1 and/or L-CDR2 from human MAb LEN. These variants

CC have the same or 2-fold lower affinity constant than HuCC49. They

CC are used in claimed methods of treating cancer and for detecting

CC cancer cells that express TAG-72.

XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 21; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7

DB 1 WASTRES 7

RESULT 8

AAV32227

ID AAV32227 standard; Peptide: 7 AA.

XX

AC AAV32227;

XX

DT 15-FEB-2000 (first entry)

XX

DE G-CSF agonist antibody mAb163-93 light chain variable region CDR2.

```

XX Granulocyte colony stimulating factor receptor; G-CSF; mouse;
KW monoclonal antibody; agonist; screening; neutropenia; therapy;
XX complementarity determining region; CDR; Mab163-93.
XX
OS Mus musculus.
PN MO9955735-A1.
XX
XX 04-NOV-1999.
XX
XX 30-APR-1999; 99WO-US09466.
XX
XX 30-APR-1998; 98US-0083575.
XX
XX (TAMO-) TAMOX INC.
XX
XX N1 B, Sun BNC, Sun CRV;
XX
XX WPI; 2000-052805/04.
XX
XX Treatment of neutropenia by stimulating proliferation of neutrophilic
XX cell lineage progenitors -
XX
XX Claim 13; Page 30; 64pp; English.
XX
XX The present sequence represents complementarity determining region
XX 2 (CD82) of the light chain variable region of murine monoclonal
XX antibody Mab163-93. This antibody is an example of an agonist
XX molecule that specifically binds to or interacts with human
XX granulocyte colony stimulating factor (G-CSF) receptor to stimulate
XX cell proliferation and differentiation, especially by dimerising
XX the receptor or activating phosphorylation of kinases associated
XX with the receptor. Agonist antibodies can be used to stimulate
XX proliferation of G-CSF-dependent cells, e.g. to differentiate
XX leading to a repopulation of neutrophilic granulocyte lineage
XX cells, especially to treat neutropenia (claimed). They can also
XX be used to detect human G-CSF receptor immunologically.
XX
XX Sequence 7 AA:
XX
SQ
XX
XX Query Match 100.0%; Score 38; DB 21; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
XX
XX QY 1 WASTRES 7
XX |||||
XX 1 WASTRES 7
XX
XX Db
XX
XX RESULT 9
XX AAE29275
XX ID AAE29275 standard; peptide; 7 AA.
XX
XX AC AAE29275;
XX
XX DT 27-JAN-2003 (first entry)
XX
XX DE Anti-ClfA monoclonal antibody variable light chain CDR2.
XX
XX Clumping factor A; ClfA; fibrinogen; fibrin; Clf40; Clf33; N3 protein;
XX immunological; staphylococcal infection; impetigo; pneumonia; furuncle;
XX septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy;
XX complementarity determining region; CDR.
XX
XX Unidentified.
XX
XX OS
XX PN WO200272600-A2.
XX
XX 19-SEP-2002.
XX
XX PD
XX PF 28-JAN-2002; 2002WO-US02296.
XX
XX

```

XX	(INH-) INHIBITEX INC.
XX	
PI	Patti JM, Hutchins JT, Domanski P, Patel P, Hall A;
DR	WPI; 2002-759834/82.
XX	
PT	New anti-clumping factor A (ClfA) monoclonal antibody, useful for
PT	treating or preventing Staphylococcus aureus infection e.g. wound
PT	infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis
XX	in a human or animal
PS	
XX	Claim 30; Page 55; 80pp: English.
CC	The invention relates to monoclonal antibody which binds the clumping
CC	factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA
CC	monoclonal antibody is useful for treating or preventing S. aureus
CC	infection in a human or animal, and for inhibiting the binding of
CC	staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
CC	S. aureus ClfA6 protein, S. aureus Clf33 protein, or the S. aureus N3
CC	protein is useful for inducing an immunological response in a human or
CC	animal. These staphylococcal infections include wound infections, sepsis,
CC	impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
CC	present sequence is an anti-ClfA monoclonal antibody variable light chain
CC	complementarity determining region (CDR).
XX	
SO	Sequence 7 AA:
Query Match	100.0%; Score 38; DB 23; Length 7;
Best Local Similarity	100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
OY	1 WASTRES 7 1 WASTRES 7
Db	
RESULT 10	
ID	ABP62361 standard; Peptide; 7 AA.
XX	
AC	ABP62361;
XX	
DT	10-OCT-2002 (first entry)
XX	
DE	Human immunopeptide to HCV E2 glycoprotein light chain CDR #38.
XX	
KW	Viruslike; human; immunopolypeptide; immunopeptide; envelope glycoprotein;
KW	nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
KW	N33 protein; viral infection.
XX	
OS	Homo sapiens.
XX	
PN	WO200259340-A1.
XX	
PD	01-AUG-2002.
XX	
PF	25-JAN-2002; 2002WO-US02303.
XX	
PR	26-JAN-2001; 2001US-264451P.
XX	
PA	(SCRI) SCRIPPS RES INST.
XX	
PI	Mariyama T, Jones IM, Burton DR, Fox RI;
XX	
DR	WPI; 2002-599801/64.
XX	
PT	New human immunopolypeptide with binding specificity for certain
PT	envelope glycoproteins and nonstructural proteins of hepatitis C virus

PT (HCV), for diagnosing or treating patients having or suspected of
PT having HCV infection
XX
XX Claim 1; Fig 17; 308pp; English.
PS
CC The present invention relates to human immunopolypeptides, produced by a
CC phage transfected cell library. The present sequence is one such
CC immunopolypeptide. The immunopolypeptides have binding specificity for
CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
CC virus (HCV). E2 glycoprotein is believed to be responsible for target
CC cell binding and contains neutralising epitopes, while NS3 is thought to
CC be involved in the replication of HCV. The immunopolypeptides are useful
CC for diagnosing and treating a patient having or suspected to be having
CC HCV infection.
XX
SQ Sequence 7 AA;
XX
Query Match 100.0%; Score 38; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 WASTRES 7
Db 1 WASTRES 7
IIIIII
RESULT 11
ABG68854 standard; Peptide: 7 AA.
XX
AC ABG68854;
XX
DT 07-OCT-2002 (first entry)
XX
DE CDR2 VL peptide.
XX
XX Cytostatic; antiviral; hepatotropic; antinflammatory; neuroprotective;
KM immunosuppressive; antiarthritic; cytokine receptor; interferon; IFN;
KM cancer; haematological malignancy; viral infection; hepatitis; human;
KM multiple sclerosis; autoimmune disease; arthritis.
XX
OS Synthetic.
XX
PN WO200244197-A2.
XX
PD 06-JUN-2002.
XX
PF 30-NOV-2001; 2001WO-CA01701.
XX
PR 01-DEC-2000; 2000US-0727388.
XX
PA (FISH/) FISH E. N.
XX
PI Fish EN;
XX
DR WPI; 2002-547689/58.
XX
N-PSDB; ABA37817.
XX
PT Cytokine receptor binding peptide construct, in particular interferon
PT receptor binding peptide construct for use as an interferon mimetic,
PT comprises a cytokine receptor binding domain incorporated in a
PT molecular scaffold
XX
XX Example 8; Page 50; 105pp; English.
XX
XX This invention relates to a novel cytokine receptor binding peptide
CC construct comprising a cytokine receptor binding domain incorporated in
CC a suitable molecular scaffold so that the scaffold maintains the binding
CC domain in a configuration suitable for binding to the cytokine receptor.
CC The peptides of the invention may have cytosolic, viral, or
CC hepatotropic, antinflammatory, neuroprotective, immunosuppressive and
CC antiarthritic activities. A new interferon receptor binding peptide
CC construct is useful in the manufacture of a medicament as an interferon

CC (IFN) mimetic. A peptide that mimics the effect of IFN is useful in
CC medical therapies for cancer, haematological malignancies, viral
CC infections (hepatitis B or C), multiple sclerosis and autoimmune
CC diseases such as arthritis, to detect modulators of IFN action, in
CC screening assays to compare the activity and/or interaction with
CC another molecule or potential IFN modulator and also in the diagnosis
CC of IFN activity related disorders. A nucleic acid encoding the
CC peptide of the invention or is useful for the treatment and therapy of
CC the mentioned medical conditions. The peptide of the invention has less
CC side effect than those of native cytokines. The present sequence
CC represents an interferon receptor binding peptide of the invention.
XX
SQ Sequence 7 AA;
XX
Query Match 100.0%; Score 38; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 WASTRES 7
Db 1 WASTRES 7
IIIIII
RESULT 12
AAU81257
ID AAU81257 standard; Peptide: 7 AA.
XX
AC AAU81257;
XX
DT 09-APR-2002 (first entry)
XX
DE Human trkC antibody light chain CDR2 of variable region #2.
XX
XX Human; mouse; anti-trkC agonist monoclonal antibody; trkC; antibody;
KM trkA; trkB; cisplatin-induced neuropathy; pyridoxine-induced neuropathy;
KM peripheral neuropathy; diabetic neuropathy; neurodegenerative disease;
KM large-fibre sensory neuropathy; amyotrophic lateral sclerosis; tumour;
KM nerve cell injury; blood cell disorder; leukopenia; eosinopenia; wound;
KM basopenia; lymphopenia; monocytopenia; neutropenia; cancer; ulcer;
KM Alzheimer's disease; Parkinson's disease; Huntington's disease; diabetes;
KM sickle cell disease; cardiac ischaemia; cerebrovascular disorder;
KM cellular degeneration; gene therapy.
XX
OS Homo sapiens.
XX
OS Homo sapiens.
XX
PN WO200198361-A2.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US20153.
XX
PR 22-JUN-2000; 2000US-213141P.
XX
PR 05-OCT-2000; 2000US-238319P.
XX
PA (GETH) GENENTECH INC.
XX
XX Devaux B, Hongo JS, Presta LG, Shelton DL;
XX
DR WPI; 2002-130790/17.
XX
PT Novel anti-trkC agonist monoclonal antibody useful for treating
PT neurodegenerative disease, shows no significant cross-reactivity with
PT trkA/trkB, and recognizes epitope in domain 5 of trkC
XX
XX Claim 13; Fig 11; 121pp; English.
XX
XX The invention relates to an anti-trkC agonist monoclonal antibody which
CC shows no significant cross-reactivity with trkA or trkB, and recognizes
CC an epitope in domain 5 of trkC. The antibodies of the invention are
CC effective in the treatment of cisplatin- or pyridoxine-induced
CC neuropathy, peripheral neuropathy, diabetic neuropathy and large-fibre
CC sensory neuropathy, neurodegenerative disease including amyotrophic
CC lateral sclerosis, nerve cell injuries, disorders of insufficient blood

CC cells such as leukopenia including eosinopenia, basopenia,
CC lymphopenia, monocytopenia, neutropenia, Alzheimer's disease,
CC Parkinson's disease, Huntington's disease and tumours. The sequences are
CC also useful for inducing angiogenesis for treating wounds, ulcers and
CC diabetic complications of sickle cell disease, for treating cardiac
CC ischaemia and cerebrovascular disorders and in the diagnosis of diseases
CC involving cellular degeneration. Sequences AA081229-AA081284 represent
CC human and mouse anti-TRC agonist monoclonal antibodies and antibody
CC fragments of the invention.
SQ Sequence 7 AA;
Query Match 100.0%; Score 38; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WASTRES 7
DB 1 WASTRES 7
RESULT 13
AA070335
ID AA070335 standard; Peptide: 7 AA.
AC AA070335;
XX 14-FEB-2002 (first entry)
DT 14-FEB-2002 (first entry)
DE Human Kappa IV light chain CDR2.
XX
KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
KW complementarity determining region; framework region; IGBP;
KW transgenic plant; immunoglobulin binding protein array;
KW Igm; Igg; Iga; Igd; Ige; Igy; Igm; kappa; lambda; CHBP.
XX
OS Homo sapiens.
XX
PN WO200183806-A1.
XX 08-NOV-2001.
PD 08-NOV-2001.
XX 02-MAY-2001; 2001WO-US14349.
PE 02-MAY-2001; 2000US-0563222.
PR 02-MAY-2000; 2000US-0563222.
XX
PA (EPIC-) EPICYTE PHARM INC.
XX Hiatt AC, Hein MB;
PI Hiatt AC, Hein MB;
XX WPI; 2002-055482/07.
DR
XX
PT Preparing immunoglobulin binding protein array in plant cells by
PT transforming the cells with different polynucleotides encoding binding
PT protein polypeptides specific to ligand, selecting plant cells for
PT preparing array
PS
XX Disclosure; Page 14; 129pp; English.
XX The invention relates to transforming a population of cells (e.g. plant
XX cells), comprising using a library of two different polynucleotides
XX encoding different immunoglobulin binding protein (IGBP) polypeptides
XX that specifically bind to a ligand or form one or more disulphide bonds
XX with polypeptides in transfected cells, to generate an IGBP that
XX binds to a ligand, and transformed plant cells are selected, and
XX preparing an IGBP array in plant cells. At least one peptide sequence has
XX at least 75% sequence identity to a framework region (FR) of a native
XX Igm, Igg, Iga, Igd, Ige, Igy, kappa or lambda immunoglobulin molecule.
XX The method is useful for preparing an immunoglobulin binding protein
XX array, preferably heavy chain binding protein (CHBP) array in eukaryotic
XX cells especially plant cells (e.g. Agrobacterium tumefaciens or maize)
XX or other eukaryotic cells (e.g. insect cells or mammalian cells). The
XX CHBP is useful for discovery of e.g. screening assays of IGBPs having

CC desired characteristics. The present sequence is a mammalian
CC immunoglobulin derived peptide that may be incorporated into an IGBP of
CC the invention.
SQ Sequence 7 AA;
Query Match 100.0%; Score 38; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WASTRES 7
DB 1 WASTRES 7
RESULT 14
AA070347
ID AA070347 standard; Peptide: 7 AA.
AC AA070347;
XX 14-FEB-2002 (first entry)
DT 14-FEB-2002 (first entry)
DE Mouse Kappa I light chain CDR2.
XX
KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
KW complementarity determining region; framework region; IGBP;
KW transgenic plant; immunoglobulin binding protein array;
KW Igm; Igg; Iga; Igd; Ige; Igy; Igm; kappa; lambda; CHBP.
XX
OS Mus musculus.
XX
PN WO200183806-A1.
XX 08-NOV-2001.
PD 08-NOV-2001.
XX 02-MAY-2001; 2001WO-US14349.
PE 02-MAY-2001; 2000US-0563222.
PR 02-MAY-2000; 2000US-0563222.
XX
PA (EPIC-) EPICYTE PHARM INC.
XX Hiatt AC, Hein MB;
PI Hiatt AC, Hein MB;
XX WPI; 2002-055482/07.
DR
XX
PT Preparing immunoglobulin binding protein array in plant cells by
PT transforming the cells with different polynucleotides encoding binding
PT protein polypeptides specific to ligand, selecting plant cells for
PT preparing array
PS
XX Disclosure; Page 14; 129pp; English.
XX The invention relates to transforming a population of cells (e.g. plant
XX cells), comprising using a library of two different polynucleotides
XX encoding different immunoglobulin binding protein (IGBP) polypeptides
XX that specifically bind to a ligand or form one or more disulphide bonds
XX with polypeptides in transfected cells, to generate an IGBP that
XX binds to a ligand, and transformed plant cells are selected, and
XX preparing an IGBP array in plant cells. At least one peptide sequence has
XX at least 75% sequence identity to a framework region (FR) of a native
XX Igm, Igg, Iga, Igd, Ige, Igy, kappa or lambda immunoglobulin molecule.
XX The method is useful for preparing an immunoglobulin binding protein
XX array, preferably heavy chain binding protein (CHBP) array in eukaryotic
XX cells especially plant cells (e.g. Agrobacterium tumefaciens or maize)
XX or other eukaryotic cells (e.g. insect cells or mammalian cells). The
XX CHBP is useful for discovery of e.g. screening assays of IGBPs having
XX immunoglobulin derived peptide that may be incorporated into an IGBP of
XX the invention.
SQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
 |||||
 Db 1 WASTRES 7

RESULT 15

ABP98681
 ID ABP98681 standard; peptide; 7 AA.

XX AC ABP98681;

XX DT 30-MAY-2003 (first entry)

XX DE Human GAH antibody light chain hypervariable region #2.

XX KM human; antibody; epitope; cytostatic; diagnosis; fluorescence wavelength;
 XX KW GAH antibody light chain; hypervariable region; cancer therapy.

XX OS Homo sapiens.

XX PN WO2003010542-A1.

XX PD 06-FEB-2003.

XX PF 25-JUL-2002; 2002WO-JP07547.

XX PR 25-JUL-2001; 2001JP-0224054.

XX PA (MITS-) MITSUBISHI PHARMA CORP.

XX PI Niki H, Tagawa T, Hosokawa S;

XX DR WPI; 2003-229648/22.

PT Cancer diagnostics based on peptide or protein recognizing part of
 PT tissue slice for staining and detection, also applicable in selecting
 PT remedies for cancer therapy and analysis of expression or behaviour of
 PT protein -

XX PS Claim 8; Page 46; 52pp; Japanese.

XX CC The invention relates to diagnostic agents comprising a peptide or a
 CC protein capable of recognizing at least a part of a tissue slice and
 CC a fluorescent substance characterized by: (a) having a fluorescence
 CC wavelength not close to the wavelength region of a non-specific
 CC autofluorescence of the tissue slice at a definite excitation wavelength;
 CC and (b) allowing simultaneous observation of image of the peptide or
 CC protein and that of the tissue slice. This peptide is an example of
 CC a peptide used in the method of the invention and represents the
 CC hypervariable region #2 from the human GAH antibody light chain.
 CC The diagnostic agents are for the detection of cancer, which are also
 CC applicable in selecting remedies for cancer therapy and analysis of
 CC expression and/or behaviour of proteins.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 24; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
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 Db 1 WASTRES 7

Search completed: October 7, 2003, 19:13:53
 Job time : 9.81034 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 19:07:41 ; Search time 3.62069 Seconds
(without alignments)
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Title: US-09-988-013a-2_COPY_56_62

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Sequence: 1 WASTRES 7

Scoring table: BLOSUM62

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Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

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Maximum Match 100%

Listing first 45 summaries

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Published Applications_AA:*

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12: /cgn2_6/ptodata/1/pubppa/US09C_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubppa/US10C_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	38	100.0	7	10	US-09-828-708-43
2	38	100.0	7	10	US-09-828-708-46
3	38	100.0	7	10	US-09-249-011A-18
4	38	100.0	7	11	US-09-563-222-15
5	38	100.0	7	11	US-09-563-222-27
6	38	100.0	7	12	US-10-071-962-19
7	38	100.0	7	14	US-10-146-305-10
8	38	100.0	7	12	US-10-078-958-15
9	38	100.0	94	9	US-09-905-243-60
10	38	100.0	101	14	US-10-025-687-25
11	38	100.0	101	15	US-10-194-975-89
12	38	100.0	101	15	US-10-125-687-25
13	38	100.0	107	12	US-10-325-694-142
14	38	100.0	107	12	US-10-325-694-148
15	38	100.0	107	12	US-10-325-694-149

16	38	100.0	107	12	US-10-325-694-152	Sequence 152, App
17	38	100.0	109	10	US-09-828-708-1	Sequence 1, Appl
18	38	100.0	109	10	US-09-828-708-4	Sequence 4, Appl
19	38	100.0	112	12	US-10-229-335-4	Sequence 4, Appl
20	38	100.0	112	12	US-10-229-335-28	Sequence 28, Appl
21	38	100.0	112	15	US-10-056-052-6	Sequence 6, Appl
22	38	100.0	112	15	US-10-056-052-10	Sequence 10, Appl
23	38	100.0	112	15	US-10-056-052-14	Sequence 14, Appl
24	38	100.0	112	15	US-10-056-052-18	Sequence 18, Appl
25	38	100.0	113	10	US-09-741-843-2	Sequence 2, Appl
26	38	100.0	113	10	US-09-741-843-6	Sequence 6, Appl
27	38	100.0	113	10	US-09-274-163E-16	Sequence 16, Appl
28	38	100.0	113	10	US-09-956-206A-80	Sequence 80, Appl
29	38	100.0	113	11	US-09-894-839-2	Sequence 2, Appl
30	38	100.0	113	11	US-09-894-839-6	Sequence 6, Appl
31	38	100.0	113	11	US-09-894-839-20	Sequence 20, Appl
32	38	100.0	113	11	US-09-895-529-6	Sequence 6, Appl
33	38	100.0	113	11	US-09-988-013A-2	Sequence 2, Appl
34	38	100.0	113	11	US-09-988-013A-6	Sequence 6, Appl
35	38	100.0	113	12	US-10-159-006-2	Sequence 2, Appl
36	38	100.0	113	12	US-10-159-006-4	Sequence 4, Appl
37	38	100.0	113	12	US-10-159-006-6	Sequence 6, Appl
38	38	100.0	113	12	US-10-159-006-32	Sequence 32, Appl
39	38	100.0	113	12	US-10-159-006-33	Sequence 33, Appl
40	38	100.0	113	12	US-10-159-006-34	Sequence 34, Appl
41	38	100.0	113	12	US-10-330-613-22	Sequence 22, Appl
42	38	100.0	113	12	US-10-330-530-22	Sequence 22, Appl
43	38	100.0	113	12	US-10-160-506-71	Sequence 71, Appl
44	38	100.0	113	12	US-10-160-506-91	Sequence 91, Appl
45	38	100.0	113	12	US-09-215-163-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1

US-09-828-708-43

Sequence 43, Application US/09828708

Patent No. US20020146753A1

GENERAL INFORMATION:

APPLICANT: Ditzel, H.

APPLICANT: Burton, D.

APPLICANT: Schaller, M.

TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their part

FILE REFERENCE: 1361.005US1

CURRENT APPLICATION NUMBER: US/09/828,708

CURRENT FILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 123

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 43

LENGTH: 7

TYPE: PRT

ORGANISM: Homo sapiens

US-09-828-708-43

Query Match 100.0%; Score 38; DB 10; Length 7;

Best Local Similarity 100.0%; Pred. No. 5.3e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

WASTRES 7

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Db 1 WASTRES 7

RESULT 2

US-09-828-708-46

Sequence 46, Application US/09828708

Patent No. US20020146753A1

GENERAL INFORMATION:

APPLICANT: Ditzel, H.

APPLICANT: Burton, D.

APPLICANT: Schaller, M.

```

; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particl
; TITLE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005051
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-46

Query Match
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
DB 1 WASTRES 7

RESULT 3
US-09-249-011A-18
; Sequence 18, Application US/09249011A
; Patent No. US20020176855A1
; GENERAL INFORMATION:
; APPLICANT: CO. MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARRENO, BEATRIZ
; APPLICANT: CELINKER, ABRIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GERTRUUDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; FILE REFERENCE: 08702.0081-00000
; CURRENT APPLICATION NUMBER: US/09/249,011A
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDR2 of humanized
US-09-249-011A-18

Query Match
Best Local Similarity 100.0%; Score 38; DB 10; Length 7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
DB 1 WASTRES 7

RESULT 4
US-09-563-222-15
; Sequence 15, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hehn, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; TITLE OF INVENTION: EUKARYOTIC CELLS
; FILE REFERENCE: 310098.406

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; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-563-222-15

Query Match
Best Local Similarity 100.0%; Score 38; DB 11; Length 7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
DB 1 WASTRES 7

RESULT 5
US-09-563-222-27
; Sequence 27, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hehn, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222-27

Query Match
Best Local Similarity 100.0%; Score 38; DB 11; Length 7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
DB 1 WASTRES 7

RESULT 6
US-10-071-962-19
; Sequence 19, Application US/10071962
; Publication No. US20030170237A1
; GENERAL INFORMATION:
; APPLICANT: Baifu NI
; APPLICANT: Bill N.C. Sun
; APPLICANT: Cedilly R.Y. Sun
; TITLE OF INVENTION: G-CSF Receptor Agonist Antibodies and
; FILE REFERENCE: 98-3
; CURRENT APPLICATION NUMBER: US/10/071,962
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US/09/303,155A
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/083,575
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 7
; TYPE: PRT
; ORGANISM: mouse
US-10-071-962-19

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Query Match 100.0%; Score 38; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
Db 1 WASTRES 7

RESULT 7

US-10-146-305-10
; Sequence 10, Application US/10146305
; Publication No. US20020173035A1
; GENERAL INFORMATION:
; APPLICANT: YUHAN CORPORATION
; TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV
; TITLE OF INVENTION: S-SURFACE ANTIGEN AND A GENE ENCODING THE SAME
; FILE REFERENCE: OY17440
; CURRENT APPLICATION NUMBER: US/10/146,305
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: KR 10-2001-26634
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 10
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-146-305-10

Query Match 100.0%; Score 38; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
Db 1 WASTRES 7

RESULT 8

US-10-078-958-15
; Sequence 15, Application US/10078958
; Publication No. US20030070185A1
; GENERAL INFORMATION:
; APPLICANT: JAKOBOVITS, AYA
; APPLICANT: KUCHERLAPATI, RAJU
; APPLICANT: KLAPHOLZ, SUSAN
; APPLICANT: MENDEZ, MICHAEL J.
; APPLICANT: GREEN, LARRY
; TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOCI INCLUDING
; TITLE OF INVENTION: PLURAL VH AND VK REGIONS AND ANTIBODIES PRODUCED
; FILE REFERENCE: CELL 4.18 CON
; CURRENT APPLICATION NUMBER: US/10/078,958
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 08/7759,620
; PRIOR FILING DATE: 1996-12-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-078-958-15

Query Match 100.0%; Score 38; DB 15; Length 82;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
Db 37 WASTRES 43

RESULT 9
US-09-905-243-60
; Sequence 60, Application US/09905243
; Patent No. US20020062009A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Alexander H
; TITLE OF INVENTION: Monoclonal Antibodies with Reduced
; TITLE OF INVENTION: Immunogenicity
; FILE REFERENCE: P50770
; CURRENT APPLICATION NUMBER: US/09/905,243
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/300,970
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Macaca cynomolgus
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (24)...(40)
; OTHER INFORMATION: CDRI
; NAME/KEY: DOMAIN
; LOCATION: (56)...(62)
; OTHER INFORMATION: CDRII
US-09-905-243-60

Query Match 100.0%; Score 38; DB 9; Length 94;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
Db 56 WASTRES 62

RESULT 10

US-10-025-687-25
; Sequence 25, Application US/10025687
; Publication No. US20020142255A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
; FILE REFERENCE: 26050-705
; CURRENT APPLICATION NUMBER: US/10/025,687
; CURRENT FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-025-687-25

Query Match 100.0%; Score 38; DB 14; Length 101;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
Db 56 WASTRES 62

RESULT 11

US-10-194-975-89
; Sequence 89, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01

```

: CURRENT APPLICATION NUMBER: US/10/194,975
: CURRENT FILING DATE: 2002-10-10
: PRIOR APPLICATION NUMBER: US 60/305,111
: PRIOR FILING DATE: 2001-07-12
: NUMBER OF SEQ ID NOS: 122
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 89
: LENGTH: 101
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-194-975-89

Query Match
Best Local Similarity 100.0%; Score 38; DB 15; Length 101;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
   |||||
Db 56 WASTRES 62

RESULT 12
US-10-125-687-25
: Sequence 25, Application US/10125687
: Publication No. US20030054407A1
: GENERAL INFORMATION:
: APPLICANT: Luo, Peter
: TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
: FILE REFERENCE: 26050-705
: CURRENT APPLICATION NUMBER: US/10/125,687
: CURRENT FILING DATE: 2002-04-17
: NUMBER OF SEQ ID NOS: 28
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 25
: LENGTH: 101
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-125-687-25

Query Match
Best Local Similarity 100.0%; Score 38; DB 15; Length 101;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
   |||||
Db 56 WASTRES 62

RESULT 13
US-10-325-694-142
: Sequence 142, Application US/10325694
: Publication No. US20030148463A1
: GENERAL INFORMATION:
: APPLICANT: KUFER, PETER
: APPLICANT: RAUM, TOBIAS
: TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
: TITLE OF INVENTION: RECEPTORS AND USES THEREOF
: FILE REFERENCE: 38164000
: CURRENT APPLICATION NUMBER: US/10/325,694
: CURRENT FILING DATE: 2002-12-19
: PRIOR APPLICATION NUMBER: US/09/403,107
: PRIOR FILING DATE: 1999-10-14
: NUMBER OF SEQ ID NOS: 152
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 142
: LENGTH: 107
: TYPE: PRT
: ORGANISM: HUMAN
US-10-325-694-142

Query Match
Best Local Similarity 100.0%; Score 38; DB 12; Length 107;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY 1 WASTRES 7
   |||||
Db 50 WASTRES 56

RESULT 14
US-10-325-694-148
: Sequence 148, Application US/10325694
: Publication No. US20030148463A1
: GENERAL INFORMATION:
: APPLICANT: KUFER, PETER
: APPLICANT: RAUM, TOBIAS
: TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
: TITLE OF INVENTION: RECEPTORS AND USES THEREOF
: FILE REFERENCE: 38164000
: CURRENT APPLICATION NUMBER: US/10/325,694
: CURRENT FILING DATE: 2002-12-19
: PRIOR APPLICATION NUMBER: US/09/403,107
: PRIOR FILING DATE: 1999-10-14
: NUMBER OF SEQ ID NOS: 152
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 148
: LENGTH: 107
: TYPE: PRT
: ORGANISM: HUMAN
US-10-325-694-148

Query Match
Best Local Similarity 100.0%; Score 38; DB 12; Length 107;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
   |||||
Db 50 WASTRES 56

RESULT 15
US-10-325-694-149
: Sequence 149, Application US/10325694
: Publication No. US20030148463A1
: GENERAL INFORMATION:
: APPLICANT: KUFER, PETER
: APPLICANT: RAUM, TOBIAS
: TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
: TITLE OF INVENTION: RECEPTORS AND USES THEREOF
: FILE REFERENCE: 38164000
: CURRENT APPLICATION NUMBER: US/10/325,694
: CURRENT FILING DATE: 2002-12-19
: PRIOR APPLICATION NUMBER: US/09/403,107
: PRIOR FILING DATE: 1999-10-14
: NUMBER OF SEQ ID NOS: 152
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 149
: LENGTH: 107
: TYPE: PRT
: ORGANISM: HUMAN
US-10-325-694-149

Query Match
Best Local Similarity 100.0%; Score 38; DB 12; Length 107;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: October 7, 2003, 19:24:24
Job time : 3.62069 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 7, 2003, 19:07:11 ; Search time 2.6069 Seconds

(without alignments)
258.231 Million cell updates/sec

Title: US-09-988-013a-2_COPY_56_62

Perfect score: 38

Sequence: 1 WASTRES 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_76:***
1: p1r1:***
2: p1r2:***
3: p1r3:***
4: p1r4:***

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	100.0	81	2 PH1048	Ig light chain V r
2	38	100.0	92	2 S37533	Ig kappa chain V r
3	38	100.0	92	2 S37530	Ig kappa chain V r
4	38	100.0	92	2 S37529	Ig kappa chain V r
5	38	100.0	92	2 S37535	Ig kappa chain V r
6	38	100.0	92	2 S37531	Ig kappa chain V r
7	38	100.0	92	2 S37534	Ig kappa chain V r
8	38	100.0	92	2 S37532	Ig kappa chain V r
9	38	100.0	98	2 S19974	Ig kappa chain V r
10	38	100.0	101	2 S26337	Ig kappa chain V r
11	38	100.0	101	2 PH1046	Ig light chain V r
12	38	100.0	101	2 PH0869	Ig kappa chain V r
13	38	100.0	102	2 A34153	Ig kappa chain V r
14	38	100.0	103	2 PH1050	Ig light chain V r
15	38	100.0	103	2 PH1051	Ig light chain V r
16	38	100.0	103	2 PH1052	Ig light chain V r
17	38	100.0	103	2 PH1054	Ig light chain V r
18	38	100.0	103	2 PH1047	Ig light chain V r
19	38	100.0	104	2 PH1101	Ig light chain V r
20	38	100.0	104	2 PH1102	Ig light chain V r
21	38	100.0	104	2 PH1103	Ig light chain V r
22	38	100.0	104	2 PH1104	Ig light chain V r
23	38	100.0	104	2 F38601	Ig kappa chain V r
24	38	100.0	106	2 A49138	Ig kappa chain V r
25	38	100.0	111	2 S03304	Ig kappa chain V r
26	38	100.0	111	2 G30502	Ig kappa chain V r
27	38	100.0	112	2 PI0265	Ig kappa chain V r
28	38	100.0	112	2 S09970	Ig kappa chain V r
29	38	100.0	112	2 S43103	Ig kappa chain V-J

30	38	100.0	113	2 S30523	Ig kappa chain V r
31	38	100.0	113	2 PI0263	Ig kappa chain V r
32	38	100.0	113	2 S34003	Ig kappa chain V r
33	38	100.0	113	2 S34002	Ig kappa chain V r
34	38	100.0	114	1 K4HUN	Ig kappa chain V r
35	38	100.0	114	2 S44116	Ig kappa chain V-J
36	38	100.0	114	2 S44119	Ig kappa chain V-J
37	38	100.0	118	2 PT0356	Ig kappa chain V r
38	38	100.0	120	2 G33932	Ig kappa chain pre
39	38	100.0	120	2 S51147	Ig kappa chain pre
40	38	100.0	121	1 K4HU	Ig kappa chain pre
41	38	100.0	129	2 S40329	Ig kappa chain pre
42	38	100.0	129	2 S40347	Ig kappa chain - h
43	38	100.0	133	1 K4HUI	Ig kappa chain pre
44	38	100.0	133	2 PS0023	Ig kappa chain pre
45	38	100.0	134	2 PC1214	Ig kappa chain pre

ALIGNMENTS

RESULT 1

PH1048
Ig light chain V region (clone 165.49) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996

C/Accession: PH1048

R/Tillman, D.M.; Jou, N.T.; Hall, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A/Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A/Reference number: PH0971; MUID:92381444; PMID:1512540

A/Accession: PH1048

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-81 <Till>

A/Experimental source: B cell, strain [NZB x NZW]F1

C/Superfamily: Immunoglobulin V region; Immunoglobulin homology

C/Keywords: Immunoglobulin

Query Match 100.0%; Score 38; DB 2; Length 81;

Best Local Similarity 100.0%; Pred. No. 0.29; 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7

Db 35 WASTRES 41

RESULT 2

S37533
Ig kappa chain V region (V-Kappa 4) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C/Accession: S37533

R/Klein, U.; Kuipers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993

A/Description: Human IGM(+)IGD(+) cells, the major B cell subset in the peripheral bl

A/Reference number: S37501

A/Accession: S37533

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-92 <Klein>

A/Cross-references: EMBL:Z26627; NID:9405708; PTDN:CA81380.1; PTD:9405709

C/Superfamily: Immunoglobulin V region; Immunoglobulin homology

C/Keywords: heterotrimer; Immunoglobulin

Query Match 100.0%; Score 38; DB 2; Length 92;

Best Local Similarity 100.0%; Pred. No. 0.34; 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7

Db 34 WASTRES 40

```
RESULT 3
S37530
Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37530
R:Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+)IGD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37530
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <RLE>
A:Cross-references: EMBL:226630; NID:g405702; PIDN:CAA81383.1; PID:g405703
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin

Query Match
Best Local Similarity 100.0%; Score 38; DB 2; Length 92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
DB 34 WASTRES 40

RESULT 4
S37529
Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37529
R:Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+)IGD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37529
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <RLE>
A:Cross-references: EMBL:226631; NID:g405700; PIDN:CAA81384.1; PID:g405701
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin

Query Match
Best Local Similarity 100.0%; Score 38; DB 2; Length 92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
DB 34 WASTRES 40

RESULT 5
S37535
Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37535
R:Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+)IGD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37535
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <RLE>
A:Cross-references: EMBL:226625; NID:g405712; PIDN:CAA81378.1; PID:g405713
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
```

```
Query Match
Best Local Similarity 100.0%; Score 38; DB 2; Length 92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
DB 34 WASTRES 40

RESULT 6
S37531
Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37531
R:Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+)IGD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37531
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <RLE>
A:Cross-references: EMBL:226629; NID:g405704; PIDN:CAA81382.1; PID:g405705
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin

Query Match
Best Local Similarity 100.0%; Score 38; DB 2; Length 92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
DB 34 WASTRES 40

RESULT 7
S37534
Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37534
R:Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+)IGD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37534
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <RLE>
A:Cross-references: EMBL:226626; NID:g405710; PIDN:CAA81379.1; PID:g405711
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin

Query Match
Best Local Similarity 100.0%; Score 38; DB 2; Length 92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
DB 34 WASTRES 40

RESULT 8
S37532
Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37532
R:Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+)IGD(+) cells, the major B cell subset in the peripheral blood
```


A:Reference number: S37501
A:Accession: S37532
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <RLE>
A:Cross-references: EMBL:Z26628; NID:q405706; PIDN:CAA81381.1; PID:q405707
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; Immunoglobulin

Query Match 100.0%; Score 38; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
|||||||
Db 34 WASTRES 40

RESULT 9

S19974
Ig kappa chain V region (M-T406) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S19974
R:Weissenborn, W.; Rietmuller, G.; Weiss, E.M.; Rieber, E.P.
Submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mab.
A:Reference number: S19963
A:Accession: S19974
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-98 <WEI>
A:Cross-references: EMBL:X65096; NID:q52294; PIDN:CAA46224.1; PID:q52295
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; Immunoglobulin
F:1-80/Domain: Immunoglobulin homology <IM>

Query Match 100.0%; Score 38; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
|||||||
Db 40 WASTRES 46

RESULT 10

S26337
Ig light chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 20-Jun-2000
C:Accession: S26337; S78449
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein
A:Reference number: S26309; MUID:91341421; PMID:1908510
A:Accession: S26337
A:Molecule type: mRNA
A:Residues: 1-101 <SFA>
A:Cross-references: EMBL:X59193
R:Caton, A.J.
Submitted to the EMBL Data Library, April 1991
A:Reference number: S78447
A:Accession: S78449
A:Molecule type: mRNA
A:Residues: 1-60, 'T', 62-91, 'S', 93-101 <CAT>
A:Cross-references: EMBL:X59193; NID:q52323; PIDN:CAA1903.1; PID:q1334067
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; Immunoglobulin
F:8-88/Domain: Immunoglobulin homology <IM>

Query Match 100.0%; Score 38; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.37;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 WASTRES 7
|||||||
Db 48 WASTRES 54

RESULT 11

PH1046
Ig light chain V region (clone 202.9) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1046
R:Trillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1046
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-101 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]P1
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: Immunoglobulin
F:16-96/Domain: Immunoglobulin homology <IM>

Query Match 100.0%; Score 38; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
|||||||
Db 56 WASTRES 62

RESULT 12

PH0869
Ig kappa chain V region (anti-DNA, H2F) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
C:Accession: PH0869
R:Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghosssein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A:Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiot
A:Reference number: PH0862; MUID:92078875; PMID:1660528
A:Accession: PH0869
A:Molecule type: DNA
A:Residues: 1-101 <MAN>
A:Note: residues 28-33 were obtained from Figure 4
C:Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that be
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; Immunoglobulin
F:1-23/Region: framework 1
F:16-96/Domain: Immunoglobulin homology <IM>
F:24-40/Region: complementarity-determining 1
F:41-55/Region: framework 2
F:56-62/Region: complementarity-determining 2
F:63-94/Region: framework 3
F:95-101/Region: complementarity-determining 3

Query Match 100.0%; Score 38; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
|||||||
Db 56 WASTRES 62

RESULT 13

A34153
Ig kappa chain V-IV region (Dep) - human
C:Species: Homo sapiens (man)

C:Date: 11-Apr-1990 #sequence_revision 11-Apr-1990 #text_change 21-Jan-2000
C:Accession: A34153
R:Milnesco, E.; Ayadi, H.; Congy, N.; Gendton, M.C.; Roy, J.P.; Heyermann, H.; Frangione
J. Biol. Chem. 264, 21481-21485, 1989
A:Title: Multiple mutations in the variable region of the kappa light chains of three mo
A:Reference number: A34153; MUID:90094313; PMID:2480953
A:Accession: A34153
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-102 <MIR>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
DB 56 WASTRES 62

RESULT 14

PH1050
Ig light chain V region (clone 111-c1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1050
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1050
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-103 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
DB 56 WASTRES 62

RESULT 15

PH1051
Ig light chain V region (clone 165.3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1051
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1051
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-103 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
|||||
DB 56 WASTRES 62

Search completed: October 7, 2003, 19:21:47
Job time : 2.6069 secs

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OM protein - protein search, using sw model

Run on: October 7, 2003, 19:03:46 ; Search time 1.42414 Seconds

(without alignments)
231.148 Million cell updates/sec

Title: US-09-988-013a-2_COPY_56_62

Perfect score: 38

Sequence: 1 WASTRES 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	100.0	109	KV4D_HUMAN	P83593 homo sapien
2	38	100.0	114	KV4A_HUMAN	P01625 homo sapien
3	38	100.0	121	KV4B_HUMAN	P06312 homo sapien
4	38	100.0	133	KV4C_HUMAN	P06313 homo sapien
5	38	100.0	134	KV4D_HUMAN	P06314 homo sapien
6	32	84.2	685	SYM_NEIM	O91290 neisseria m
7	31	81.6	382	THRC_SYNY3	P71193 synecocyst
8	30	78.9	497	GLPK_PYRKO	O93623 pyrococcus
9	30	78.9	668	COAT_FCVF4	P27405 feline cali
10	30	78.9	675	SG1_RAT	O35314 rattus norv
11	30	78.9	677	SG1_MOUSE	O35314 rattus norv
12	30	78.9	1139	HMW1_MOUSE	O49413 mycoplasma
13	30	78.9	2365	CCAH_MOUSE	O88427 mus musculu
14	30	78.9	3414	POLG_TBRYH	O01299 t genome po
15	30	78.9	3414	POLG_TBRYH	P14336 t genome po
16	29	76.3	227	ATP6_BRAFL	O47426 branchiosto
17	29	76.3	227	ATP6_BRAFL	O02104 branchiosto
18	29	76.3	413	RCA_CUCSA	O01587 cucumis sat
19	29	76.3	420	O63A_DROME	O92528 drosophila
20	29	76.3	425	RCA_HORVU	O42450 hordeum vul
21	29	76.3	430	HEMA_CVMS	P31614 murine coro
22	29	76.3	433	RCA_MALIZ	O92100 zea mays (m
23	29	76.3	437	RCA_MALIZ	O40281 malus domes
24	29	76.3	439	HEMA_CVMS	O83356 murine coro
25	29	76.3	439	RCA_MALIZ	O40565 nicotiana t
26	29	76.3	441	RCA_PHAVU	O64981 phaseolus v
27	29	76.3	442	RCA_TORAC	O40460 nicotiana t
28	29	76.3	451	TIN2_HUMAN	O93514 homo sapien
29	29	76.3	459	RCA_LYCPN	O49074 lycopersico
30	29	76.3	472	RCA_SPIOL	P10871 spinacia ol
31	29	76.3	474	RCA_ARAFH	P10896 arabidopsis
32	29	76.3	574	MP12_RAT	P48966 rattus norv
33	29	76.3	580	MP12_HUMAN	P30305 homo sapien

34	29	76.3	685	SYM_NEIM	O91290 neisseria m
35	29	76.3	717	MCCA_MOUSE	O99m8 mus musculu
36	29	76.3	1653	YFHM_ECOLI	P76578 escherichia
37	28	73.7	79	Y52A_MYCLE	O05755 mycobacteri
38	28	73.7	179	KPFA_FUSNN	O8113 mus musculu
39	28	73.7	203	SP24_MOUSE	P35783 vesipula fla
40	28	73.7	204	VAS_VESFL	P35784 vesipula fla
41	28	73.7	204	VAS_VESGE	P35760 vesipula ger
42	28	73.7	204	VAS_VESMC	P35785 vesipula pen
43	28	73.7	205	VAS_VESPE	O92528 homo sapien
44	28	73.7	217	TAL_CAUCR	O92521 caulobacter
45	28	73.7	217	TAL_CAUCR	O92521 caulobacter

ALIGNMENTS

RESULT 1					
KV4D_HUMAN	STANDARD;	PRT;	109 AA.		
AC P83593;					
DT 15-SEP-2003 (Rel. 42, Created)					
DT 15-SEP-2003 (Rel. 42, Last sequence update)					
DT 15-SEP-2003 (Rel. 42, Last annotation update)					
DE 19 kappa chain V-IV region STR (Fragment).					
OS Homo sapiens (Human).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
OX NCBI_TaxID=9606;					
RN [1]					
RP SEQUENCE.					
RC TISSUE=Abdominal adipose tissue;					
RA PubMed-9588180;					
RX Olsen K.E., Sletten K., Westermarck P.;					
RT "Extended analysis of Al-amyloid protein from abdominal wall					
RT subcutaneous fat biopsy: kappa IV immunoglobulin light chain.";					
RL Biochem. Biophys. Res. Commun. 245:713-716(1998).					
CC -1 - FUNCTION: May play an important role in fibrillogenesis.					
DR InterPro: IPR003599; Ig.					
DR InterPro: IPR007110; Ig-like.					
DR InterPro: IPR003596; Ig-V.					
DR Pfam: PF00047; Ig_1.					
DR PROSITE: PS50835; IG-LIKE; 1.					
KW Immunoglobulin V region.					
FT DOMAIN 1 23					
FT DOMAIN 24 40					
FT DOMAIN 41 55					
FT DOMAIN 56 62					
FT DOMAIN 63 94					
FT DOMAIN 95 101					
FT DISULFD 102 109					
FT DISULFD 23 94					
FT UNSURE 23 23					
FT UNSURE 94 94					
FT NON_TER 109 109					
SO SEQUENCE 109 AA; 12060 MW; 0C4F31EA11E12A0B CRC64;					
Query Match 100.0%; Score 38; DB 1; Length 109;					
Best Local Similarity 100.0%; Pred. NO. 0.21;					
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
OY 1 WASTRES 7					
DB 56 WASTRES 62					
RESULT 2					
KV4A_HUMAN	STANDARD;	PRT;	114 AA.		
ID KV4A_HUMAN					
AC P01625;					
DT 21-JUN-1986 (Rel. 01, Created)					
DT 01-OCT-1996 (Rel. 34, Last sequence update)					
DT 15-SEP-2003 (Rel. 42, Last annotation update)					

```

DE Ig kappa chain V-IV region Len.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=76004342; PubMed=50995;
RA Schneider M., Hilschmann N.;
RT "The primary structure of a monoclonic immunoglobulin-L-chain of
RT subgroup IV of the kappa type (Bence-Jones protein Len).";
RL Hoppe-Sejler's Z. Physiol. Chem. 356:507-557(1975).
RN [2]
RP REVISION TO 9.
RA Salomon A.;
RC Submitted (AUG-1996) to the SWISS-PROT data bank.
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DR PDB: 1LEO; 01-FEB-01.
DR PDB: 1LEU; 03-FEB-01.
DR PDB: 1ER3; 09-FEB-01.
DR PDB: 1ER3; 06-MAR-01.
DR PDB: 1LVE; 21-JAN-98.
DR PDB: 1LVE; 18-MAY-99.
DR PDB: 1LVE; 28-MAR-01.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR pfam: PF00047; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Bence-Jones protein; 3D-structure.
KW DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 40 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 41 55 FRAMEWORK-2.
FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 63 94 FRAMEWORK-3.
FT DOMAIN 95 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 113 FRAMEWORK-4.
FT DISULFID 23 94 BY SIMILARITY.
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12640 MW; 0647FD17F236485 CRC64;

Query Match 100.0%; Score 38; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
DB 56 WASTRES 62

RESULT 3
KV40_HUMAN STANDARD; PRT; 121 AA.
AC P06312;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-IV region precursor (Fragment).
GN IGKV4-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=86041853; PubMed=2997712;
RA Kloebeck H.G., Bornkamm G.W., Combrato G., Mocklat R., Pohlentz H.D.,
RA Zachau H.G.;

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RT *Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene."
RL Nucleic Acids Res. 13:6515-6529(1985).
CC -1- MISCELLANEOUS: THERE IS ONLY ONE IG KAPPA V-IV GENE.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; 200023; CAA77318.1; .
DR PIR; A01902; K4HD.
DR HSSP; P80362; 1WTL.
DR GeneW; HGNC:5834; IGKV4-1.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR pfam: PF00047; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL 1 20
FT CHAIN 21 >121 IG KAPPA CHAIN V-IV REGION.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 114 BY SIMILARITY.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13380 MW; 9586AD4188D33974 CRC64;

Query Match 100.0%; Score 38; DB 1; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
DB 76 WASTRES 82

RESULT 4
KV4B_HUMAN STANDARD; PRT; 133 AA.
AC P06313;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region JI precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=86041853; PubMed=2997712;
RA Kloebeck H.G., Bornkamm G.W., Combrato G., Mocklat R., Pohlentz H.D.,
RA Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene."
RL Nucleic Acids Res. 13:6515-6529(1985).
CC -----
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CC EMBL: Z00022; CAA77317.1; -
CC PIR: A01904; K4HUIJ.
CC HSSP: P80362; 1MTL.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
DR PROSITE: PS50835; IG-LIKE; 1.
KM Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133 IG KAPPA CHAIN V-IV REGION JT.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 122 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 123 132 FRAMEWORK-4.
FT DISULFID 43 114 BY SIMILARITY.
FT NON_TER 133 133
SQ SEQUENCE 133 AA; 14632 MW; 5FB3953066744AF4 CRC64;
Query Match 100.0%; Score 38; DB 1; Length 133;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 76 WASTRES 82

OY 1 WASTRES 7
DB 76 WASTRES 82

RESULT 5
KVAC_HUMAN STANDARD; PRT; 134 AA.
ID P06314;
AC 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region B17 precursor.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:86041854; PubMed:2997713;
RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned cDNA probe."
RL Nucleic Acids Res. 13:6531-6544(1985).
RN [2]
RP REVISION TO 76.
RA Marsh P.;
CC Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
CC -----
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CC or send an email to license@isb-sib.ch).

CC EMBL: X02990; CAA26733.1; -
CC HSSP: P80362; 1MTL.

DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
DR PROSITE: PS50835; IG-LIKE; 1.
KM Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 134 IG KAPPA CHAIN V-IV REGION B17.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 121 FRAMEWORK-4.
FT DOMAIN 122 133 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 114 BY SIMILARITY.
FT NON_TER 134 134
SQ SEQUENCE 134 AA; 14966 MW; 6413A22ED0738832 CRC64;
Query Match 100.0%; Score 38; DB 1; Length 134;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 76 WASTRES 82

OY 1 WASTRES 7
DB 76 WASTRES 82

RESULT 6
SYM_NEIMA STANDARD; PRT; 685 AA.
ID Q0JWP0;
AC 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Methionyl-tRNA synthetase (EC 6.1.1.10) (methionine--tRNA ligase)
DE (metrs).
GN METG OR NMA0275.
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OC NCBI_TaxID:65699;
RN [1]
RP SEQUENCE FROM N.A.
RC SYRAIN-22491 / Serogroup A / Serotype 4A;
RX MEDLINE:20222556; PubMed:10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holtroyd S.,
RA Jagers K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrall B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491."
RL Nature 404:502-506(2000).
CC -I- FUNCTION: is required not only for elongation of protein synthesis
CC but also for the initiation of all mRNA translation through
CC initiator tRNA(fmet) aminoacylation (by similarity).
CC -I- CATALYTIC ACTIVITY: ATP + L-methionine + tRNA(Met) -> AMP +
CC diphosphate + L-methionyl-tRNA(Met).
CC -I- COFACTOR: Binds 1 zinc ion per subunit (by similarity).
CC -I- SUBUNIT: Homodimer (by similarity).
CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
CC -I- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC Metg subfamily 1.
CC -I- SIMILARITY: Contains 1 tRNA-binding domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL, AL162752; CAB83583.1; -
CC PIR, G82022; G82022.
CC HSSP, P00959; IMEX.
CC HAMAP, MF_00098; fused; 1.
CC InterPro, IPR004495; Metc_Cterm.
CC InterPro, IPR002300; tRNA-synt_1a.
CC InterPro, IPR001412; tRNA-synt_1.
CC InterPro, IPR002304; tRNA-synt_mec.
CC InterPro, IPR002347; tRNA-synt.
CC Pfam, PF00133; tRNA-synt_1; 1.
CC Pfam, PF01588; tRNA-synt_1; 1.
CC PIRSF, PIRSF001528; Metrs_dimerising; 1.
CC PRINTS, PR01041; TRNASYNTHMET.
CC TIGRFAMs, TIGR00398; metc; 1.
CC TIGRFAMs, TIGR00399; metc_C-term; 1.
CC PROSITE, PS00178; AA_TRNA_LIGASE_I; 1.
CC PROSITE, PS00886; TRBD; 1.
CC Aminoacyl-tRNA synthetase; Protein biosynthesis; ligase; ATP-binding;
CC tRNA-binding; tRNA-binding; Metal-binding; Zinc; Complete proteome.
CC SITE 12 22 "HIGH" REGION.
CC SITE 339 343 "MASKS" REGION.
CC DOMAIN 582 685 tRNA-BINDING.
CC METAL 143 143 ZINC (BY SIMILARITY).
CC METAL 146 146 ZINC (BY SIMILARITY).
CC METAL 156 156 ZINC (BY SIMILARITY).
CC METAL 159 159 ZINC (BY SIMILARITY).
CC BINDING 342 342 ATP (BY SIMILARITY).
CC SEQUENCE 685 AA; 76984 MW; 07FD45915ED3BEF3 CRC64;

Query Match 84.2%; Score 32; DB 1; Length 685;
Best Local Similarity 71.4%; Pred. No. 29;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
DB 520 WANTRET 526
|:|:|:|:

RESULT 7
THRC_SYNY3 STANDARD; PRT; 382 AA.
AC THRC_SYNY3
DT 15-DEC-1998 (rel. 37; Created)
DT 15-DEC-1998 (rel. 37; Last sequence update)
DT 28-FEB-2003 (rel. 41; Last annotation update)
DE Threonine synthase (EC 4.2.3.1).
GN THRC OR SLI172.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905221;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hikosawa M., Sugita A., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naidu K., Okumura S.,
RA Shimpou S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT *Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Rep. 3:109-116(1996).
CC -1- CATALYTIC ACTIVITY: O-phospho-L-homoserine + H(2)O -> L-threonine +
CC phosphate.
CC -1- COFACTOR: Pyridoxal phosphate (By similarity).
CC -1- PATHWAY: Threonine biosynthesis.
CC -1- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL, D90913; BAA18282.1; -
CC PIR, S75823; S75823.
CC HSSP, Q95785; 1ESX.
CC InterPro, IPR001926; B6_enzyme_beta.
CC InterPro, IPR000634; S/T_denhydrtase.
CC InterPro, IPR004450; Thr_synthase.
CC Pfam, PF00291; PALP; 1.
CC TIGRFAMs, TIGR00260; thrC; 1.
CC PROSITE, PS00165; DEHYDRATASE_SER_THR; 1.
CC Threonine biosynthesis; Lyase; Pyridoxal phosphate; Complete proteome.
CC BINDING 93 93 PYRIDOXAL PHOSPHATE (PROBABLE).
CC SEQUENCE 382 AA; 40414 MW; FBC9AEEC2B7F6F35 CRC64;

Query Match 81.6%; Score 31; DB 1; Length 382;
Best Local Similarity 71.4%; Pred. No. 26;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7
DB 265 WASTRES 291
|:|:|:|:

RESULT 8
GLPK_PYRKO STANDARD; PRT; 497 AA.
AC GLPK_PYRKO
DT 30-MAY-2000 (rel. 39; Created)
DT 30-MAY-2000 (rel. 39; Last sequence update)
DT 28-FEB-2003 (rel. 41; Last annotation update)
DE Glycerol kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase)
DE (Glycerokinase) (GK).
GN GLPK.
OS Pyrococcus kodakarensis.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Thermococcus.
OX NCBI_TaxID=69014;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN-KOD1;
RX MEDLINE=99127861; PubMed=9930671;
RA Koga Y., Morikawa M., Haruki M., Nakamura H., Imanaka T., Kanaya S.;
RT "The most stable glycerol kinase from a hyperthermophilic archaeon: gene
RT cloning and characterization of the recombinant enzyme.";
RL Protein Eng. 11:1219-1227(1998).
CC -1- FUNCTION: Key enzyme in the regulation of glycerol uptake and
CC metabolism. Can utilize other nucleoside triphosphates than ATP as
CC a phosphoryl donor.
CC -1- CATALYTIC ACTIVITY: ATP + glycerol -> ADP + glycerol 3-phosphate.
CC -1- PATHWAY: Glycerol utilization; rate-limiting step.
CC -1- SUBUNIT: Homodimer.
CC -1- MISCELLANEOUS: The optimum pH and temperature are 8.0 and 80
CC degrees Celsius respectively.
CC -1- SIMILARITY: BELONGS TO THE GLUCOKINASE / GLUCONOKINASE /
CC GLYCEROKINASE / XYLOKINASE FAMILY.
CC -----
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CC -----
CC EMBL, AB012099; BAA34909.1; -

DR PIR: T43888; T43888.
 DR HMAP: P08859; 1GLC.
 DR HAMAP: MF-00186; -; 1.
 DR InterPro: IPR000577; FGXY_kin.
 DR InterPro: IPR005999; Glycerol_kin.
 DR Pfam: PF00370; FGXY_1.
 DR Pfam: PF02782; FGXY_C_1.
 DR TIGRfam: TIGR01311; glycerol_kin; 1.
 DR PROSITE: PS00445; FGXY_KINASES_2; 1.
 DR PROSITE: PS00933; FGXY_KINASES_1; 1.
 DR Glycerol metabolism; transferase; kinase; ATP-binding.
 FT NE_BIND 151 163 ATP (PROBABLY).
 SO SEQUENCE 497 AA; 55904 MW; 91A0A16D9735B56 CRC64;

Query Match 78.9%; Score 30; DB 1; Length 497;
 Best Local Similarity 83.3%; Pred. No. 56;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WASTRE 6
 |||||
 DB 445 WADTRE 450

RESULT 9

COAT_FCVF4 STANDARD; PRT; 668 AA.
 AC P27405;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE Coat protein (capsid protein).
 OS Feline calicivirus (strain Japanese F4) (FCV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
 OC Vesivirus.
 NC NCB1_Taxid=11980;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=91306470; PubMed=1853578;
 RA Tshya Y., Taniguchi Y., Takahashi E., Utagawa E., Takeda N.,
 RA Miyamura K., Yamazaki S., Mikami T.;
 RT "Sequence analysis of the 3'-end of feline calicivirus genome.";
 RL Virology 183:810-814(1991).
 CC -1- SIMILARITY: TO CAPSID PROTEIN OF OTHER CALICIVIRUSES.
 CC -----
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DR EMBL: D90357; BAAL4371.1; -.
 DR PIR: B40481; VCMWRC.
 DR InterPro: IPR004005; Calic1_coat.
 DR Pfam: PF00915; Calic1_coat; 1.
 KW Coat protein; Glycoprotein.
 FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 304 304 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 399 399 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 668 AA; 73589 MW; 85BDCB85804E503 CRC64;

Query Match 78.9%; Score 30; DB 1; Length 668;
 Best Local Similarity 71.4%; Pred. No. 76;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WASTRES 7
 |||||
 DB 72 WASTHEA 78

RESULT 10

SG1_RAT STANDARD; PRT; 675 AA.
 AC 035314; 090YGB; 090VH1;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Secretogranin I precursor (Sg1) (Chromogranin B) (Cgb) (Glucagonoma
 peptide) [Contains: GAWK peptide; CCB peptide].
 GN CGB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NC NCB1_Taxid=101116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley;
 RX MEDLINE=90351888; PubMed=2641278;
 RA Forsa-Petter S., Danielson P., Battenberg E., Bloom F.,
 RA Sutcliffe J.G.;
 RT "Nucleotide sequence and cellular distribution of rat chromogranin B
 (secretogranin I) mRNA in the neuroendocrine system.";
 RL J. Mol. Neurosci. 1:63-75(1989).
 CC [2]
 CC PARTIAL SEQUENCE.
 CC TISSUE=Glucagonoma;
 RX MEDLINE=92063871; PubMed=1954895;
 RA Nielsen E., Welinder B.S., Madsen O.D.;
 RT "Chromogranin-B, a putative precursor of eight novel rat glucagonoma
 peptides through processing at mono-, di-, or tribasic residues.";
 RL Endocrinology 129:3147-3156(1991).
 CC -1- FUNCTION: NEUROENDOCRINE SECRETORY GRANULE PROTEIN, WHICH MAY BE
 CC THE PRECURSOR FOR OTHER BIOLOGICALLY ACTIVE PEPTIDES.
 CC -1- SUBCELLULAR LOCATION: NEUROENDOCRINE AND ENDOCRINE SECRETORY
 CC GRANULES (BY SIMILARITY).
 CC -1- PTM: EXTENSIVELY PROCESSED IN GLUCAGONOMA TISSUE BY LIMITED
 CC PROTEOLYSIS AT CONSERVED BASIC RESIDUES. ALTERNATIVE PROCESSING
 CC ARE SEEN IN DIFFERENT TISSUES. THE PROGLUCAGON-CONVERTING ENZYMES
 CC PRESENT IN TRANSFORMED ALPHA-CELLS ARE LIKELY CANDIDATES TO BE
 CC INVOLVED IN TISSUE-SPECIFIC PROCESSING.
 CC -1- SIMILARITY: BELONGS TO THE CHROMOGRANIN / SECRETOGANIN PROTEIN
 CC FAMILY.
 CC -----
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DR EMBL: AF019974; AAB72089.1; -.
 DR InterPro: IPR001819; Chromogranin_AB.
 DR InterPro: IPR001900; Granin.
 DR Pfam: PF01271; Granin; 1.
 DR PRINTS: PR00659; CHROMOGRANIN.
 DR PROSITE: PS00422; GRANINS_1; 1.
 DR PROSITE: PS00423; GRANINS_2; 1.
 KW Sulfation; Cleavage on pair of basic residues; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 675
 FT PEPTIDE 435 508 SECRETORANIN I.
 FT PEPTIDE 615 674 GAWK PEPTIDE (BY SIMILARITY).
 FT DISULFID 36 57 CCB PEPTIDE (BY SIMILARITY).
 FT MOD_RES 171 171 BY SIMILARITY.
 FT MOD_RES 339 339 SULEFATION (POTENTIAL).
 SO SEQUENCE 675 AA; 77392 MW; 2D3D71DB4C0ABE48 CRC64;

Query Match 78.9%; Score 30; DB 1; Length 675;
 Best Local Similarity 83.3%; Pred. No. 77;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRE 6
DB 97 WASSRE 102

RESULT 11

SG1_MOUSE STANDARD; PRT; 677 AA.

AC P16014;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Secretogranin I precursor (Sgi) (Chromogranin B) (cgb).
GN CHGB OR SCG1 OR SCG-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]

RP SEQUENCE FROM N.A.
RC TISSUE=pituitary;
MEDLINE=90206804; PubMed=2320426;
RA Linard C.G., Mikiy M., Seldah N.G., Chretien M.;
RT "Primary structure of mouse chromogranin B deduced from cDNA
sequence."
RL Nucleic Acids Res. 18:1298-1298(1990).
RN [2]

RP SEQUENCE FROM N.A.
RC MEDLINE=90242932; PubMed=2335203;
RA Pohl T.M., Phillips E., Song K., Gerdes H.H., Huttner W.B.,
RT Ruehner U.;
RT "The organization of the mouse chromogranin B (secretogranin I)
gene."

RT FEBS Lett. 262:219-224(1990).
CC -1- FUNCTION: SECRETOGRANIN I IS A NEUROENDOCRINE SECRETORY GRANULE
PROTEIN, WHICH MAY BE THE PRECURSOR FOR OTHER BIOLOGICALLY ACTIVE
PEPTIDES.

CC -1- SUBCELLULAR LOCATION: Neuroendocrine and endocrine secretory
granules.

CC -1- SIMILARITY: BELONGS TO THE CHROMOGRANIN / SECRETOGRANIN PROTEIN
FAMILY.

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CC EMBL: X53028; CAA37199.1; -;
CC EMBL: X51429; CAA35792.1; -;
CC PIR: S09078; S09078.
CC MGI: 88395; Chgb.
CC InterPro: IPR001819; Chromogranin.
CC InterPro: IPR001990; Granin.
CC Pfam: PFO1271; Granin; 1.
CC PRINTS: PR00659; CHROMOGRANIN.
CC PROSITE: PS00422; GRANINS_1; 1.
CC PROSITE: PS00423; GRANINS_2; 1.
CC Sulfation; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 20
FT CHAIN 1 677
FT DISULFID 36 57
FT MOD_RES 348 348
FT CONFLICT 422 424
SO SEQUENCE 677 AA; 77969 MW; C7391E781E4F9B9 CRC64;

Query Match 78.9%; Score 30; DB 1; Length 677;
Best Local Similarity 83.3%; Pred. No. 78;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRE 6

DB 97 WASSRE 102

RESULT 12

HMW1_MYCGE STANDARD; PRT; 1139 AA.

AC Q49413; Q49365;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome high molecular weight protein 1 (cytochrome accessory
protein 1).
GN HMW1 OR MG312.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2097;
[1]

RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Frithman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhmann J.L.,
RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.-F., Dougherty B.A., Bort R.F., Hu P.-C., Lueker T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT "The minimal gene complement of Mycoplasma genitalium.";
Science 270:397-403(1995).
RN [2]

RP SEQUENCE OF 721-847 FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RA MEDLINE=94075230; PubMed=8253680;
RA Peterson S.N., Hu P.-C., Bort R.F., Hutchison C.A. III;
RT "A survey of the Mycoplasma genitalium genome by using random
sequencing."
J. Bacteriol. 175:7918-7930(1993).

CC -1- FUNCTION: COMPONENT OF THE CYTOSKELETON-LIKE STRUCTURE WHICH
STABILIZES THE SHAPE OF THE WALL-LESS MYCOPLASMA. THIS
CYTOSKELETON-LIKE NETWORK OF ACCESSORY PROTEINS CONTAINING HMW
PROTEINS 1 TO 5 ALLOWS THE PROPER ANCHORING OF CYTADHESIN PROTEINS
IN THE MYCOPLASMA MEMBRANE AT THE ATTACHMENT ORGANELLE (BY
SIMILARITY).

CC -1- SUBCELLULAR LOCATION: LOCALIZES SPECIFICALLY TO THE ATTACHMENT
MEMBRANE (BY SIMILARITY).

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CC EMBL: U39712; AAC71534.1; -;
CC EMBL: U02261; AAD12527.1; -;
CC PIR: E64234; E64234.
CC TIGR: MG312; -;
CC Cytochrome; Structural protein; Complete proteome.
SO SEQUENCE 1139 AA; 130531 MW; 0011D3286C3DD856 CRC64;

Query Match 78.9%; Score 30; DB 1; Length 1139;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WASTRES 7
DB 123 WISTRES 129

RESULT 13
CCAH_MOUSE STANDARD; PRT; 2365 AA.

AC 008427; 09JUK5; 38, Created)
 DT 15-JUL-1999 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Voltage-dependent T-type calcium channel alpha-1H subunit (Cav3.2).
 GN CACNA1H.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/c;
 RA Miltman S.;
 RT "Exon organization of mouse Cacna1h.";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 1823-1952 FROM N.A.
 RC STRAIN=CS7BL/6J;
 RA Cribbs L.L., Lee J.-H., Yang J., Daud A.N., Perez-Reyes E.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDATE THE
 ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
 IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
 CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
 CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1H
 CC GIVES RISE TO T-TYPE CALCIUM CURRENTS. T-TYPE CALCIUM CHANNELS
 BELONG TO THE "LOW-VOLTAGE ACTIVATED (LVA)" GROUP AND ARE STRONGLY
 CC BLOCKED BY NICKEL AND MIBEFRADIL. A PARTICULARITY OF THIS TYPE OF
 CC CHANNELS IS AN OPENING AT QUITE NEGATIVE POTENTIALS, AND A
 CC VOLTAGE-DEPENDENT INACTIVATION. T-TYPE CHANNELS SERVE PACEMAKING
 CC FUNCTIONS IN BOTH CENTRAL NEURONS AND CARDIAC NODAL CELLS AND
 CC SUPPORT CALCIUM SIGNALING IN SECRETORY CELLS AND VASCULAR SMOOTH
 CC MUSCLE. THEY MAY ALSO BE INVOLVED IN THE MODULATION OF FIRING
 CC PATTERNS OF NEURONS WHICH IS IMPORTANT FOR INFORMATION PROCESSING
 CC AS WELL AS IN CELL GROWTH PROCESSES.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
 CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
 CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
 CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
 CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
 CC -1- PWM: IN RESPONSE TO RAISING OF INTRACELLULAR CALCIUM, THE T-TYPE
 CC CHANNELS ARE ACTIVATED BY CAM-KINASE II.
 CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
 CC FAMILY.
 CC -----
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 CC -----
 DR EMBL; AF226868; AAK1607.2; -
 DR EMBL; AF026385; AAK21607.2; JOINED.
 DR EMBL; AF051947; AAC67240.1; -
 DR MGI; MGI:1928842; Cacna1h.
 DR InterPro; IPR001682; Ca/Na_pore.
 DR InterPro; IPR002111; Cal_channel_TTPl.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR005820; M-channel_nlg.
 DR Pfam; PF00520; Ion_trans_4.
 DR Iodic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Calcium channel; Glycoprotein; Repeat; Multigene family;
 KM Phosphorylation.
 FT REPEAT 87 422 I.
 FT REPEAT 776 1015 II.
 FT REPEAT 1292 1569 III.
 FT REPEAT 1613 1874 IV.
 FT DOMAIN 1 100 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 101 119 SI OF REPEAT I (POTENTIAL).

FT	DOMAIN	120	139	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	140	160	S2 OF REPEAT I (POTENTIAL).
FT	DOMAIN	161	169	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	170	184	S3 OF REPEAT I (POTENTIAL).
FT	DOMAIN	185	193	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	194	212	S4 OF REPEAT I (POTENTIAL).
FT	DOMAIN	213	232	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	233	253	S5 OF REPEAT I (POTENTIAL).
FT	DOMAIN	254	394	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	395	419	S6 OF REPEAT I (POTENTIAL).
FT	DOMAIN	420	790	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	791	811	S1 OF REPEAT II (POTENTIAL).
FT	DOMAIN	812	824	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	825	856	S2 OF REPEAT II (POTENTIAL).
FT	DOMAIN	847	862	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	853	871	S3 OF REPEAT II (POTENTIAL).
FT	DOMAIN	872	879	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	880	903	S4 OF REPEAT II (POTENTIAL).
FT	DOMAIN	904	914	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	915	935	S5 OF REPEAT II (POTENTIAL).
FT	DOMAIN	936	987	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	988	1012	S6 OF REPEAT II (POTENTIAL).
FT	DOMAIN	1013	1301	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1302	1324	S1 OF REPEAT III (POTENTIAL).
FT	DOMAIN	1325	1342	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1343	1363	S2 OF REPEAT III (POTENTIAL).
FT	DOMAIN	1364	1373	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1374	1393	S3 OF REPEAT III (POTENTIAL).
FT	DOMAIN	1394	1407	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1408	1429	S4 OF REPEAT III (POTENTIAL).
FT	DOMAIN	1430	1439	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1440	1463	S5 OF REPEAT III (POTENTIAL).
FT	DOMAIN	1464	1540	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1541	1566	S6 OF REPEAT III (POTENTIAL).
FT	DOMAIN	1567	1627	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1628	1648	S1 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1649	1662	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1663	1684	S2 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1685	1691	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1692	1710	S3 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1711	1724	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1725	1748	S4 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1749	1762	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1763	1783	S5 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1784	1846	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1847	1874	S6 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1875	2365	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	521	531	POLY-HIS.
FT	DOMAIN	1594	1597	POLY-ARG.
FT	SITE	378	378	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	971	971	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	1515	1515	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	1819	1819	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	CARBOHD	192	192	N-LINKED (GLCNAc. . .) (POTENTIAL).
FT	CARBOHD	271	271	N-LINKED (GLCNAc. . .) (POTENTIAL).
FT	CARBOHD	1477	1477	N-LINKED (GLCNAc. . .) (POTENTIAL).
FT	CONFLICT	1823	1825	GIM -> ARG (IN REF. 2).
FT	CONFLICT	1914	1914	D -> E (IN REF. 2).
FT	CONFLICT	1945	1947	APA -> LLO (IN REF. 2).
FT	CONFLICT	1952	1952	S -> A (IN REF. 2).
FT	CONFLICT	1953	2351	MISSING (IN REF. 2).
SO	SEQUENCE	2365	AA; 261944	MW; 9A8A1750C210596 CRC64;

Query Match 78.9%; Score 30; DB 1; Length 2365;
 Best Local Similarity 71.4%; Pred. No. 3e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 WASTRES 7
 1:111

Db 1276 WCSSRES 1282

RESULT 14
POLG_TBEVH STANDARD; PRT; 3414 AA.

AC 001299;
ID POLG_TBEVH STANDARD; PRT; 3414 AA.

DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Genome polyprotein [contains: Capsid protein C (Core protein); Matrix protein (Envelope protein M); Major envelope protein E; Nonstructural proteins NS1, NS2a, NS2b, NS4a and NS4B; Protease/helicase (EC 3.4.21.98) (NS3); RNA-directed RNA polymerase (EC 2.7.7.48) (NS5)].
DE (EC 3.4.21.98) (NS3); RNA-directed RNA polymerase (EC 2.7.7.48)
DE (NS5)].
OS tick-borne encephalitis virus (strain Hypr) (TBEV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
OX NCBI_TaxID=70733;
RN [1]
RP SEQUENCE FROM N.A.
RA Wallner G., Mandl C.W., Ecker M., Holmann H., Sulasny K.,
RA Kunz C., Heinz F.X.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 3357-3414 FROM N.A.
RX MEDLINE=91303656; PubMed=1712858;
RA Mandl C.W., Kunz C., Heinz F.X.;
RT *Presence of poly(A) in a flavivirus: significant differences between
RT the 3' noncoding regions of the genomic RNAs of tick-borne
RT encephalitis virus strains*;
RL J. Virol. 65:4070-4077(1991).
CC -1- FUNCTION: THE SMALL PROTEINS NS2a, NS2b, NS4a AND NS4b ARE
CC HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.
CC NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the viral
CC precursor polyprotein, commonly with Asp or Glu in the p6
CC position, Cys or Thr in p1 and Ser or Ala in p1'.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate -> N diphosphate +
CC (RNA)(N).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPID-PROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND RNA.
CC -1- MISCELLANEOUS: THE NONSTRUCTURAL PROTEINS NS1 PRESENTS TWO
CC ALTERNATIVE CLEAVAGE SITES FOR ITS C-TERMINUS, WHICH MAY DEFINE A
CC SOLUBLE OR A MEMBRANE-BOUND FORM OF NS1.
CC CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U39293; AAB53095.1; -
CC EMBL: M76660; AAA47904.1; -
CC HSSP: P14336; ISVB.
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR000336; Flav1_capsidC.
DR InterPro: IPR001122; Flav1_glycoprote.
DR InterPro: IPR001850; Flav1_helicase.
DR InterPro: IPR000069; Flav1_M.
DR InterPro: IPR001157; Flav1_NS1.
DR InterPro: IPR000752; Flav1_NS2a.
DR InterPro: IPR000487; Flav1_NS2b.
DR InterPro: IPR000404; Flav1_NS4a.
DR InterPro: IPR001528; Flav1_NS4b.
DR InterPro: IPR000208; Flav1_NS5.
DR InterPro: IPR002535; Flav1_propep.
DR InterPro: IPR002877; FtsJ.
DR InterPro: IPR001650; Helicase_C.

DR InterPro: IPR007095; RNA_pol_DS_PS.
DR InterPro: IPR007094; RNA_pol_PSVir.
DR Pfam: PF01003; Flav1_capsid. 1.
DR Pfam: PF02832; Flav1_glycoprot. 1.
DR Pfam: PF00869; Flav1_glycoprot. 1.
DR Pfam: PF00949; Flav1_helicase. 1.
DR Pfam: PF01004; Flav1_M. 1.
DR Pfam: PF00948; Flav1_NS1. 1.
DR Pfam: PF01005; Flav1_NS2a. 1.
DR Pfam: PF01002; Flav1_NS2b. 1.
DR Pfam: PF01350; Flav1_NS4a. 1.
DR Pfam: PF01349; Flav1_NS4b. 1.
DR Pfam: PF00972; Flav1_NS5. 1.
DR Pfam: PF01570; Flav1_propep. 1.
DR Pfam: PF01728; Flav1. 1.
DR Pfam: PF00271; helicase_C. 1.
DR ProDom: PD001556; Flav1_glycoprote. 1.
DR ProDom: PD001496; Flav1_NS1. 1.
DR SMART: SM00487; DEXDC. 1.
DR SMART: SM00490; HELICC. 1.
DR PolyProtein: Glycoprotein; Transferase: RNA-directed RNA polymerase;
KW Core protein; Coat protein; Envelope protein; Hydrolase; Helicase;
KW ATP-binding; Transmembrane; Nonstructural protein.
ET INIT_MER 1 1
ET CHAIN 1 112
ET PROPEP 113 205
ET CHAIN 206 280
ET CHAIN 281 776
ET CHAIN 777 21128
ET CHAIN 21129 1358
ET CHAIN 1359 1489
ET CHAIN 1490 2110
ET CHAIN 2111 2259
ET CHAIN 2260 2511
ET CHAIN 2512 3414
ET NP_BIND 1688 1695
ET SITE 1779 1782
ET TRANSMEM 101 112
ET TRANSMEM 247 259
ET TRANSMEM 266 280
ET TRANSMEM 738 751
ET DISULFID 283 310
ET DISULFID 340 396
ET DISULFID 354 385
ET DISULFID 372 401
ET DISULFID 466 570
ET DISULFID 587 618
ET CARBOHYD 144 144
ET CARBOHYD 434 434
ET CARBOHYD 861 861
ET CARBOHYD 983 983
ET CARBOHYD 999 999
ET CARBOHYD 1649 1649
ET CARBOHYD 1988 1988
ET CARBOHYD 2044 2044
ET CARBOHYD 2447 2447
ET CARBOHYD 2529 2529
ET CARBOHYD 2726 2726
SO SEQUENCE 3414 AA; 378539 MW; EC0B1A5325A08C19 CRC64;

Query Match Best Local Similarity 78.9%; Score 30; DB 1; Length 3414;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WASTRES 7
Db 2931 WASTRES 2937

RESULT 15
POLG_TBEVH STANDARD; PRT; 3414 AA.

AC P14336; 088493;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Genome polypeptide [contains: Capsid protein C (Core protein); Matrix
 DE protein (Envelope protein M); Major envelope protein E; Nonstructural
 DE proteins NS1, NS2A, NS2B, NS4A and NS4B; Protease/helicase
 DE (EC 3.4.21.98); RNA-directed RNA polymerase (EC 2.7.7.48)
 DE (NS5)].
 OS Tick-borne encephalitis virus (Western subtype) (TBEV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Flavivirus.
 OX NCBI_TaxID=11088;
 RN [1]
 RP SEQUENCE FROM N.A., AND REVISIONS.
 RC STRAIN=Neudoerfl;
 RX MEDLINE=96036491; PubMed=7483260;
 RA Wallner G., Mandl C.W., Kunz C., Heinz F.X.;
 RT The flavivirus 3'-noncoding region: extensive size heterogeneity
 RT independent of evolutionary relationships among strains of tick-borne
 RT encephalitis virus.";
 RL Virology 213:169-178(1995).
 RN [2]
 RP SEQUENCE OF 1-779 FROM N.A.
 RC STRAIN=Neudoerfl;
 RX MEDLINE=88322870; PubMed=3413985;
 RA Mandl C.W., Heinz F.X., Kunz C.;
 RT *Sequence of the structural proteins of tick-borne encephalitis virus
 RT (Western subtype) and comparative analysis with other flaviviruses.";
 RL Virology 166:197-205(1988).
 RN [3]
 RP SEQUENCE OF 767-3414 FROM N.A.
 RC STRAIN=Neudoerfl;
 RX MEDLINE=90051080; PubMed=2554575;
 RA Mandl C.W., Heinz F.X., Stoeckl E., Kunz C.;
 RT *Genome sequence of tick-borne encephalitis virus (Western subtype)
 RT and comparative analysis of nonstructural proteins with other
 RT flaviviruses.";
 RL Virology 173:291-301(1989).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 281-680.
 RX MEDLINE=95272700; PubMed=753193;
 RA Rey F.A., Heinz F.X., Mandl C.W., Harrison S.C.;
 RT The envelope glycoprotein from tick-borne encephalitis virus at 2-A
 RT resolution.";
 RL Nature 375:291-298(1995).
 CC -1- FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE
 CC HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.
 CC NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the viral
 CC precursor polypeptide, commonly with Asp or Glu in the P6
 CC position, Cys or Thr in P1 and Ser or Ala in P1'.
 CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
 CC [RNA](N). THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
 CC LIPID-PROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
 CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
 CC PROTEIN C AND MRNA.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U27495; AAA86870.1; -.
 DR PIR: A31052; GNMVNE.
 DR PDB: 1SVB; 10-JUN-96.
 DR MEROPS: S07; UPW; -.
 DR InterPro: IPR001410; DEAD.
 DR InterPro: IPR001122; Flav1_capsidC.

DR InterPro: IPR000336; Flav1_glycoprote.
 DR InterPro: IPR001850; Flav1_helicase.
 DR InterPro: IPR000069; Flav1_M.
 DR InterPro: IPR001157; Flav1_NS1.
 DR InterPro: IPR000752; Flav1_NS2A.
 DR InterPro: IPR000487; Flav1_NS2B.
 DR InterPro: IPR000404; Flav1_NS4A.
 DR InterPro: IPR001528; Flav1_NS4B.
 DR InterPro: IPR002008; Flav1_NS5.
 DR InterPro: IPR002535; Flav1_proppep.
 DR InterPro: IPR002877; FtsJ.
 DR InterPro: IPR001650; Helicase_C.
 DR InterPro: IPR007095; RNA_pol_DS_PS.
 DR InterPro: IPR007094; RNA_pol_PSVIR.
 DR Pfam: PF01003; Flav1_capsid; 1.
 DR Pfam: PF02832; Flav1_glycop_C; 1.
 DR Pfam: PF00869; Flav1_glycoprot; 1.
 DR Pfam: PF00949; Flav1_helicase; 1.
 DR Pfam: PF01004; Flav1_M; 1.
 DR Pfam: PF00948; Flav1_NS1; 1.
 DR Pfam: PF01005; Flav1_NS2A; 1.
 DR Pfam: PF01002; Flav1_NS2B; 1.
 DR Pfam: PF01350; Flav1_NS4A; 1.
 DR Pfam: PF01349; Flav1_NS4B; 1.
 DR Pfam: PF00972; Flav1_NS5; 1.
 DR Pfam: PF01570; Flav1_proppep; 1.
 DR Pfam: PF01728; FtsJ; 1.
 DR Pfam: PF00271; helicase_C; 1.
 DR ProDom: PD001556; Flav1_glycoprote; 1.
 DR ProDom: PD001456; Flav1_NS1; 1.
 DR SMART: SM00487; DEXDC; 1.
 DR SMART: SM00490; HELIC_C; 1.
 KW Polypeptide; Glycoprotein; Transferase; RNA-directed RNA polymerase;
 KW Core protein; Coat protein; Envelope protein; Hydrolyase; Helicase;
 KW ATP-binding; Transmembrane; Nonstructural protein; 3D-structure;
 KW INIT_MET 1
 FT CHAIN 1 112
 FT PROPEP 113 205
 FT CHAIN 206 280
 FT CHAIN 281 776
 FT CHAIN 777 1128
 FT CHAIN 1129 1358
 FT CHAIN 1359 1489
 FT CHAIN 1490 2110
 FT CHAIN 2111 2259
 FT CHAIN 2260 2511
 FT CHAIN 2512 3414
 FT DOMAIN 378 391
 FT NP_BIND 1688 1695
 FT SITE 1779 1782
 FT TRANSMEM 101 112
 FT TRANSMEM 247 259
 FT TRANSMEM 266 280
 FT TRANSMEM 738 751
 FT DISULFID 283 310
 FT DISULFID 340 396
 FT DISULFID 354 385
 FT DISULFID 372 401
 FT DISULFID 466 570
 FT DISULFID 587 618
 FT CARBOHYD 144 144
 FT CARBOHYD 434 434
 FT CARBOHYD 861 861
 FT CARBOHYD 983 983
 FT CARBOHYD 999 999
 FT CARBOHYD 2447 2447
 FT HELIX 282 285
 FT STRAND 290 294
 FT STRAND 300 306
 FT TURN 307 308
 FT STRAND 311 315
 FT TURN 316 317
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 ENVELOPE GLYCOPROTEIN M.
 MAJOR ENVELOPE PROTEIN E.
 NONSTRUCTURAL PROTEIN NS1.
 NONSTRUCTURAL PROTEIN NS2A.
 NONSTRUCTURAL PROTEIN NS2B.
 PROTEASE/HELICASE (NS3).
 NONSTRUCTURAL PROTEIN NS4A.
 NONSTRUCTURAL PROTEIN NS4B.
 RNA-DIRECTED RNA POLYMERASE (NS5).
 INVOLVED IN FUSION.
 ATP (POTENTIAL).
 DEAD BOX.
 HYDROPHOBIC SIGNAL SEQUENCE (POTENTIAL).
 POTENTIAL.
 POTENTIAL.
 POTENTIAL.

FT	STRAND	318	331
FT	STRAND	334	340
FT	STRAND	343	352
FT	TURN	355	356
FT	HELIX	363	366
FT	TURN	368	369
FT	STRAND	370	379
FT	HELIX	381	383
FT	TURN	384	384
FT	STRAND	389	401
FT	TURN	403	404
FT	STRAND	406	411
FT	TURN	414	416
FT	STRAND	418	425
FT	TURN	433	434
FT	TURN	438	439
FT	STRAND	441	446
FT	TURN	447	448
FT	STRAND	449	449
FT	STRAND	451	455
FT	HELIX	457	459
FT	STRAND	460	467
FT	HELIX	468	470
FT	TURN	475	476
FT	STRAND	477	481
FT	TURN	484	485
FT	TURN	487	488
FT	STRAND	492	496
FT	HELIX	497	501
FT	TURN	502	502
FT	STRAND	507	508
FT	TURN	510	511
FT	STRAND	516	516
FT	TURN	517	517
FT	HELIX	518	521
FT	STRAND	522	524
FT	STRAND	528	528
FT	TURN	529	530
FT	STRAND	531	531
FT	STRAND	534	536
FT	HELIX	541	547
FT	TURN	548	550
FT	STRAND	553	557
FT	TURN	558	559
FT	STRAND	560	562
FT	STRAND	567	573
FT	TURN	575	576
FT	STRAND	577	577
FT	TURN	582	583
FT	STRAND	586	586
FT	TURN	589	590
FT	STRAND	592	600
FT	STRAND	606	612

Query Match 78.9%; Score 30; DB 1; Length 3414;
Best Local Similarity 71.4%; Pred. No. 4.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WASTRES 7
||| ||:
Db 2931 WASAREA 2937

Search completed: October 7, 2003, 19:14:58
Job time : 2.42414 secs

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OM protein - protein search, using sw model

Run on: October 7, 2003, 19:04:06 ; Search time 6.97586 Seconds
(without alignments)
258.946 Million cell updates/sec

Title: us-09-988-013a-2_COPY_56_62
Perfect score: 38
Sequence: 1 WASTRES 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mmc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	92.1	130	4 Q9NP29	Q9NP29 homo sapien
2	34	86.5	980	16 Q9PL66	Q9PL66 xanthomonas
3	33	86.8	1317	3 Q8TF23	Q8TF23 aspergillus
4	32	84.2	347	16 Q915J7	Q915J7 pseudomonas
5	31	81.6	171	5 Q9NSV2	Q9NSV2 caenorhabdi
6	31	81.6	183	2 Q57000	Q57000 zymomonas m
7	31	81.6	226	2 Q88087	Q88087 enterococu
8	31	81.6	230	16 Q8NU75	Q8NU75 corynebacte
9	31	81.6	404	2 Q9AMJ2	Q9AMJ2 streptomyce
10	31	81.6	564	5 Q9NA93	Q9NA93 caenorhabdi
11	31	81.6	572	16 Q9ZX10	Q9ZX10 rhizobium m
12	31	81.6	642	2 Q8RMG0	Q8RMG0 nostoc sp.
13	31	81.6	642	16 Q9A805	Q9A805 caulobacter
14	31	81.6	642	16 Q8Z0C9	Q8Z0C9 anabaena sp
15	31	81.6	727	5 Q9BNW8	Q9BNW8 scutigerell
16	31	81.6	735	16 Q989J7	Q989J7 rhizobium 1

17	31	81.6	783	2 Q8KJN0	Q8KJN0 rhizobium 1
18	31	81.6	1499	10 Q9LH44	Q9LH44 arabidopsis
19	30	78.9	29	11 Q8C837	Q8C837 mus musculu
20	30	78.9	51	4 Q9UJ11	Q9UJ11 homo sapien
21	30	78.9	62	12 Q8B8F5	Q8B8F5 hepatitis b
22	30	78.9	103	17 Q8Z272	Q8Z272 pyrobaculum
23	30	78.9	118	6 Q9BGP0	Q9BGP0 macaca fasc
24	30	78.9	119	12 Q8JYX1	Q8JYX1 hepatitis b
25	30	78.9	119	12 Q8JYX2	Q8JYX2 hepatitis b
26	30	78.9	119	12 Q8JYX3	Q8JYX3 hepatitis b
27	30	78.9	130	4 Q8MWL9	Q8MWL9 homo sapien
28	30	78.9	206	11 Q9CTW1	Q9CTW1 mus musculu
29	30	78.9	207	15 Q9UB47	Q9UB47 human immun
30	30	78.9	209	2 P94650	P94650 chlorobium
31	30	78.9	256	16 Q913X8	Q913X8 pseudomonas
32	30	78.9	285	16 Q9B838	Q9B838 rhizobium 1
33	30	78.9	301	12 Q8JMA5	Q8JMA5 manestria co
34	30	78.9	310	10 Q9C939	Q9C939 arabidopsis
35	30	78.9	349	4 Q8TC24	Q8TC24 homo sapien
36	30	78.9	349	11 Q9W001	Q9W001 mus musculu
37	30	78.9	356	10 Q8RYX9	Q8RYX9 oryza sativ
38	30	78.9	409	16 Q8UG04	Q8UG04 agrobacteri
39	30	78.9	415	17 Q8TFM2	Q8TFM2 methanosarc
40	30	78.9	462	16 Q9E4H6	Q9E4H6 rhizobium 1
41	30	78.9	489	16 Q8UE58	Q8UE58 agrobacteri
42	30	78.9	528	5 Q8SVE2	Q8SVE2 encephalito
43	30	78.9	558	17 Q8TQ86	Q8TQ86 methanosarc
44	30	78.9	650	16 Q8Y005	Q8Y005 ralsstonia s
45	30	78.9	677	11 Q8BP91	Q8BP91 mus musculu

ALIGNMENTS

RESULT 1

Q9NP29 ID Q9NP29 PRELIMINARY; PRT; 130 AA.

AC Q9NP29;

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Microfibrillar protein 2 (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Theria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96354815; PubMed=8753791;

RA Ozsvath K.J., Xia S., Hirose H., Tilson M.D.;

RT "Two hypothetical proteins of human aortic adventitia, with Ig kappa,

RT collagenous, and aromatic-rich motifs.";

RL Biochem. Biophys. Res. Commun. 225:500-504(1996).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=97367690; PubMed=9224393;

RA Ozsvath K.J., Hirose H., Xia S., Chew D., Knoetgen J. III,

RT Tilson M.D.;

RT "Expression of two novel recombinant proteins from aortic adventitia

RT (kappaIbs) sharing amino acid sequences with cytomegalovirus.";

RL J. Surg. Res. 69:277-282(1997).

RN [3]

RP SEQUENCE FROM N.A.

RA Ozsvath K.J., Xia S., Hirose H., Tilson M.D.;

RT Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF206020; AAF62402.1; -.

DR HSSP; P80362; IWTL.

FT NON_TER 130

SO SEQUENCE 130 AA; 14128 MW; 51275185ACGFAIE CRC64;

Query Match 92.1%; Score 35; DB 4; Length 130;

Best Local Similarity 85.7%; Pred. No. 11;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY      1 WASTRES 7
       |||||:|
Db      76 WASTRDS 82

RESULT 2
O8PL66 PRELIMINARY; PRT: 980 AA.
ID O8PL66
AC O8PL66;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
GN GGDPE family protein.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OX Xanthomonadaceae; Xanthomonas.
NCBI_TaxID=92829;

RP SEQUENCE FROM N.A.
RX STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Qunggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Canavan F., Cardozo J., Chamberg F., Clapina L.P.,
RA Ciccarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locelli E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Melandris J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sana J.A.D., Silva C., de Souza R.F.,
RA Spicola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitejima J.P.,
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL: AE011829; AAM36802.1; -.
DR InterPro: IPR000160; GGDPEF.
DR Pfam: PF00990; GGDPEF.1.
DR TIGRFAMs: TIGR00254; GGDPEF.1.
KM Complete proteome.
SQ SEQUENCE 980 AA; 107940 MW; 47179C81E6DCE442 CRC64;

Query Match
Best Local Similarity 89.5%; Score 34; DB 16; Length 980;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 WASTRE 6
       |||||
Db      492 WASTRE 497

RESULT 3
O8TF23 PRELIMINARY; PRT: 1317 AA.
ID O8TF23
AC O8TF23;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Conserved hypothetical protein.
AF AFA35G10.09C.
OS Aspergillus fumigatus (Sartorya fumigata).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillius.
NCBI_TaxID=5085;
[1]
RN RP SEQUENCE FROM N.A.
RX STRAIN=Af293;

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RA Knowles D.G., Warren T., Hall N., Quail M., Woodward J.R.,
RA Denning D.W., Anderson M.J., Bartell B.;
RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL: AL731691; CAD29602.1; -.
DR InterPro: IPR01680; WD40.
DR Pfam: PF00400; WD40; 2.
DR SMART: SM00320; WD40; 3.
KM Hypothetical protein; Repeat. Repeat.
SQ SEQUENCE 1317 AA; 148645 MW; 0DCA80BD149A45DE CRC64;

Query Match
Best Local Similarity 86.8%; Score 33; DB 3; Length 1317;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 WASTRES 7
       |||||
Db      979 WASTRES 985

RESULT 4
O9I5J7 PRELIMINARY; PRT: 347 AA.
ID O9I5J7
AC O9I5J7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Hypothetical protein PA0732.
GN PA0732.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
[1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Huynh W.O., Kowalik D.J., Lagrou M.,
RA Garner R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lapidis R., Llin R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.,
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT opportunistic pathogen."
RL Nature 406:959-964(2000).
DR EMBL: AE004508; AAG04121.1; -.
DR InterPro: IPR005490; ERFK_YBIS_Yhng.
DR Pfam: PF03734; ERFK_YBIS_Yhng.1.
KM Hypothetical protein; Complete proteome.
SQ SEQUENCE 347 AA; 37161 MW; 264E4DC064290CC3 CRC64;

Query Match
Best Local Similarity 84.2%; Score 32; DB 16; Length 347;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY      1 WASTRES 7
       |||||
Db      318 WASTRDT 324

RESULT 5
O9NSV2 PRELIMINARY; PRT: 171 AA.
ID O9NSV2
AC O9NSV2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical 17.6 kDa protein.
GN CC8.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode *C. elegans*: a platform for
investigating biology." the *C. elegans* Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RX Kemp K., Le T.T.";
RT "The sequence of *C. elegans* cosmid CC8.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RX Waterston R.";
RT "Direct Submission.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006626; AAF39788.1; -
DR WormPep; CC8.1; CE20616.
SO Hypothetical protein.
SQ SEQUENCE 171 AA; 17643 MW; 03AD996B9A627CFD CRC64;

Query Match 81.6%; Score 31; DB 5; Length 171;
Best Local Similarity 83.3%; Pred. No. 97;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRE 6
DB 122 WASTRE 127

RESULT 6
057000 PRELIMINARY; PRT; 183 AA.
AC 057000;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JAN-1999 (TReMBLrel. 09, Last annotation update)
DE Secretion activator protein.
GN ZLITS.
OS *Zymomonas mobilis*.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; *Zymomonas*.
OX NCBI_TaxID=542;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-IP013756;
RX Kondo Y., Toyoda A., Fukushi H., Yanase H., Tonomura K., Kawasaki H.,
RA Sakai T.";
RT "Cloning and characterization of a pair of genes that stimulate the
production and secretion of *Zymomonas mobilis* extracellular
levansucrase and invertase.";
RL Biosci. Biotechnol. Biochem. 0:0-0(1994).
DR EMBL; D17522; BAA0473.1; -
SQ SEQUENCE 183 AA; 20629 MW; F8F00828108BD66F CRC64;

Query Match 81.6%; Score 31; DB 2; Length 183;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WASTRES 7
DB 145 WAKTREN 151

RESULT 7
088087 PRELIMINARY; PRT; 226 AA.
AC 088087;
DT 01-NOV-1998 (TReMBLrel. 08, Created)

DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE ABC transporter ATP-binding protein.
OS *Enterococcus faecalis* (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; *Enterococcus*.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-OG1RF;
RX MEDLINE=98380380; PubMed=9712783;
RA Xu Y., Murray B.E., Weinstock G.M.";
RT "A cluster of genes involved in polysaccharide biosynthesis from
Enterococcus faecalis OG1RF.";
RL Infect. Immun. 66:4313-4323(1998).
DR EMBL; AF071085; AAC35926.1; -
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding.
SQ SEQUENCE 226 AA; 25420 MW; 68C6D5CE85CD2A25 CRC64;

Query Match 81.6%; Score 31; DB 2; Length 226;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WASTRES 7
DB 219 WASTRES 225

RESULT 8
08NU75 PRELIMINARY; PRT; 230 AA.
AC 08NU75;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Nicotinamide mononucleotide transporter.
GN CGL0064.
OS *Corynebacterium glutamicum* (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; *Corynebacterium*.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.";
RT "Complete genomic sequence of *Corynebacterium glutamicum* ATCC 13032.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005274; BAB97457.1; -
DR InterPro; IPR007056; NNN_transporter.
DR InterPro; IPR006419; NNN_trans_PnuC.
DR Pfam; PF04973; NNN_transporter; 1.
DR TIGRFAMs; TIGR01528; NNN_trans_PnuC; 1.
KW Complete proteome.
SQ SEQUENCE 230 AA; 25546 MW; 93429B9438A8AE45 CRC64;

Query Match 81.6%; Score 31; DB 16; Length 230;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRE 6
DB 113 WASTRE 118

RESULT 9
09AMJ2 PRELIMINARY; PRT; 404 AA.
AC 09AMJ2;
DT 09AMJ2;

DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE Putative ketosynthase Sima2 (Sim3).
 GN SIMA2 OR SIM3.
 OS Streptomyces antibioticus.
 OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
 OC Streptomycetaceae; Streptomyces.
 OC NCBI_TaxID=1890;
 OX NCBI_TaxID=1890;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Tue6040;
 RA Trefter A., Bechthold A.;
 RT "The streptomycin biosynthetic gene cluster isolated from
 RT Streptomyces antibioticus Tue6040."
 RT Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Tu 6040;
 RA Galin U., Li S.-M., Schimana J., Fiedler H.-P., Heide L.;
 RT "Identification of the Streptomycin Biosynthetic Gene Cluster of
 RT Streptomyces antibioticus Tu 6040."
 RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF324838; AAK06785.1; -;
 DR EMBL: AF322256; AAL15581.1; -;
 DR HSSP: P73283; 1ESM.
 DR InterPro: IPR000794; Ketoacyl-synt.
 DR Pfam: PF00109; ketoacyl-synt. 1.
 DR Pfam: PF02801; ketoacyl-synt. C. 1.
 SQ SEQUENCE 404 AA; 41905 MW; CDE4A9DD54DD6B8 CRC64;

Query Match 81.6%; Score 31; DB 2; Length 404;
 Best Local Similarity 83.3%; Pred. No. 2.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRE 6
 |||||
 Db 24 WASTRE 29

RESULT 10
 O9NA93 PRELIMINARY; PRT; 564 AA.
 AC O9NA93;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE Y53F4B.27 protein.
 GN Y53F4B.27.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Smye R.;
 RL Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99069613; PubMed-9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology."
 RT Science 282:2012-2018(1998).
 RL EMBL: AL132949; CAB61101.2; -;
 DR WormPep: Y53F4B.27; CE26159.
 SQ SEQUENCE 564 AA; 62463 MW; 950BB275855E1C8 CRC64;

Query Match 81.6%; Score 31; DB 5; Length 564;
 Best Local Similarity 83.3%; Pred. No. 3.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRE 6
 |||||

Db 33 WASTRE 38
 |||||

RESULT 11
 O92X10 PRELIMINARY; PRT; 572 AA.
 ID O92X10;
 AC O92X10;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE Hypothetical protein RB0152.
 GN RB0152 OR SMD20152.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OG Plasmid pSymb (megaplasmid 2).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-1021;
 RX MEDLINE-21396508; PubMed-11481431;
 RA Finn T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
 RA Vorholter F.J., Hernandez-Lucas I., Becker A., Gouzy J.,
 RA Golding B., Fuenler A.;
 RT "The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-
 RT fixing endosymbiont Sinorhizobium meliloti."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
 DR EMBL: AL036442; CAC48552.1; -;
 DR InterPro: IPR004843; M-peptidase.
 DR Pfam: PF00149; Metallophos; 1.
 DR PfamId: Hypothetical protein; Complete proteome.
 SQ SEQUENCE 572 AA; 62894 MW; B0E25EC10F213353 CRC64;

Query Match 81.6%; Score 31; DB 16; Length 572;
 Best Local Similarity 71.4%; Pred. No. 3.4e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WASTRES 7
 |||||

Db 41 WADTROS 47

RESULT 12
 O8RMGO PRELIMINARY; PRT; 642 AA.
 ID O8RMGO;
 AC O8RMGO;
 DT 01-JUN-2002 (TREMblrel. 21, Created)
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE Cyclomaltoextrin glucanotransferase.
 OS Nostoc sp. (strain PCC 9229).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 OX NCBI_TaxID=70817;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wouters J., Janson S., Bergman B.;
 RC STRAIN-PCC 9229;
 RT "Cloning and of expression of a putative cyclomaltoextrin
 RT glucanotransferase from the symbiotically competent cyanobacterium
 RT Nostoc sp. PCC 9229."
 RT Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
 RL EMBL: AF497477; AAM16154.1; -;
 DR EMBL: AF497477; AAM16154.1; -;
 DR InterPro: IPR006048; Alpha-amyl-C.
 DR InterPro: IPR006047; Alpha-amyl-C.
 DR InterPro: IPR006589; Alp-amyl-cat.
 DR InterPro: IPR002044; CBD_4.
 DR Pfam: PF00128; alpha-amylase; 1.
 DR Pfam: PF02806; alpha-amylase_C; 1.
 DR Pfam: PF00686; CBL_20; 1.
 DR SMART: SM00642; Amy; 1.
 KW Translasease.
 SQ SEQUENCE 642 AA; 74063 MW; A3806A00720797B6 CRC64;

Query Match 81.6%; Score 31; DB 2; Length 642;
 Best Local Similarity 85.7%; Pred. No. 3.9e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WASTRES 7
 DB 636 WASTRES 642

RESULT 13

O9A805 PRELIMINARY; PRT; 642 AA.
 AC O9A805;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE TolC protein.
 GN CCL1298.
 OS Caulobacter crescentus.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
 OC Caulobacteraceae; Caulobacter.
 OX NCBI_TaxID=155892;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 19089 / CB15;
 RX MEDLINE=21173698; PubMed=11259647;
 RA Nierman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
 RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Holt D.H.,
 RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
 RA Ueberback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
 RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
 RT "Complete genome sequence of Caulobacter crescentus.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
 DR EMBL: AEO05805; AAK23279.1; -.
 DR TIGR: CC1298; -.
 DR InterPro: IPR002173; PFKB.
 DR Pfam: PF00294; PFKB; 1.
 DR PROSITE: PS00583; PFKB_KINASES_1; 1.
 DR PROSITE: PS00584; PFKB_KINASES_2; 1.
 KW Complete proteome.
 SQ SEQUENCE 642 AA; 70888 MW; 2410A43215415889 CRC64;

Query Match 81.6%; Score 31; DB 16; Length 642;
 Best Local Similarity 83.3%; Pred. No. 3.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRE 6
 DB 352 WASTRE 357

RESULT 14

O8Z0C9 PRELIMINARY; PRT; 642 AA.
 AC O8Z0C9;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Cyclomalodextrin glucanotransferase.
 GN ALR0169.
 OS Anabaena sp. (strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 OX NCBI_TaxID=103690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21595285; PubMed=11759840;
 RA Kaneo T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
 RA Matsunabe A., Iriyuchi M., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kohara M., Matsunoto M., Matsuno A., Muraki A.,
 RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,

RA Yasuda M., Tabata S.;
 RT "Complete genomic sequence of the filamentous nitrogen-fixing
 cyanobacterium Anabaena sp. strain PCC 7120.";
 RL DNA Res. 8:205-213(2001).
 DR EMBL: AP003581; BAB77693.1; -.
 DR InterPro: IPR006048; Alpha_amy1_C.
 DR InterPro: IPR006047; Alpha_amy1_cat.
 DR InterPro: IPR006589; Alp_amy1_cat_sub.
 DR InterPro: IPR002044; CBD_4.
 DR InterPro: IPR006046; Glyco_hydro_13.
 DR Pfam: PR00128; alpha-amy1ase; 1.
 DR Pfam: PF02806; alpha-amy1ase-C; 1.
 DR Pfam: PF00686; CBM_20; 1.
 DR PRINTS: PR00110; ALPHAMYLASE.
 DR SMART: SM00642; Amy; 1.
 KW Transferase; Complete proteome.
 SQ SEQUENCE 642 AA; 74287 MW; 9F0991CD452F9FC CRC64;

Query Match 81.6%; Score 31; DB 16; Length 642;
 Best Local Similarity 85.7%; Pred. No. 3.9e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WASTRES 7
 DB 636 WASTRES 642

RESULT 15

O9BNW8 PRELIMINARY; PRT; 727 AA.
 AC O9BNW8;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Elongation factor-2 (Fragment).
 OS Scutigera sp. 'Scut2'.
 OC Eukaryota; Metazoa; Arthropoda; Myriapoda; Symphyla; Scutigerellidae;
 OC Scutigerella.
 OX NCBI_TaxID=109756;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21317060; PubMed=11421654;
 RA Regier J.C., Shultz J.W.;
 RT "Elongation factor-2: a useful gene for arthropod phylogenetics.";
 RL Mol. Phylogenet. Evol. 20:136-148(2001).
 DR EMBL: AF240827; AAK12352.1; -.
 DR HSSP: P13551; IDAR.
 DR InterPro: IPR005517; EFG_IV.
 DR InterPro: IPR004161; EFTU_D2.
 DR InterPro: IPR00795; EF_GTPbind.
 DR Pfam: PF03764; EFG_IV; 1.
 DR Pfam: PF00009; GTP_EFTU; 1.
 DR Pfam: PF03144; GTP_EFTU_D2; 1.
 DR PRINTS: PR00315; ELONGACTNCT.
 DR PROSITE: PS00301; EFATOR_GTP; 1.
 KW GTP-binding; Protein biosynthesis.
 FT NON_TER 1
 FT NON_TER 727
 SQ SEQUENCE 727 AA; 81422 MW; 577371F1AA122178 CRC64;

Query Match 81.6%; Score 31; DB 5; Length 727;
 Best Local Similarity 71.4%; Pred. No. 4.4e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WASTRES 7
 DB 256 WASTRES 262

Search completed: October 7, 2003, 19:19:57
 Job time : 8.97586 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 19:03:26 ; Search time 10.069 Seconds
(without alignments)
126.112 Million cell updates/sec

Title: US-09-988-013a-2_COPY_95_102
Perfect score: 48
Sequence: 1 HQYLSSWT 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	112	15	AA54932
2	48	100.0	112	15	AA54933
3	48	100.0	113	17	AA92215
4	48	100.0	113	17	AA92217
5	48	100.0	113	18	AA27695
6	48	100.0	115	18	AA27697
7	48	100.0	263	20	AA90226
8	48	100.0	268	20	AA90228
9	48	100.0	268	20	AA90222

10	48	100.0	273	20	AA90224
11	48	100.0	301	18	AAW11507
12	48	100.0	301	20	AAW73217
13	48	100.0	301	22	AA85454
14	48	100.0	301	22	AA61959
15	48	100.0	352	20	AA706272
16	48	100.0	353	18	AAW11508
17	48	100.0	553	20	AAW73223
18	48	100.0	553	22	AA85455
19	48	100.0	553	22	AA61960
20	48	100.0	556	20	AA90218
21	48	100.0	580	20	AA90217
22	44	91.7	272	23	ABG31024
23	43	89.6	86	22	AA996679
24	43	89.6	86	22	AA42489
25	39	81.2	8	23	AAE29276
26	39	81.2	112	23	AAE29266
27	39	81.2	112	23	AAE29268
28	39	81.2	112	23	AAE29270
29	37	77.1	154	21	AA825131
30	37	77.1	154	21	AA825449
31	37	77.1	625	21	AA97397
32	37	77.1	629	21	AA97395
33	36	75.0	117	22	AA69071
34	36	75.0	417	21	AA77953
35	36	75.0	690	21	AA825101
36	36	75.0	795	22	AAU34003
37	36	75.0	904	22	AAU36814
38	36	75.0	1135	22	ABG18470
39	35	72.9	10	23	AA52796
40	35	72.9	107	12	AA811985
41	35	72.9	107	12	AA811987
42	35	72.9	112	23	AAE29264
43	35	72.9	130	22	AA000064
44	35	72.9	351	22	AB60572
45	35	72.9	453	23	ABP74050

ALIGNMENTS

RESULT 1
ID AAR54932 standard; peptide: 112 AA.
AC AAR54932:
XX
DT 25-MAR-2003 (updated)
DT 19-OCT-1994 (first entry)
XX
DE FC receptor humanized VK chain 022 HuVK.
XX
KW FC receptor; FcR; humanized antibody; hAb; IgG; cancer; allergy;
KW autoimmune disease; heteroantibody; bifunctional antibody;
KW immunotoxin; CDR; complementarity determining region; VH;
KW heavy chain variable region; VK; kappa chain variable region;
KW monoclonal phagocyte; PCR; polymerase chain reaction; primer;
KW site-directed mutagenesis; HuVK; monoclonal antibody; hAb.
XX
OS Homo sapiens; Mus sp.
XX
PN MO9410332-A1.
XX
PD 11-MAY-1994.
XX
PF 04-NOV-1993; 93MO-US10384.
XX
PR 04-NOV-1992; 92GB-0023377.
XX
PA (MEDA-) MEDAREX INC.
XX
PI Carr FU, Harris WJ, Tempest PR.
XX

DR WPI: 1994-167486/20.
XX New humanised antibodies to Fc receptors - used for diagnosis or
PT for treatment of e.g. cancer, allergies and infectious and
PR auto-immune diseases
PS
XX Disclosure: Page 16; 36pp; English.
XX
CC Humanised antibodies (habs) for IgG Fc receptors on human phagocytes
CC comprise the CDR of mouse monoclonal antibody 22 (from hybridoma
CC 022MCL-1), VH chains from human Igs NEMM or KOL, and VK chains from
CC Ig REI. Sequences are provided for mouse 022 VH (AAR54931),
CC humanized NEMM-based VH (022 NMVH, AAR54929), humanized KOL-
CC based VH (022 KLVH, AAR54930), mouse 022 VK (AAR54933) and humanized
CC REI-based VK (022 HUVK, AAR54932). During hAb production, VH and VK
CC CDNA's were PCR amplified using primers given in AA065378-87.
CC Mutagenesis of clone M13VHPCR2 KOL VH (L71R) was performed using
CC oligos AA065388-89. The habs can be used in heteroantibody,
CC bifunctional antibody and immunotoxin production.
CC (Updated on 25-MAR-2003 to correct PN field.)
CC
CC
SQ Sequence 112 AA;

Query Match 100.0%; Score 48; DB 15; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSSWT 8
| | | | | | | |
DB 95 HOYLSSWT 102

RESULT 2

AAR54933
ID AAR54933 standard; peptide; 112 AA.

XX AAR54933;

XX 25-MAR-2003 (updated)
DT 19-OCT-1994 (first entry)
XX

DE MAb 022 VK chain.

XX Fc receptor; FcR; humanized antibody; hAb; IgG; cancer; allergy;
KM auto-immune disease; heteroantibody; bifunctional antibody;
KM immunotoxin; CDR; complementarity determining region; VH;
KM heavy chain variable region; VK; kappa chain variable region;
KM mononuclear phagocyte; PCR; polymerase chain reaction; primer;
KM site-directed mutagenesis; monoclonal antibody; MAb.

OS Mus sp.

PN WO9410332-A1.

XX 11-MAY-1994.

XX 04-NOV-1993; 93WO-US10384.

XX 04-NOV-1992; 92GB-0023377.

XX (MEDA-) MEDAREX INC.

XX Carr FU, Harris WJ, Tempest PR;

DR WPI: 1994-167486/20.

XX New humanised antibodies to Fc receptors - used for diagnosis or
PT for treatment of e.g. cancer, allergies and infectious and
PR auto-immune diseases
PS
XX Disclosure: Page 23; 36pp; English.

XX Humanized antibodies (habs) for IgG Fc receptors on human phagocytes

CC comprise the CDR of mouse monoclonal antibody 22 (from hybridoma
CC 022MCL-1), VH chains from human Igs NEMM or KOL, and VK chains from
CC Ig REI. Sequences are provided for mouse 022 VH (AAR54931),
CC humanized NEMM-based VH (022 NMVH, AAR54929), humanized KOL-
CC based VH (022 KLVH, AAR54930), mouse 022 VK (AAR54933) and humanized
CC REI-based VK (022 HUVK, AAR54932). During hAb production, VH and VK
CC CDNA's were PCR amplified using primers given in AA065378-87.
CC Mutagenesis of clone M13VHPCR2 KOL VH (L71R) was performed using
CC oligos AA065388-89. The habs can be used in heteroantibody,
CC bifunctional antibody and immunotoxin production.
CC (Updated on 25-MAR-2003 to correct PN field.)
CC
CC
SQ Sequence 112 AA;

Query Match 100.0%; Score 48; DB 15; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSSWT 8
| | | | | | | |
DB 95 HOYLSSWT 102

RESULT 3

AAR92215
ID AAR92215 standard; Protein; 113 AA.

XX AAR92215;

XX 28-MAY-1996 (first entry)
DT

XX LL2 MAb VK region.

XX Humanised antibody; monoclonal antibody; MAb; LL2; B-cell lymphoma;
KM Leukemia; therapy; diagnosis; complementarity determining region;
KM CDR; antibody engineering.

XX Mus musculus.

OS

XX

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XX

XX

XX

Location/Qualifiers
Key 24..40
FT Region /label= CDR1
FT Region /note="claim 6, page 44"
FT Region /note="claim 62
FT Region /label= CDR2
FT Region /note="claim 7, page 44"
FT Region /note="claim 7, page 44"
FT Region /label= CDR3
FT Region /note="claim 8, page 44"

PN WO9604925-A1.

XX 22-FEB-1996.

XX 11-AUG-1995; 95WO-US09641.

XX 12-AUG-1994; 94US-0289576.

XX (IMMU-) IMMUNOMEDICS INC.

XX Hansen H, Leung S;

XX WPI: 1996-139454/14.

XX N-PSDB; AAT15802.

XX Chimeric and humanised LL2 antibodies - used to produce conjugates
PT for the therapy and diagnosis of B-cell lymphoma(s) and
PR Leukaemia(s).

XX Claim 5; Page 35-36; 70pp; English.

XX The complementarity determining regions (CDRs) of mouse monoclonal
CC antibody (MAb) LL2 VK (AAR92215) and VH (AAR92216) regions were

CC recombinantly linked to the framework sequences of human VK and VH
 CC regions, respectively, to give humanised LL2 VK (AAR92217) and VH
 CC (AAR92218). These were subsequently linked, respectively, to human
 CC kappa and IgG1 constant regions. A humanised Mab was obtd. that
 CC retained the B-lymphoma and leukaemia cell targeting and
 CC internalisation characteristics of the parental LL2 Mab, and which
 CC exhibited a lowered HAMA reaction. It can be linked to e.g. a
 CC cytostatic agent for therapeutic appln.

XX
 SQ Sequence 113 AA;

Query Match 100.0%; Score 48; DB 17; Length 113;
 Best Local Similarity 100.0%; Pred. No. 0.59; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0;

OY 1 HOYLSSWT 8
 |||||
 DB 95 HOYLSSWT 102

RESULT 4
 AAR92217

ID AAR92217 standard; Protein; 113 AA.

AC AAR92217;

DT 28-MAY-1996 (first entry)

XX Humanised LL2 Mab VK region.

DE Humanised antibody; monoclonal antibody; Mab; LL2; B-cell lymphoma;
 KW leukaemia; therapy; diagnosis; complementarity determining region;
 KM CDR; antibody engineering.

XX Synthetic.

OS
 FH Key Location/Qualifiers
 FT Region 24..40
 FT /label= CDR1
 FT Region 56..62
 FT /label= CDR2
 FT Region 95..103
 FT /label= CDR3

XX MO9604925-A1.

XX 22-FEB-1996.

XX 11-AUG-1995; 95WO-US09641.

XX 12-AUG-1994; 94US-0289576.

XX (IMMU-) IMMUNOMEDICS INC.

XX Hansen H, Leung S;

XX WPI; 1996-139454/14.

XX DR N-PSDB; AAT15803.

XX Chimeric and humanised LL2 antibodies - used to produce conjugates
 PT for the therapy and diagnosis of B-cell lymphoma(s) and
 PT leukaemia(s).

XX
 PS Claim 5; Page 38; 70pp; English.

XX The complementarity determining regions (CDRs) of mouse monoclonal
 CC antibody (Mab) LL2 VK (AAR92215) and VH (AAR92216) regions were
 CC recombinantly linked to the framework sequences of human VK and VH
 CC regions, respectively, to give humanised LL2 VK (AAR92217) and VH
 CC (AAR92218). These were subsequently linked, respectively, to human
 CC kappa and IgG1 constant regions. A humanised Mab was obtd. that
 CC retained the B-lymphoma and leukaemia cell targeting and
 CC internalisation characteristics of the parental LL2 Mab, and which

CC exhibited a lowered HAMA reaction. It can be linked to e.g. a
 CC cytostatic agent for therapeutic appln.

XX
 SQ Sequence 113 AA;

Query Match 100.0%; Score 48; DB 17; Length 113;
 Best Local Similarity 100.0%; Pred. No. 0.59; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0;

OY 1 HOYLSSWT 8
 |||||
 DB 95 HOYLSSWT 102

RESULT 5
 AAM27695

ID AAM27695 standard; Protein; 113 AA.

AC AAM27695;

DT 14-APR-1998 (first entry)

XX Variable kappa chain of Mab LL2.

DE Variable kappa chain; B cell; monoclonal antibody; Mab; LL2;
 KW B cell lymphoma; lymphocytic leukaemia cell; murine;
 KM diagnosis; treatment; B cell malignancy; non-Hodgkins lymphoma;
 KW chronic lymphocytic leukaemia.

OS Mus sp.
 OS Synthetic.

XX
 FH Key Location/Qualifiers
 FT Region 18..20
 FT /note= "potential N-linked glycosylation site"
 FT Region 24..40
 FT /note= "complementarity determining region 1"
 FT Region 56..62
 FT /note= "complementarity determining region 2"
 FT Region 95..102
 FT /note= "complementarity determining region 3"

XX MO9734632-A1.

XX 25-SEP-1997.

XX 19-MAR-1997; 97WO-US04196.

XX 20-MAR-1996; 96US-0013709.

XX (IMMU-) IMMUNOMEDICS INC.

XX Hansen H, Leung S, Qu Z;

XX WPI; 1997-479995/44.

XX DR N-PSDB; AAT88128.

XX Monoclonal antibody engineered to contain glycosylation site - in
 PT non-Fc constant heavy or light chain region, useful to diagnose or
 PT treat B cell malignancies, e.g. non-Hodgkins lymphoma
 PT
 XX Example 3; Fig 4A; 88pp; English.

XX The present sequence is the variable kappa chain of the
 CC B cell specific monoclonal antibody (Mab) LL2, which contains an
 CC engineered tri-peptide N-glycan acceptor sequence. LL2 is a highly
 CC specific anti-B cell lymphoma and anti-lymphocytic leukaemia cell
 CC murine Mab. The Mab can be used to diagnose or treat B
 CC cell malignancies, e.g. non-Hodgkins lymphoma or chronic
 CC lymphocytic leukaemia. The glycosylation site allows a label or
 CC therapeutic agent of increased size to be conjugated to the
 CC carbohydrate moiety, without affecting the Mab's binding affinity
 CC or specificity.

```

XX      SQ      Sequence      113 AA:
Query Match      100.0%; Score 48; DB 18; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.59;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 HOYLSSWT 8
      11111111
DB      95 HOYLSSWT 102

RESULT 6
ID      AAW27697
AAW27697 standard; Protein: 115 AA.
XX
XX      AAW27697;
XX
XX      14-APR-1998 (first entry)
XX
XX      Variable kappa chain of MAb hLL2.
XX
XX      Variable kappa chain; B cell; monoclonal antibody; MAb: hLL2;
XX      B cell lymphoma; lymphocytic leukaemia cell; murine; humanised;
XX      diagnosis; treatment; B cell malignancy; non-Hodgkins lymphoma;
XX      chronic lymphocytic leukaemia.
XX      Chimeric - Mus sp.
XX      Chimeric - Homo sapiens.
XX
XX      Key      Location/Qualifiers
XX      Region      24..40      "complementarity determining region 1"
XX      Region      56..62      "complementarity determining region 2"
XX      Region      95..102     "complementarity determining region 3"
XX      /note="complementarity determining region 3"
XX
XX      WO9734632-A1.
XX
XX      25-SEP-1997.
XX
XX      19-MAR-1997; 97WO-US04196.
XX
XX      20-MAR-1996; 96US-0013709.
XX
XX      (IMMU-) IMMUNOMEDICS INC.
XX
XX      Hansen H, Leung S, Qu Z;
XX
XX      WPI: 1997-479995/44.
XX      N-PSDB: AAT8130.
XX
XX      Monoclonal antibody engineered to contain glycosylation site - in
XX      non-Fc constant heavy or light chain region, useful to diagnose or
XX      treat B cell malignancies, e.g. non-Hodgkins lymphoma
XX
XX      Example 3; Fig 5a; 88pp; English.
XX
XX      The present sequence is the variable kappa chain of the
XX      B cell specific monoclonal antibody (MAb) hLL2. hLL2 is a highly
XX      specific anti-B cell lymphoma and anti-lymphocytic leukaemia cell
XX      humanised murine MAb. The MAb can be used to diagnose or treat B
XX      cell malignancies, e.g. non-Hodgkins lymphoma or chronic
XX      lymphocytic leukaemia.
XX
XX      Sequence      115 AA:
Query Match      100.0%; Score 48; DB 18; Length 115;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 HOYLSSWT 8

```

```

DB      95 HOYLSSWT 102
      11111111
RESULT 7
ID      AAW90226
AAW90226 standard; Protein: 263 AA.
XX
XX      AAW90226;
XX
XX      10-MAY-1999 (first entry)
XX
XX      Anti-B7.2 monospecific triabody 1G10.
XX
XX      B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;
XX      CD86; T cell activation; inhibitor; graft versus host disease;
XX      transplant rejection; allograft rejection; autoimmune disease;
XX      allergy; therapy; human; triabody; antibody; 1G10.
XX
XX      Chimeric - Mus sp.
XX      Chimeric - synthetic.
XX
XX      Key      Location/Qualifiers
XX      Peptide      1..24      "pe1B signal peptide"
XX      Region      25..144     "ant1 B7.2 MAb VH region"
XX      Peptide      145..257     "ant1 B7.2 MAb VL region"
XX      Peptide      258..263     "H1s6 tag"
XX      /note="H1s6 tag"
XX
XX      WO9858965-A2.
XX
XX      30-DEC-1998.
XX
XX      22-JUN-1998; 98WO-EP03791.
XX
XX      20-JUN-1997; 97EP-0870092.
XX
XX      (INNO-) INNOGENETICS NV.
XX
XX      Bosman A, Buyse M, Lotte K, Sablon E;
XX
XX      WPI: 1999-105615/09.
XX      N-PSDB: AAX01660.
XX
XX      New molecules which bind B7.1 and B7.2 - useful to prevent and treat
XX      immune diseases including allograft rejection
XX
XX      Example 7.3; Fig 34; 182pp; English.
XX
XX      This polypeptide comprises a 1G10 monospecific triabody composed
XX      of the VH region of anti-B7.2 monoclonal antibody (MAb) 1G10
XX      joined to the VL region of 1G10. A triabody is a mono- or bi- or
XX      a trispecific molecule recognising simultaneously e.g. two B7.2
XX      and one B7.1 molecules. It has a rigid structure that prevents
XX      simultaneous binding to the 3 targets. Each antigen-binding site
XX      is formed by pairing of one VH and one VL domain from the same or
XX      from two different polypeptides. The invention relates to novel
XX      molecules, including triabodies, which can cross-link and/or
XX      cross-react with the costimulatory molecules B7.1 and B7.2 expressed
XX      on professional antigen-presenting cells, leading to the inhibition
XX      of antigen-specific T cell activation. Methods are provided for
XX      the production of such B7-binding molecules, and for their use in
XX      the treatment or prevention of diseases of the immune system, in
XX      particular graft rejection, graft versus host disease, allergy and
XX      autoimmune diseases (claimed).
XX
XX      Sequence      263 AA:
Query Match      100.0%; Score 48; DB 20; Length 263;
Best Local Similarity 100.0%; Pred. No. 1.4;

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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 HOYLSSWT 8
| | | | | | | |
Db 239 HOYLSSWT 246

RESULT 8
AAW90228
ID AAW90228 standard; Protein; 268 AA.

AAW90228;

10-MAY-1999 (first entry)

Anti-B7.1/anti-B7.2 bispecific triabody II.

B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;
CD86; T cell activation; inhibitor; graft versus host disease;
transplant rejection; allograft rejection; autoimmune disease;
allergy; therapy; human; triabody; antibody; B7-24; 1G10.

Chimeric - Mus sp.
Chimeric - synthetic.

Key Location/Qualifiers

Peptide 1..39 /note="g3p signal peptide"

Region 40..155 /note="anti B7.1 MAB VH region"

Peptide 156..268 /note="anti B7.2 MAB VL region"

WO9858965-A2.

30-DEC-1998.

22-JUN-1998; 98WO-EP03791.

20-JUN-1997; 97EP-0870092.

(INNO-) INNOGENETICS NV.

Bosman A, Buyse M, Lorre K, Sablon E;

WPI: 1999-105615/09.

N-Psdb; AAX01662.

New molecules which bind B7.1 and B7.2 - useful to prevent and treat
immune diseases including allograft rejection

Example 7.3; Fig 38; 182pp; English.

This polypeptide comprises a bispecific triabody composed of the VH
region of anti-B7.1 monoclonal antibody (Mab) B7-24 joined to the
VL region of anti-B7.2 Mab 1G10. A triabody is a mono- a bi- or
a trispecific molecule recognising simultaneously e.g. two B7.2
and one B7.1 molecules. It has a rigid structure that prevents
simultaneous binding to the 3 targets. Each antigen-binding site
is formed by pairing of one VH and one VL domain from the same or
from two different polypeptides. The invention relates to novel
molecules, including triabodies, which can cross-link and/or
cross-react with the costimulatory molecules B7.1 and B7.2 expressed
on professional antigen-presenting cells, leading to the inhibition
of antigen-specific T cell activation. Methods are provided for
the production of such B7-binding molecules, and for their use in
the treatment or prevention of diseases of the immune system, in
particular graft rejection, graft versus host disease, allergy and
autoimmune diseases (claimed).

Sequence 268 AA;

Query Match 100.0%; Score 48; DB 20; Length 268;

Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 HOYLSSWT 8
| | | | | | | |
Db 250 HOYLSSWT 257

RESULT 9
AAW90222
ID AAW90222 standard; Protein; 268 AA.

AAW90222;

10-MAY-1999 (first entry)

Anti-B7.2 monospecific diabody 1G-10.

B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;
CD86; T cell activation; inhibitor; graft versus host disease;
transplant rejection; allograft rejection; autoimmune disease;
allergy; therapy; human; diabody; antibody; 1G-10.

Chimeric - Mus sp.
Chimeric - synthetic.

Key Location/Qualifiers

Peptide 1..24 /note="pe1b signal peptide"

Region 25..144 /note="anti B7.2 MAB VH region"

Peptide 145..149 /note="G4S flexible linker"

Region 150..262 /note="anti B7.2 MAB VL region"

Peptide 263..268 /note="His6 tag"

WO9858965-A2.

30-DEC-1998.

22-JUN-1998; 98WO-EP03791.

20-JUN-1997; 97EP-0870092.

(INNO-) INNOGENETICS NV.

Bosman A, Buyse M, Lorre K, Sablon E;

WPI: 1999-105615/09.

N-Psdb; AAX01656.

New molecules which bind B7.1 and B7.2 - useful to prevent and treat
immune diseases including allograft rejection

Example 7.2; Fig 26; 182pp; English.

This polypeptide comprises a 1G-10 monospecific diabody composed
of the VH region of anti-B7.2 monoclonal antibody (Mab) 1G-10
joined via a short, flexible linker to the VL region of 1G-10.
Mono- or bispecific bivalent molecules are generated by shortening
the flexible linker sequence between the VH and VL of the anti-B7.1
scFv B7-24, the anti-B7.2 scFv 1G10 and the scFv molecule with
dual specificity for B7.1 and B7.2 (B7.12) to 5-10 residues, and
for bispecific molecules by cross-pairing the VH and VL domains
from the 2 scFvs with different antigen recognition (B7.1/B7.2 and
B7.12/B7.12). The invention relates to novel molecules, including
diabodies, which can cross-link and/or cross-react with the
costimulatory molecules B7.1 and B7.2 expressed on professional
antigen-presenting cells, leading to the inhibition of antigen-
specific T cell activation. Methods are provided for the
production of such B7-binding molecules, and for their use in the

CC treatment or prevention of diseases of the immune system, in
 CC particular graft rejection, graft versus host disease, allergy and
 CC autoimmune diseases (claimed).
 CC
 XX Sequence 268 AA;
 SQ

Query Match 100.0%; Score 48; DB 20; Length 268;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYLSSWT 8
 |||||
 Db 244 HOYLSSWT 251

RESULT 10
 ID AAW90224 standard; Protein; 273 AA.
 XX
 AC AAW90224;
 XX
 DT 10-MAY-1999 (first entry)
 XX
 DE Anti-B7.1/anti-B7.2 bispecific diabody II.
 XX
 DE B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;
 KW CD86; T cell activation; inhibitor; graft versus host disease;
 KW transplant rejection; allograft rejection; autoimmune disease;
 KW allergy; therapy; human; diabody; antibody; B7-24; Ig10.
 XX
 OS Chimeric - Mus sp.
 OS Chimeric - synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..39
 FT /note= "g3p signal peptide"
 FT 40..155
 FT /note= "anti B7.1 MAb VH region"
 FT 156..160
 FT /note= "G4S flexible linker"
 FT 161..273
 FT /note= "anti B7.2 MAB VL region"
 FT Misc-difference 21
 FT /note= "encoded by TCA"
 FT
 XX
 PN WO9858965-A2.
 XX
 PD 30-DEC-1998.
 XX
 PE 22-JUN-1998; 98WO-EP03791.
 XX
 PR 20-JUN-1997; 97EP-0870092.
 XX
 PA (INNO-) INNOGENETICS NV.
 XX
 PI Bosman A, Buysse M, Loree K, Sablon E;
 DR WPI: 1999-105615/09.
 DR N-PSDB; AAX01658.
 XX
 PT New molecules which bind B7.1 and B7.2 - useful to prevent and treat
 PT immune diseases including allograft rejection
 XX
 XX Example 7.2; Fig 30; 182pp; English.
 XX
 CC This polypeptide comprises a bispecific diabody composed of the VH
 CC region of anti-B7.1 monoclonal antibody (MAb) B7-24 joined via a
 CC short, flexible linker to the VL region of anti-B7.2 MAb Ig10.
 CC Mono- or bispecific bivalent molecules are generated by shortening
 CC the flexible linker sequence between the VH and VL of the anti-B7.1
 CC scfv B7-24, the anti-B7.2 scfv Ig10 and the scfv molecule with
 CC dual specificity for B7.1 and B7.2 (B7.12) to 5-10 residues and
 CC for bispecific molecules by cross-pairing the VH and VL domains

CC from the 2 scfvs with different antigen recognition (B7.1/B7.2 and
 CC B7.12/B7.12). The invention relates to novel molecules, including
 CC diabodies, which can cross-link and/or cross-react with the
 CC costimulatory molecules B7.1 and B7.2 expressed on professional
 CC antigen-presenting cells, leading to the inhibition of antigen-
 CC specific T cell activation. Methods are provided for the
 CC production of such B7-binding molecules, and for their use in the
 CC treatment or prevention of diseases of the immune system, in
 CC particular graft rejection, graft versus host disease, allergy and
 CC autoimmune diseases (claimed).
 CC
 XX Sequence 273 AA;
 SQ

Query Match 100.0%; Score 48; DB 20; Length 273;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYLSSWT 8
 |||||
 Db 255 HOYLSSWT 262

RESULT 11
 ID AAW11507 standard; Protein; 301 AA.
 XX
 AC AAW11507;
 XX
 DT 24-SEP-1997 (first entry)
 XX
 DE Single chain, humanised anti-Fc gamma RI antibody H22.
 XX
 KW Humanised antibody; anti-Fc receptor; H22; bifunctional; bispecific;
 KW fusion protein; chimera; carcinoembryonic antigen; CEA.
 XX
 OS Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= signal_peptide
 FT 20..139
 FT /label= VH
 FT /note= "H22 heavy chain variable region"
 FT 140..154
 FT /label= linker
 FT 155..266
 FT /label= VL
 FT /note= "H22 light chain variable domain"
 FT 267..281
 FT /label= linker
 FT 282..292
 FT /label= c-myc_tag
 FT 296..301
 FT /label= His-6_tail
 FT /note= "6 histidine residues"
 FT
 XX
 PN WO9640789-A1.
 XX
 PD 19-DEC-1996.
 XX
 PE 07-JUN-1996; 96WO-US09988.
 XX
 PR 07-JUN-1995; 95US-0484172.
 XX
 PA (MEDA-) MEDAREX INC.
 XX
 PI Deo YM, Goldstein J, Graziano R, Somasundaram C;
 DR WPI: 1997-052242/05.
 DR N-PSDB; AAT58129.
 XX

PT Recombinant, multi-specific anti-Fc receptor antibody molecules -
 PT also comprise an anti-target portion, used for the treatment of
 PT cancer, autoimmune disease and pathogenic infection
 XX
 PS Example 8; Fig 39; 115pp; English.
 CC A mammalian expression construct encoding a single chain antibody
 CC having binding specificity for Fc gamma RI, derived from the
 CC humanised anti-Fc gamma RI monoclonal antibody H22 was prepared
 CC (see A4158129). A bispecific single chain polypeptide was produced
 CC by fusing the H22 scFv to an anti-carcinoembryonic antigen (CEA)
 CC antibody. The H22-anti-CEA fusion protein was shown to bind both
 CC Fc gamma RI and CEA.
 XX
 SQ Sequence 301 AA;
 QY
 Query Match 100.0%; Score 48; DB 18; Length 301;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 249 HOYLSSWT 256
 QY 1 HOYLSSWT 8
 |||||
 DB 249 HOYLSSWT 256
 RESULT 12
 AAW73217
 ID AAW73217 standard; Protein; 301 AA.
 XX AAW73217;
 AC 25-JAN-1999 (first entry)
 DT
 XX
 DE Multispecific single chain antibody H22.
 XX
 KM Multispecific single chain antibody; antibody H22; tumour cell; therapy;
 KM antibody-dependent cellular cytotoxicity; ADCC; HER 2/neu; infection;
 KM epidermal growth factor receptor; breast cancer; ovarian cancer.
 KW
 XX Homo sapiens.
 OS
 XX
 PN US5837243-A.
 PD 17-NOV-1998.
 XX
 XX 07-JUN-1996; 96US-0661052.
 PF
 XX 07-JUN-1996; 96US-0661052.
 PR 07-JUN-1995; 95US-0484172.
 XX
 PA (MEDA-) MEDAREX INC.
 PI Deo YM, Goldstein J, Graziano R, Somasundaram C;
 XX
 DR WPI; 1999-023374/02.
 DR N-PSDB; AAV08175.
 XX
 PT Specific killing of tumour cells - using a multi-specific molecule
 PT comprising an anti-Fc receptor antibody and a portion which binds to
 PT a target cell
 XX
 PS Claim 14; Fig 39; 57pp; English.
 CC This sequence is the multispecific single chain antibody designated
 CC H22. The antibody can be used in the method of the invention for inducing
 CC antibody-dependent cellular cytotoxicity (ADCC) against a tumour cell
 CC which is characterised by overexpression of HER 2/neu or epidermal growth
 CC factor receptor (EGFR), comprises contacting the tumour cell with a
 CC multispecific protein molecule (preferably a single chain antibody)
 CC comprising: (a) an anti-Fc receptor antibody or an antigen binding
 CC fragment; (b) a portion which binds to HER 2/neu; and (c) a portion which
 CC binds to EGFR. The method can be used for treating cancers especially
 CC breast cancer or ovarian cancer. The multispecific antibody can also

CC be administered prophylactically to vaccinate a subject against infection
 CC by a target cell.
 CC
 SQ Sequence 301 AA;
 QY
 Query Match 100.0%; Score 48; DB 20; Length 301;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 249 HOYLSSWT 256
 QY 1 HOYLSSWT 8
 |||||
 DB 249 HOYLSSWT 256
 RESULT 13
 AAB85454
 ID AAB85454 standard; Protein; 301 AA.
 XX AAB85454;
 AC 25-SEP-2001 (first entry)
 DT
 XX
 DE Single chain humanised anti-Fc gamma RI antibody sequence.
 XX
 KM HER 2/neu; epidermal growth factor receptor; EGFR; multispecific protein;
 KM Fc receptor; FCR; tumour cell; breast; cancer; sarcoma; HIV;
 KM pathogenic; Toxoplasma gondii; candidiasis; systemic lupus; cytostatic;
 KM immune thrombocytopenia purpura; immunosuppressive; antiviral;
 KM antifungal; antiprotzoal.
 KW
 XX Homo sapiens.
 OS
 XX
 FH Key
 FH Peptide
 FT Location/Qualifiers
 FT 1..19
 FT /note= "signal sequence"
 FT 20..139
 FT /note= "H22 Vh"
 FT 140..154
 FT /note= "linker"
 FT 155..266
 FT /note= "H22 Vh"
 FT 267..281
 FT /note= "linker"
 FT 282..292
 FT /note= "c-mys tag"
 FT 296..301
 FT /note= "His-6 tail"
 XX
 XX US6270765-B1.
 PN
 XX
 PD 07-AUG-2001.
 XX
 XX 06-NOV-1998; 98US-0188082.
 PF
 XX 07-JUN-1996; 96US-0661052.
 PR 07-JUN-1995; 95US-0484172.
 XX
 PA (MEDA-) MEDAREX INC.
 PI Deo YM, Goldstein J, Graziano R, Somasundaram C;
 XX
 DR WPI; 2001-475189/51.
 DR N-PSDB; AAH23382.
 XX
 PT Inducing killing of tumor cells which expresses HER 2/neu or epidermal
 PT growth factor receptor (EGFR) by contacting the cell with multispecific
 PT proteins comprising an anti-Fc receptor, -Her 2/neu or -EGFR antibody,
 PT useful for treating cancer -
 XX
 PS Example 8; Fig 39A-B; 57pp; English.
 CC The invention relates to a new method for inducing killing of a tumor
 CC cell which expresses HER 2/neu or epidermal growth factor receptor

CC monoclonal antibody produced by cell line HA022CL1 (ATCC CRL 11177).
CC The fusion protein is encoded by expression vector pUG717 (see
CC AX58935). The H22 SFV was expressed on the surface of murine tumour
CC cells transformed with this vector. These transformed tumour cells,
CC when in the presence of macrophages, engaged and activated Fc gamma
CC RI, resulting in specific lysis of the tumour cells. Induction of
CC cytokines by H22-TM transformed tumour cells was also demonstrated.
CC This is an example of cells of the invention that have been
CC transformed to express on their surface a component which binds to
CC an Fc receptor of an effector cell. The transformed cell is
CC targeted to an effector cell via the Fc binding component, and can
CC be used as a vehicle to increase an effector cell-mediated immune
CC response, such as cell lysis and phagocytosis, against an antigen
CC associated with the cell. The transformed cells are used to treat
CC cancer and infectious diseases or used as vaccines. The method
CC allows for killing of target cells without targeting any particular
CC antigen on the cell. This is advantageous since many tumour cells
CC and other target cells do not have defined antigens for targeting.
XX

SQ Sequence 352 AA;

Query Match

100.0%; Score 48; DB 20; Length 352;

Best Local Similarity 100.0%; Pred. No. 1.9; Mismatches 0; Indels 0; Gaps 0;

Matches 8; Conservative 0; Indels 0; Gaps 0;

QY 1 HQYLSWT 8

|||||||

Db 132 HQYLSWT 139

Search completed: October 7, 2003, 19:13:54
Job time : 11.069 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 19:07:41 ; Search time 4.13793 Seconds
(without alignments)
305.878 Million cell updates/sec

Title: US-09-988-013a-2_COPY_95_102
Perfect score: 48
Sequence: 1 HQRLSSWT 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapect 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubppaa/PCPN_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep:*
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- 18: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	100.0	112	12	US-10-229-335-4
2	48	100.0	112	12	US-10-229-335-28
3	48	100.0	113	10	US-09-741-843-2
4	48	100.0	113	10	US-09-741-843-6
5	48	100.0	113	11	US-09-894-839-2
6	48	100.0	113	11	US-09-894-839-6
7	48	100.0	113	11	US-09-894-839-20
8	48	100.0	113	11	US-09-888-013a-2
9	48	100.0	113	11	US-09-888-013a-6
10	44	91.7	272	12	US-10-053-530-14
11	44	91.7	272	15	US-10-207-655-14
12	39	81.2	112	15	US-10-056-052-10
13	39	81.2	112	15	US-10-056-052-14
14	39	81.2	112	15	US-10-056-052-18
15	37	77.1	154	15	US-10-101-464a-99

16	37	77.1	154	15	US-10-101-464a-768	Sequence 768, App
17	36	75.0	417	12	US-10-342-224-58	Sequence 58, Appl
18	36	75.0	690	15	US-10-101-464a-69	Sequence 69, Appl
19	36	75.0	795	9	US-09-815-242-5499	Sequence 5499, Ap
20	36	75.0	904	9	US-09-815-242-12407	Sequence 12407, A
21	35	72.9	10	9	US-09-813-653-35	Sequence 35, Appl
22	35	72.9	112	15	US-10-056-052-6	Sequence 6, Appl1
23	35	72.9	453	12	US-10-032-585-7887	Sequence 7887, Ap
24	34	70.8	613	15	US-10-013-477-18	Sequence 18, Appl
25	34	70.8	613	15	US-10-013-477-26	Sequence 26, Appl
26	34	70.8	613	15	US-10-207-655-204	Sequence 204, App
27	33	68.8	35	15	US-10-106-698-8340	Sequence 8340, Ap
28	33	68.8	249	11	US-09-880-748-363	Sequence 363, App
29	33	68.8	886	15	US-09-815-242-12501	Sequence 12501, A
30	33	68.8	886	15	US-10-195-144-61	Sequence 61, Appl
31	32	66.7	70	10	US-09-796-692-1821	Sequence 1821, Ap
32	32	66.7	70	10	US-09-796-692-2076	Sequence 2076, Ap
33	32	66.7	70	15	US-10-040-862-1821	Sequence 1821, Ap
34	32	66.7	70	15	US-10-040-862-2076	Sequence 2076, Ap
35	32	66.7	115	10	US-09-796-692-1443	Sequence 1443, Ap
36	32	66.7	115	10	US-09-796-692-1539	Sequence 1539, Ap
37	32	66.7	115	10	US-09-796-692-1893	Sequence 1893, Ap
38	32	66.7	115	10	US-09-796-692-2021	Sequence 2021, Ap
39	32	66.7	115	15	US-10-040-862-1443	Sequence 1443, Ap
40	32	66.7	115	15	US-10-040-862-1539	Sequence 1539, Ap
41	32	66.7	115	15	US-10-040-862-1893	Sequence 1893, Ap
42	32	66.7	115	15	US-10-040-862-2021	Sequence 2021, Ap
43	32	66.7	235	11	US-09-870-406a-46	Sequence 46, Appl
44	32	66.7	235	15	US-10-159-901-46	Sequence 46, Appl
45	32	66.7	235	11	US-09-870-406a-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1
Sequence 4, Application US/10229335
Publication No. US20030144483A1

GENERAL INFORMATION:
APPLICANT: MEDAREX, INC.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO FC RECEPTORS FOR IMMUNOBULBULIN G ON HUMAN MONONUCLEAR PHAGOCYTES
NUMBER OF SEQUENCES: 28
STREET: P.O. Box 953, 1545 Route 22 East
CITY: Annandale
STATE: New Jersey
COUNTRY: USA
ZIP: 08801

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/229, 335
FILING DATE: 26-Aug-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/435, 516
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35, 430
REFERENCE/DOCKET NUMBER: KAI-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: Peptide
FRAGMENT TYPE: Internal
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-229-335-4

Query Match
Best Local Similarity 100.0%; Score 48; DB 12; Length 112;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSSWT 8
|||||
DB 95 HOYLSSWT 102

RESULT 2
US-10-229-335-28
Sequence 28, Application US/10229335
Publication No. US20030144483A1
GENERAL INFORMATION:
APPLICANT: MEDAREX, INC.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO FC RECEPTORS FOR
IMMUNOBLOBLIN G ON HUMAN MONONUCLEAR PHAGOCYTES
NUMBER OF SEQUENCES: 28
STREET: P.O. Box 953, 1545 Route 22 East
CITY: Annandale
STATE: New Jersey
COUNTRY: USA
ZIP: 08801
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/229,335
FILING DATE: 26-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/435,516
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-229-335-28

Query Match
Best Local Similarity 100.0%; Score 48; DB 12; Length 112;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSSWT 8
|||||
DB 95 HOYLSSWT 102

RESULT 3
US-09-741-843-2
Sequence 2, Application US/09741843
Patent No. US20020102254A1
GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
APPLICANT: HANSEN, Hans

TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL
TITLE OF INVENTION: AND LEUKEMIA CELLS
FILE REFERENCE: 018733/0996
CURRENT APPLICATION NUMBER: US/09/741,843
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/127,902
PRIOR FILING DATE: 1998-08-03
PRIOR APPLICATION NUMBER: US 08/690,102
PRIOR FILING DATE: 1996-07-06
PRIOR APPLICATION NUMBER: US 08/289,576
PRIOR FILING DATE: 1994-08-12
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 113
TYPE: PRT
ORGANISM: Murinae gen. sp.
US-09-741-843-2

Query Match
Best Local Similarity 100.0%; Score 48; DB 10; Length 113;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSSWT 8
|||||
DB 95 HOYLSSWT 102

RESULT 4
US-09-741-843-6
Sequence 6, Application US/09741843
Patent No. US20020102254A1
GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
APPLICANT: HANSEN, Hans
TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL
TITLE OF INVENTION: AND LEUKEMIA CELLS
FILE REFERENCE: 018733/0996
CURRENT APPLICATION NUMBER: US/09/741,843
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/127,902
PRIOR FILING DATE: 1998-08-03
PRIOR APPLICATION NUMBER: US 08/690,102
PRIOR FILING DATE: 1996-07-06
PRIOR APPLICATION NUMBER: US 08/289,576
PRIOR FILING DATE: 1994-08-12
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 113
TYPE: PRT
ORGANISM: Homo sapiens
US-09-741-843-6

Query Match
Best Local Similarity 100.0%; Score 48; DB 10; Length 113;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSSWT 8
|||||
DB 95 HOYLSSWT 102

RESULT 5
US-09-894-839-2
Sequence 2, Application US/09894839
Publication No. US20030035800A1
GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
APPLICANT: HANSEN, Hans
APPLICANT: OU, Zhengxing
TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
FILE REFERENCE: 018733/1049

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; CURRENT APPLICATION NUMBER: US/09/894,839
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/155,107
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 60/013,709
; PRIOR FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-894-839-2
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Query Match          100.0%; Score 48; DB 11; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 HOYLSWT 8
        |||||||
Db       95 HOYLSWT 102
```

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RESULT 6
US-09-894-839-6
; Sequence 6, Application US/09894839
; Publication No. US20030035800A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; APPLICANT: QU, Zhengxing
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/1049
; CURRENT APPLICATION NUMBER: US/09/894,839
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/155,107
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 60/013,709
; PRIOR FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-894-839-6
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```
Query Match          100.0%; Score 48; DB 11; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 HOYLSWT 8
        |||||||
Db       95 HOYLSWT 102
```

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RESULT 7
US-09-894-839-20
; Sequence 20, Application US/09894839
; Publication No. US20030035800A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; APPLICANT: QU, Zhengxing
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/1049
; CURRENT APPLICATION NUMBER: US/09/894,839
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/155,107
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 60/013,709
; PRIOR FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 47
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-894-839-20
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Query Match          100.0%; Score 48; DB 11; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HOYLSWT 8
        |||||||
Db       95 HOYLSWT 102
```

```
RESULT 8
US-09-988-013a-2
; Sequence 2, Application US/09988013A
; Publication No. US20030103979A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
; FILE REFERENCE: 18733/1082
; CURRENT APPLICATION NUMBER: US/09/988,013A
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 09/741,843
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/127,902
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/690,102
; PRIOR FILING DATE: 1996-07-06
; PRIOR APPLICATION NUMBER: US 08/289,576
; PRIOR FILING DATE: 1994-08-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-988-013a-2
```

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Query Match          100.0%; Score 48; DB 11; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 HOYLSWT 8
        |||||||
Db       95 HOYLSWT 102
```

```
RESULT 9
US-09-988-013a-6
; Sequence 6, Application US/09988013A
; Publication No. US20030103979A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
; FILE REFERENCE: 18733/1082
; CURRENT APPLICATION NUMBER: US/09/988,013A
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 09/741,843
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/127,902
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/690,102
; PRIOR FILING DATE: 1996-07-06
; PRIOR APPLICATION NUMBER: US 08/289,576
; PRIOR FILING DATE: 1994-08-12
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; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-988-013A-6

Query Match 100.0%; Score 48; DB 11; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYLSSWT 8
DB 95 HOYLSSWT 102

RESULT 10
US-10-053-530-14
; Sequence 14, Application US/10053530
; Publication No. US20030133939A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey
; APPLICANT: Hayden-Ledbetter, Martha
; TITLE OF INVENTION: Binding Domain-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 390069.401
; CURRENT APPLICATION NUMBER: US/10/053,530
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: US 09/765,208
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(272)
; OTHER INFORMATION: MOUSE ANTI-HUMAN CD22 SCFV
US-10-053-530-14

Query Match 91.7%; Score 44; DB 12; Length 272;
Best Local Similarity 87.5%; Pred. No. 5.6;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYLSSWT 8
DB 115 HOYLSSWT 122

RESULT 11
US-10-207-655-14
; Sequence 14, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(272)
; OTHER INFORMATION: MOUSE ANTI-HUMAN CD22 SCFV
US-10-207-655-14

Query Match 91.7%; Score 44; DB 15; Length 272;
Best Local Similarity 87.5%; Pred. No. 5.6;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYLSSWT 8
DB 115 HOYLSSWT 122

RESULT 12
US-10-056-052-10
; Sequence 10, Application US/10056052
; Publication No. US2003009656A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLPA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/10/056,052
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-056-052-10

Query Match 81.2%; Score 39; DB 15; Length 112;
Best Local Similarity 87.5%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYLSSWT 8
DB 95 HOYLSSWT 102

RESULT 13
US-10-056-052-14
; Sequence 14, Application US/10056052
; Publication No. US2003009656A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLPA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/10/056,052
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1

SEQ ID NO 14
LENGTH: 112
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-056-052-14

Query Match 81.2%; Score 39; DB 15; Length 112;
Best Local Similarity 87.5%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYLSWT 8
|||||:|
Db 95 HOYLSYT 102

RESULT 14
US-10-056-052-18
Sequence 18, Application US/10056052
Publication No. US20030099636A1
GENERAL INFORMATION:
APPLICANT: PATTI, Joseph M
APPLICANT: HUTCHINS, Jeff T
APPLICANT: DOMANSKI, Paul
APPLICANT: PATEL, Pratiksha
APPLICANT: HALL, Andrea
TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
FILE REFERENCE: P07069US04/BAS
CURRENT APPLICATION NUMBER: US/10/056,052
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/308,116
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/298,413
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/274,611
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: 60/264,072
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 112
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-056-052-18

Query Match 81.2%; Score 39; DB 15; Length 112;
Best Local Similarity 87.5%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYLSWT 8
|||||:|
Db 95 HOYLSYT 102

RESULT 15
US-10-101-464A-99
Sequence 99, Application US/10101464A
Publication No. US20030046728A1
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000,1020c2
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01

PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 99
LENGTH: 154
TYPE: PRT
ORGANISM: Pinus radiata
US-10-101-464A-99

Query Match 77.1%; Score 37; DB 15; Length 154;
Best Local Similarity 62.5%; Pred. No. 52;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYLSWT 8
||:|:|:|
Db 66 HEWLSNWT 73

Search completed: October 7, 2003, 19:24:25
Job time : 5.13793 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 19:07:11 ; Search time 2.97931 Seconds
(without alignments)
258.231 Million cell updates/sec

Title: US-09-988-013a-2_COPY_95_102

Perfect score: 48
Sequence: 1 HOYLSWT 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	81.2	103	2 PH1054	Ig light chain V r
2	39	81.2	111	2 G30502	Ig kappa chain V r
3	38	79.2	686	2 T13490	NADH2 dehydrogenas
4	38	79.2	686	2 T13561	NADH2 dehydrogenas
5	38	79.2	686	2 T13680	NADH2 dehydrogenas
6	38	79.2	688	2 T09836	NADH2 dehydrogenas
7	36	75.0	597	2 A35928	hypothetical 86k p
8	36	75.0	737	2 T28481	hypothetical prote
9	36	75.0	737	2 A72156	C2L protein - vari
10	36	75.0	737	2 T30795	hypothetical prote
11	36	75.0	737	2 F42508	E2L protein - vacc
12	36	75.0	737	2 E36841	conserved hypotet
13	36	75.0	901	2 G89810	hypothetical prote
14	36	75.0	2109	2 T31352	Ig light chain V r
15	35	72.9	101	2 S26337	hypothetical prote
16	35	72.9	174	2 T29783	hypothetical prote
17	35	72.9	381	2 T13666	NADH2 dehydrogenas
18	35	72.9	581	2 A05204	hypothetical prote
19	35	72.9	693	2 T13175	NADH2 dehydrogenas
20	35	72.9	694	2 T13573	NADH2 dehydrogenas
21	35	72.9	694	2 T13572	NADH2 dehydrogenas
22	35	72.9	697	2 T13370	NADH2 dehydrogenas
23	35	72.9	697	2 T13670	NADH2 dehydrogenas
24	35	72.9	698	2 T12625	NADH2 dehydrogenas
25	35	72.9	698	2 T12627	NADH2 dehydrogenas
26	35	72.9	699	2 T12673	NADH2 dehydrogenas
27	35	72.9	701	2 T13587	NADH2 dehydrogenas
28	35	72.9	701	2 T13588	NADH2 dehydrogenas
29	35	72.9	701	2 T13056	NADH2 dehydrogenas

30	35	72.9	702	2 T12624	NADH2 dehydrogenas
31	35	72.9	702	2 T12677	NADH2 dehydrogenas
32	35	72.9	702	2 T13655	NADH2 dehydrogenas
33	35	72.9	702	2 T13409	NADH2 dehydrogenas
34	35	72.9	702	2 T13505	NADH2 dehydrogenas
35	35	72.9	702	2 T13058	NADH2 dehydrogenas
36	35	72.9	703	2 T12696	NADH2 dehydrogenas
37	35	72.9	703	2 T13074	NADH2 dehydrogenas
38	35	72.9	703	2 T13393	NADH2 dehydrogenas
39	35	72.9	703	2 T13696	NADH2 dehydrogenas
40	35	72.9	704	2 T13503	NADH2 dehydrogenas
41	35	72.9	704	2 T13665	NADH2 dehydrogenas
42	35	72.9	705	2 T04400	NADH2 dehydrogenas
43	35	72.9	706	2 T12748	NADH2 dehydrogenas
44	35	72.9	706	2 T13391	NADH2 dehydrogenas
45	35	72.9	734	1 DER2N5	NADH2 dehydrogenas

ALIGNMENTS

RESULT 1

PH1054
Ig light chain V region (clone 202.135) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C/Accession: PH1054
R/Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A/Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A/Reference number: PH0971; M01D:92381444; PMID:1512540
A/Accession: PH1054
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-103 <RTL>
A/Experimental source: B cell, strain [NZB x NZM]F1
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
C/Keywords: Immunoglobulin
F/16-96/Domain: Immunoglobulin homology <IMM>

Query Match 81.2% Score 39; DB 2; Length 103;

Best Local Similarity 87.5%; Pred. No. 2.6;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYLSWT 8
|||||:|
Db 95 HOYLSWT 102

RESULT 2

G30502
Ig kappa chain V region (A52) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000
C/Accession: G30502
R/Ellat, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A/Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1
A/Reference number: A30502; M01D:86315787; PMID:2457627
A/Accession: G30502
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-111 <RTL>
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
C/Keywords: heterotetramer; Immunoglobulin
F/16-96/Domain: Immunoglobulin homology <IMM>

Query Match 81.2% Score 39; DB 2; Length 111;

Best Local Similarity 75.0%; Pred. No. 2.8;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HOYLSWT 8
||:||||

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DB 95 HQHFSWT 102

RESULT 3
T13490
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Mentha x rotundifolia chloroplast
C:Species: chloroplast Mentha x rotundifolia
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
C:Accession: T13490
R:Magstalt, S.J.; Hickerson, L.; Spangler, R.; Reeves, P.A.; Olmstead, R.G.
Plant Syst. Evol. 209, 265-274, 1998
A>Title: Phylogeny of Labiatae s.l. Inferred from cpDNA sequences.
A:Reference number: 217580
A:Accession: T13490
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-686 <MAG>
A:Cross-references: EMBL:U78696; NID:g1695962; PID:g1695963; PIDN:AAB37149.1
C:Genetics:
A:Genome: chloroplast
A>Note: ndhf
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match
Best Local Similarity 79.2%; Score 38; DB 2; Length 686;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HQYLSWT 8
|||: |||
50 HQYVSWT 57

RESULT 4
T13561
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Plectranthus barbatus chloroplast
C:Species: chloroplast Plectranthus barbatus
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
C:Accession: T13561
R:Magstalt, S.J.; Hickerson, L.; Spangler, R.; Reeves, P.A.; Olmstead, R.G.
Plant Syst. Evol. 209, 265-274, 1998
A>Title: Phylogeny of Labiatae s.l. Inferred from cpDNA sequences.
A:Reference number: 217580
A:Accession: T13561
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-686 <MAG>
A:Cross-references: EMBL:U78698; NID:g1695968; PID:g1695969; PIDN:AAB37152.1
C:Genetics:
A:Genome: chloroplast
A>Note: ndhf
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match
Best Local Similarity 79.2%; Score 38; DB 2; Length 686;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HQYLSWT 8
|||: |||
50 HQYVSWT 57

RESULT 5
T13680
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Salvia divinorum chloroplast (fr
C:Species: chloroplast Salvia divinorum
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
C:Accession: T13680
R:Magstalt, S.J.; Hickerson, L.; Spangler, R.; Reeves, P.A.; Olmstead, R.G.
Plant Syst. Evol. 209, 265-274, 1998
A>Title: Phylogeny of Labiatae s.l. Inferred from cpDNA sequences.
A:Reference number: 217580

A:Accession: T13680
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-686 <MAG>
A:Cross-references: EMBL:U78703; NID:g1695982; PID:g1695983; PIDN:AAB37159.1
C:Genetics:
A:Genome: chloroplast
A>Note: ndhf
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match
Best Local Similarity 79.2%; Score 38; DB 2; Length 686;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HQYLSWT 8
|||: |||
50 HQYVSWT 57

RESULT 6
T09836
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - upland cotton chloroplast (fr
C:Species: chloroplast Gossypium hirsutum (upland cotton)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002
C:Accession: T09836
R:Seelanan, T.; Wendel, J.F.; Schnabel, A.
Syst. Bot. 22, 259-290, 1997
A>Title: Congruence and consensus in the cotton tribe (Malvaceae).
A:Reference number: 216766
A:Accession: T09836
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-688 <SEE>
A:Cross-references: EMBL:U55340; NID:g1654247; PID:g1654248
C:Genetics:
A:Genome: chloroplast
A>Note: ndhf
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match
Best Local Similarity 79.2%; Score 38; DB 2; Length 686;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HQYLSWT 8
|||: |||
57 HQYVSWT 64

RESULT 7
A35928
hypothetical 86k protein E2L - vaccinia virus
C:Species: vaccinia virus
C>Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 19-Apr-2002
C:Accession: A35928
R:Ahm, B.Y.; Gershon, P.D.; Jones, E.V.; Moss, B.
Mol. Cell. Biol. 10, 5433-5441, 1990
A>Title: Identification of rpo30, a vaccinia virus RNA polymerase gene with structure
A:Reference number: A35928; MUID:90377234; PMID:2398897
A:Accession: A35928
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-597 <AHN>
A:Cross-references: GB:M36339
C:Superfamily: vaccinia virus hypothetical protein 49L

Query Match
Best Local Similarity 75.0%; Score 36; DB 2; Length 597;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 OYLSWT 8
:|||||
```

Db 572 RYLSSWT 578

RESULT 8
T28481
hypothetical protein E2L - variola major virus
C:Species: variola major virus
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C:Accession: T28481
R:Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin
Nature 366, 748-751, 1993
A:Title: Potential virulence determinants in terminal regions of variola smallpox virus
A:Reference number: Z20488; MUID:9408874; PMID:8264798
A:Accession: T28481
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-737 <MAS>
A:Cross-references: EMBL:L22579; NID:g623595; PIDN:AAA60791.1; PID:g438961
C:Superfamily: vaccinia virus hypothetical protein 49L

Query Match 75.0%; Score 36; DB 2; Length 737;
Best Local Similarity 85.7%; Pred. No. 73;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYLSWT 8
:|||||

Db 572 RYLSSWT 578

RESULT 9
A72156
C2L protein - variola minor virus (strain Garcia-1966)
C:Species: variola minor virus
C>Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 20-Jun-2000
C:Accession: A72156
R:Shchelkunov, S.N.; Tomenin, A.V.; Gutrov, V.V.; Safonov, P.F.; Massung, R.F.; Lopat
submitted to GenBank, March 1998
A:Description: Analysis of the complete coding sequence of DNA of alastrim variola minor
A:Reference number: A72150
A:Accession: A72156
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-737 <SHC>
A:Cross-references: GB:Y16780; NID:g5830555; PIDN:CAB54643.1; PID:g5830604
A:Experimental source: strain Garcia-1966
C:Genetics:
A:Gene: C2L
C:Superfamily: vaccinia virus hypothetical protein 49L

Query Match 75.0%; Score 36; DB 2; Length 737;
Best Local Similarity 85.7%; Pred. No. 73;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYLSWT 8
:|||||

Db 572 RYLSSWT 578

RESULT 10
T30795
hypothetical protein 49L - vaccinia virus (strain Ankara)
N:Alternate names: probable 85.9k protein
C:Species: vaccinia virus
A:Variety: strain Ankara
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jun-2000
C:Accession: T30795
R:Autoune, G.; Schellinger, F.; Falkner, F.G.; Dorner, F.
submitted to the EMBL Data Library, March 1997
A:Description: The complete genomic sequence of the Modified Vaccinia Ankara (MVA) strain
A:Reference number: Z20877
A:Accession: T30795
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-737 <ANT>
A:Cross-references: EMBL:U94848; PIDN:AAB96427.1
A:Experimental source: strain Ankara
C:Genetics:
A:Note: MVA049L
C:Superfamily: vaccinia virus hypothetical protein 49L

Query Match 75.0%; Score 36; DB 2; Length 737;
Best Local Similarity 85.7%; Pred. No. 73;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYLSWT 8
:|||||

Db 572 RYLSSWT 578

RESULT 11
F42508
E2L protein - vaccinia virus (strain Copenhagen)
C:Species: vaccinia virus
A:Note: host Homo sapiens (man)
C>Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 20-Jun-2000
C:Accession: F42508
R:Johnson, G.P.
submitted to GenBank, June 1990
A:Reference number: A33172
A:Accession: F42508
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-737 <JOH>
C:Superfamily: vaccinia virus hypothetical protein 49L

Query Match 75.0%; Score 36; DB 2; Length 737;
Best Local Similarity 85.7%; Pred. No. 73;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYLSWT 8
:|||||

Db 572 RYLSSWT 578

RESULT 12
E36841
E2L protein - variola virus (strain India-1967)
C:Species: variola virus
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001
C:Accession: E36841
R:Blinov, V.M.
submitted to GenBank, November 1992
A:Reference number: A36859
A:Accession: E36841
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-737 <BLI>
A:Cross-references: GB:X69198; NID:g456758; PIDN:CAA48984.1; PID:g297224
C:Superfamily: vaccinia virus hypothetical protein 49L

Query Match 75.0%; Score 36; DB 2; Length 737;
Best Local Similarity 85.7%; Pred. No. 73;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYLSWT 8
:|||||

Db 572 RYLSSWT 578

RESULT 13
G89810
conserved hypothetical protein SA0412 [imported] - Staphylococcus aureus (strain N315
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: G89810

R.Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A>Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: G89810
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-901 <KUR>
A:Cross-references: GB:BA000018; PID:g13700344; PIDN:BAB41642.1; GSPDB:GN00149
C:Genetics:
A:gene: SA0412

Query Match 75.0%; Score 36; DB 2; Length 901;
Best Local Similarity 85.7%; Pred. No. 89;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 QYLSWT 8
1:|||||
Db 177 QYLSWT 183

RESULT 14
T31352
hypothetical protein - Pelargonium x hortorum
C:Species: Pelargonium x hortorum
C>Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
C:Accession: T31352
R:Downie, S.R.; Katz-Downie, D.S.; Wolfe, K.H.; Calle, P.J.; Palmer, J.D.
Curr. Genet. 25, 367-378, 1994
A>Title: Structure and evolution of the largest chloroplast gene (ORF280): internal pla
A:Reference number: 221012; MUID:94363755; PMID:8082181
A:Accession: T31352
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2109 <DOM>
A:Cross-references: EMBL:M83200; NID:g468913; PID:g468914; PIDN:AAA73173.1

Query Match 75.0%; Score 36; DB 2; Length 2109;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 HQYLSWT 8
1:|||||
Db 28 HQYLSWT 35

RESULT 15
S26337
Ig light chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 20-Jun-2000
C:Accession: S26337; S78449
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A>Title: Antibodies that are specific for a single amino acid interchange in a protein e
A:Reference number: S26309; MUID:91341421; PMID:1908510
A:Accession: S26337
A:Molecule type: mRNA
A:Residues: 1-101 <STA>
A:Cross-references: EMBL:X59193
R:Caton, A.J.
submitted to the EMBL Data Library, April 1991
A:Reference number: S78447
A:Accession: S78449
A:Molecule type: mRNA
A:Residues: 1-60, 'T', 62-91, 'S', 93-101 <CAT>
A:Cross-references: EMBL:X59193; NID:g52323; PIDN:CAA41903.1; PID:g1334067
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:8-86/Domain: Immunoglobulin homology <IMK>

Query Match 72.9%; Score 35; DB 2; Length 101;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 HQYLSWT 8
1:|||||
Db 87 HQYLSWT 94

Search completed: October 7, 2003, 19:21:48
Job time : 3.97931 secs

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OM protein - protein search, using sw model

Run on: October 7, 2003, 19:03:46 ; Search time 1.62759 Seconds
(without alignments)
231.148 Million cell updates/sec

Title: US-09-988-013a-2_COPY_95_102
Perfect score: 48
Sequence: 1 HQTLSSWT 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwisProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	37	77.1	612	1	PCD8_MOUSE
2	36	75.0	426	1	HEML_SYNEU
3	36	75.0	737	1	VE02_VACCC
4	36	75.0	737	1	VE02_VACCV
5	35	75.0	737	1	VE02_VARY
6	35	72.9	702	1	NU5C_POAPR
7	35	72.9	702	1	NU5C_SORBI
8	35	72.9	705	1	NU5C_HORVU
9	35	72.9	734	1	NU5C_ORISA
10	35	72.9	738	1	NU5C_ORIAZ
11	35	72.9	739	1	NU5C_MHAT
12	35	72.9	742	1	NU5C_SPIOL
13	35	72.9	2280	1	YCF2_OENHO
14	35	72.9	2280	1	YCF2_TOBAC
15	34	70.8	238	1	Y825_CHIMU
16	34	70.8	340	1	SNB2_HUMAN
17	34	70.8	612	1	PCD8_HUMAN
18	34	70.8	613	1	PCD8_HUMAN
19	34	70.8	2131	1	YCF2_SPIOL
20	34	70.8	2216	1	YCF2_EPIVI
21	34	70.8	2294	1	YCF2_ARATH
22	34	70.8	3066	1	POLG_BCMVN
23	33	68.8	238	1	Y538_CHLTR
24	33	68.8	863	1	AMPN_CAUCR
25	33	68.8	869	1	AMPN_ECOLI
26	33	68.8	869	1	AMPN_HAETN
27	32	66.7	171	1	VP19_TBSY8
28	32	66.7	172	1	VP19_AMCV
29	32	66.7	172	1	VP19_TBSYA
30	32	66.7	172	1	VP19_TBSYB
31	32	66.7	172	1	VP19_TBSYC
32	32	66.7	172	1	VP19_TBSYJ
33	32	66.7	172	1	VP19_TBSYV

34	32	66.7	220	1	PRT1_PICAN
35	32	66.7	226	1	UNG_VIBCH
36	32	66.7	227	1	UNG_ECOL6
37	32	66.7	228	1	UCRI_SCHPO
38	32	66.7	228	1	UNG_ECO57
39	32	66.7	228	1	UNG_ECOLI
40	32	66.7	228	1	UNG_SALTY
41	32	66.7	236	1	PEBA_SYNPY
42	32	66.7	237	1	DUP1_YEAS
43	32	66.7	241	1	DJCA_HUMAN
44	32	66.7	261	1	TPIS_ENTHI
45	32	66.7	296	1	YDEH_ECOLI

ALIGNMENTS

RESULT 1
PCD8_MOUSE
ID PCD8_MOUSE STANDARD; PRT; 612 AA.
AC Q920X1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Programmed cell death protein 8, mitochondrial precursor (EC 1.-.-.-)
DE (Apoptosis-inducing factor).
GN PCD8 OR AIF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
RN (1)
RP SEQUENCE FROM N.A., SEQUENCE OF N-TERMINUS, AND SEQUENCE OF 322-336.
RX MEDLINE=99142517; PubMed=9989411;
RA Sustin S.A., Lorenzo H.K., Zamzami N., Marzo I., Snow B.E.,
RA Brothers G.M., Mangion J., Jacotot E., Costantini P., Loeffler M.,
RA Larocquette N., Goodlett D.R., Aebersold R., Siderovski D.P.,
RA Penninger J.M., Kroemer G.,
RT "Molecular characterization of mitochondrial apoptosis-inducing factor."
RT Nature 397:441-446(1999).
RL
CC -I- FUNCTION: PROBABLE OXIDOREDUCTASE THAT ACTS AS A CASPASE-
CC INDEPENDENT MITOCHONDRIAL EFFECTOR OF APOPTOTIC CELL DEATH.
CC EXTRAMITOCHONDRIAL AIF INDUCES NUCLEAR CHROMATIN CONDENSATION AND
CC LARGE SCALE DNA FRAGMENTATION (IN VITRO).
CC -I- CORFACTOR: FAD (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: Mitochondrial intermembrane space.
CC TRANSLOCATED TO THE NUCLEUS UPON INDUCTION OF APOPTOSIS.
CC -I- SIMILARITY: BELONGS TO THE FAD-DEPENDENT OXIDOREDUCTASE
CC SUPERFAMILY.
CC -----
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CC -----
DR EMBL, AF100927; AAD16435.1; -;
DR PDB; 1GV4; 31-MAY-02.
DR MGD; MGI:1349419; Pcd8.
DR InterPro: IPR001327; FAD_Pyr_redox.
DR InterPro: IPR001100; Pyr_redox.
DR Pfam: PF00070; Pyr_redox; 1.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00411; PNDRPASE1.
KW Oxidoreductase; Flavoprotein; FAD; Mitochondrion; Transl. peptide;
KW Nuclear protein; Apoptosis; 3D-structure.
FT TRANSIT 1 101 MITOCHONDRION.
FT CHAIN 102 612 PROGRAMMED CELL DEATH PROTEIN 8.
FT DOMAIN 133 438 FAD-DEPENDENT OXIDOREDUCTASE.
FT DOMAIN 445 450 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

SO SEQUENCE 612 AA; 66765 MW; A17EDP5CF77BB85 CRC64;

Query Match 77.1%; Score 37; DB 1; Length 612;
Best Local Similarity 85.7%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 OYLSWT 8
11111111
DB 345 OYLSWNT 351

RESULT 2

HEM1_SYNEL STANDARD; PRT; 426 AA.
AC Q8D13;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Glutamyl-tRNA reductase (EC 1.2.1.-) (GluTR).
GN HEMA OR TLL1738.
OS Synechococcus elongatus (Thermosynechococcus elongatus).
OC Bacteria; Cyanobacteria; Cyanoecoccales; Synechococcus.
OX NCBI_TaxID=32046;
[1]
RN RP SEQUENCE FROM N.A.
RC STRAIN-BP-1;
RX MEDLINE-22225144; PubMed-12240834;
RA Nakamura Y., Kaneo T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
RA Watanabe A., Iriyuchi M., Kawashima K., Kimura T., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
RA Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Nakata S.;
RT "Complete genome structure of the thermophilic cyanobacterium
Thermosynechococcus elongatus BP-1.";
RL DNA Res. 9:123-130(2002).

CC -1- SEMIALDEHYDE + NADP(+) + tRNA(Glu) -
CC -1- PATHWAY: Porphyrin biosynthesis by the C5 pathway; first step.
CC Involved in chlorophyll biosynthesis
CC -1- SIMILARITY: Belongs to the glutamyl-tRNA reductase family.
CC -----
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CC EMBL: AF005375; BAC09290.1; -;
CC HAMAP: MF_00087; -1;
DR InterPro: IPR000343; GluTR.
DR InterPro: IPR000594; Thif_domain.
DR Pfam: PF00745; GluTR_dimer; 1.
DR Pfam: PF05201; GluTR_N; 1.
DR Pfam: PF05200; GluTR_NAD_bind; 1.
DR TIGRfam: TIGR01035; hema; 1.
DR PROSITE: PS00747; GluTR; FALSE_NEG.
KW Porphyrin biosynthesis; Chlorophyll biosynthesis; Oxidoreductase;
KW NADP; Complete proteome.
FT ACT_SITE 50 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 99 BASE (BY SIMILARITY).
SO SEQUENCE 426 AA; 47596 MW; D84CE5A1D2AA777E CRC64;

Query Match 75.0%; Score 36; DB 1; Length 426;
Best Local Similarity 62.5%; Pred. No. 24;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 HOYLSWT 8
11111111
DB 70 HOFLSEMS 77

RESULT 3

VE02_VACC STANDARD; PRT; 737 AA.

AC P21080;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein E2.
GN E2L.
OS Vaccinia virus (strain Copenhagen).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10249;

RN [1]
RN RP SEQUENCE FROM N.A.
RX MEDLINE-91021027; PubMed-2219722;
RA Goebel S.J., Johnson G.P., Perkins M.E., Davis S.W., Winslow J.P.,
RA Paolelli E.;
RT "The complete DNA sequence of vaccinia virus.";
RL Virology 179:247-266(1990).
RN [2]
RN RP COMPLETE GENOME.
RA Goebel S.J., Johnson G.P., Perkins M.E., Davis S.W., Winslow J.P.,
RA Paolelli E.;
RT "Appendix to 'The complete DNA sequence of vaccinia virus.'";
RL Virology 179:517-563(1990).
CC -1- SIMILARITY: TO VACCINIA VIRUS PROTEIN E2.

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CC EMBL: M35027; AAA48039.1; -;
DR PIR: F42508; F42508
DR Pfam: PF04497; Fox_E2; 1.
SO SEQUENCE 737 AA; 85916 MW; 4DBEB8A1BFC2E2F4 CRC64;

Query Match 75.0%; Score 36; DB 1; Length 737;
Best Local Similarity 85.7%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 OYLSWT 8
11111111
DB 572 OYLSWNT 578

RESULT 4

VE02_VACCV STANDARD; PRT; 737 AA.
AC P21604;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-NOV-1991 (Rel. 20, Last annotation update)
DE Protein E2.
GN E2L.
OS Vaccinia virus (strain WR).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10254;

RN [1]
RN RP SEQUENCE FROM N.A.
RA Gershon P.D., Jones E.V., Moss B., Ahn B.-Y.;
RL Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.
RN [2]
RN RP SEQUENCE OF 1-597 FROM N.A.
RX MEDLINE-90377234; PubMed-2398897;
RA Ahn B.-Y., Gershon P.D., Jones E.V., Moss B.;
RT "Identification of rpo30, a vaccinia virus RNA polymerase gene with
RT structural similarity to a eucaryotic transcription elongation
RT factor.";


```

RL MOL. Cell. Biol. 10:5433-5441(1990).
CC -1- SIMILARITY: TO VACCINIA VIRUS PROTEIN E2.
CC -----
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CC -----
DR EMBL: M36339; AAB59822.1; -.
DR PIR: A35928; A35928.
DR PIR: PF04497; Pox_E2; 1.
SQ SEQUENCE 737 AA; 85957 MW; D5BAF09E2F944A9E CRC64;

Query Match 75.0%; Score 36; DB 1; Length 737;
Best Local Similarity 85.7%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYLSWT 8
Db 572 RYLSWT 578

RESULT 5
VE02_VARY STANDARD; PRT; 737 AA.
AC P33862;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein E2.
GN E2L.
OS Variola virus.
OS Viruses: dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OC NCBI_TaxID=10255;
OX [1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN-India-1967 / Isolate Ind3;
RX MEDLINE=94152154; PubMed=8109158;
RA Sandakchnev S.N., Blinov V.M., Resenchuk S.M., Totmenin A.V.,
RA Sandakchnev L.S.;
RT "Analysis of the nucleotide sequence of a 43 kbp segment of the
RT genome of variola virus India-1967 strain.";
RL Virus Res. 30:239-258(1993).
RN [2]
RP COMPLETE GENOME.
RC STRAIN-India-1967 / Isolate Ind3;
RX MEDLINE=93202281; PubMed=8384129;
RA Shchelkunov S.N., Blinov V.M., Sandakchnev L.S.;
RT "Genes of variola and vaccinia viruses necessary to overcome the host
RT protective mechanisms.";
RL FEBS Lett. 319:80-83(1993).
RN -1- SIMILARITY: TO VACCINIA VIRUS PROTEIN E2.
CC -----
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CC -----
DR EMBL: X69198; CAA48984.1; -.
DR PIR: E36841; E36841.
DR Pfam: PF04497; Pox_E2; 1.
SQ SEQUENCE 737 AA; 85957 MW; F8CA3A5A6EFA17E0 CRC64;

Query Match 75.0%; Score 36; DB 1; Length 737;
Best Local Similarity 85.7%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 QYLSWT 8
Db 572 RYLSWT 578

RESULT 6
NU5C_POAPR STANDARD; PRT; 702 AA.
ID NU5C_POAPR
AC Q32880;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE NAD(P)H-quinone oxidoreductase chain 5, chloroplast (EC 1.6.5.-)
DE (NAD(P)H dehydrogenase, chain 5) (NADH-plastoquinone oxidoreductase
DE chain 5) (Fragment).
GN NDHF.
OS Poa pratensis (Kentucky bluegrass).
OS Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Poaceae; Poa.
OX NCBI_TaxID=4545;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RA Clark L.G., Zhang W., Wendel J.F.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: NAD(P)H + plastoquinone = NAD(P)(+) +
CC plastoquinol.
CC -----
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CC -----
DR EMBL: U21980; AAA64698.1; -.
DR PIR: T13655; T13655.
DR InterPro: IPR003916; NADHdb_oxrds.
DR InterPro: IPR001750; Oxidored_q1.
DR InterPro: IPR002128; Oxidored_q1_C.
DR InterPro: IPR001516; Oxidored_q1_N.
DR Pfam: PF00361; Oxidored_q1; 1.
DR Pfam: PF01010; Oxidored_q1_C; 1.
DR Pfam: PF00662; Oxidored_q1_N; 1.
DR DR PRINTS: PR01434; NADHdGNASES.
DR Oxidoreductase; NAD; NADP; Quinone; Plastoquinone; Chloroplast.
FT NON_TER 1
FT NON_TER 1
FT SEQUENCE 702 AA; 78718 MW; 7D7E2C64F961185F CRC64;

Query Match 72.9%; Score 35; DB 1; Length 702;
Best Local Similarity 75.0%; Pred. No. 60;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSWT 8
Db 61 YOYLSWT 68

RESULT 7
NU5C_SORBI STANDARD; PRT; 702 AA.
ID NU5C_SORBI
AC Q33066;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE NAD(P)H-quinone oxidoreductase chain 5, chloroplast (EC 1.6.5.-)
DE (NAD(P)H dehydrogenase, chain 5) (NADH-plastoquinone oxidoreductase
DE chain 5) (Fragment).

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```
GN NDHF.
OS Sorghum bicolor (Sorghum) (Sorghum vulgare).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Sorghum.
OX NCBI_TaxID=4558;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RA Clark L.G., Zhang W., Wendel J.F.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: NAD(P)H + plastocquinone = NAD(P)(+) +
CC plastocquinol.
-----
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-----
CC EMBL: U21981; AAA64699.1; -
CC InterPro: IPR003916; NADhub_oxred5.
CC InterPro: IPR001750; Oxidored_g1.
CC InterPro: IPR002128; Oxidored_g1_C.
CC InterPro: IPR001516; Oxidored_g1_N.
CC Pfam: PF00361; oxidored_g1; 1.
CC Pfam: PF01010; oxidored_g1_C; 1.
CC Pfam: PF00662; oxidored_g1_N; 1.
CC PRINTS: PR01434; NADHGNAS5.
CC Oxidoreductase; NAD; NADP; Quinone; Plastocquinone; Chloroplast.
FT NON_TER 1 702
FT SEQUENCE 702 AA; 78504 MW; 1868EAF2F956F851 CRC64;
SQ
Query Match 72.9%; Score 35; DB 1; Length 702;
Best Local Similarity 75.0%; Pred. No. 60;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 HOYLSSWT 8
DB 61 YQYLMSWT 68
RESULT 8
NU5C_HORVU STANDARD; PRT; 705 AA.
ID NU5C_HORVU 032440;
AC 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE NAD(P)H-quinone oxidoreductase chain 5, chloroplast (EC 1.6.5.-)
DE (NAD(P)H dehydrogenase, chain 5) (NADH-plastocquinone oxidoreductase
DE chain 5) (Fragment).
GN NDHF.
OS Hordeum vulgare (Barley).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticaceae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RA Clark L.G., Zhang W., Wendel J.F.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: NAD(P)H + plastocquinone = NAD(P)(+) +
CC plastocquinol.
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-----
CC EMBL: U22003; AAA64207.1; -
CC PIR: T04400; T04400.
CC InterPro: IPR003916; NADhub_oxred5.
CC InterPro: IPR001750; Oxidored_g1.
CC InterPro: IPR002128; Oxidored_g1_C.
CC InterPro: IPR001516; Oxidored_g1_N.
CC Pfam: PF00361; oxidored_g1; 1.
CC Pfam: PF01010; oxidored_g1_C; 1.
CC Pfam: PF00662; oxidored_g1_N; 1.
CC PRINTS: PR01434; NADHGNAS5.
CC Oxidoreductase; NAD; NADP; Quinone; Plastocquinone; Chloroplast.
FT NON_TER 1 705
FT SEQUENCE 705 AA; 78841 MW; ACC63E07C070ADE6 CRC64;
SQ
Query Match 72.9%; Score 35; DB 1; Length 705;
Best Local Similarity 75.0%; Pred. No. 61;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 HOYLSSWT 8
DB 61 YQYLMSWT 68
RESULT 9
NU5C_ORYSA STANDARD; PRT; 734 AA.
ID NU5C_ORYSA P12129;
AC 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE NAD(P)H-quinone oxidoreductase chain 5, chloroplast (EC 1.6.5.-)
DE (NAD(P)H dehydrogenase, chain 5) (NADH-plastocquinone oxidoreductase
DE chain 5).
GN NDHF.
OS Oryza sativa (Rice).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RC MEDLINE=89364698; PubMed=2770692;
RA Hiratsuka J., Shimada H., Whittier R., Ishibashi T., Sakamoto M.,
RA Mori M., Kondo C., Honji Y., Sun C.-R., Meng B.-Y., Li Y.-Q.,
RA Kanno A., Nishizawa Y., Hirai A., Shinzaki K., Suglura M.;
RT "The complete sequence of the rice (Oryza sativa) chloroplast genome:
RT intermolecular recombination between distinct tRNA genes accounts for
RT a major plastid DNA inversion during the evolution of the cereals.";
RT Mol. Gen. Genet. 217:185-194(1989).
CC -1- CATALYTIC ACTIVITY: NAD(P)H + plastocquinone = NAD(P)(+) +
CC plastocquinol.
-----
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-----
CC EMBL: X15901; CAA33950.1; -
CC PIR: J00286; DERZNS.
CC InterPro: IPR003916; NADhub_oxred5.
DR
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DR InterPro: IPR001750; Oxidored_q1.
DR InterPro: IPR002128; Oxidored_q1_C.
DR InterPro: IPR001516; Oxidored_q1_N.
DR Pfam: PF00361; Oxidored_q1; 1.
DR Pfam: PF01010; Oxidored_q1_C; 1.
DR Pfam: PF00662; Oxidored_q1_N; 1.
DR PRINTS: PR01434; NADHGNASE5.
KW Oxidoreductase; NAD; NADP; Quinone; Plastoquinone; Chloroplast.
SQ SEQUENCE 734 AA; 82597 MW; BFEFE20A01632B2 CRC64;

Query Match 72.9%; Score 35; DB 1; Length 734;
Best Local Similarity 75.0%; Pred. No. 63;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HOYLSWT 8
Db 69 YOYLSWT 76

RESULT 10
ID NUSC_MAIZE STANDARD; PRT; 738 AA.
AC P46620;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE NAD(P)H-quinone oxidoreductase chain 5, chloroplast (EC 1.6.5.-)
DE (NAD(P)H dehydrogenase, chain 5) (NADH-plastoquinone oxidoreductase chain 5).
GN NDHF OR NDH5.
OS Zea mays (Maize).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RX MEDLINE=95395841; PubMed=7666415;
RA Maier R.M., Neckermann K., Igloi G.L., Koessel H.;
RT "Complete sequence of the maize chloroplast genome: gene content, hotspots of divergence and fine tuning of genetic information by transcript editing.";
RT J. Mol. Biol. 251:614-628(1995).
RL [2]
RP SEQUENCE OF 9-709 FROM N.A.
RC TISSUE=Leaf;
RA Clark L.G., Zhang W., Wendel J.F.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: NAD(P)H + plastoquinone = NAD(P)(+) + plastoquinol.
CC -----
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CC -----
CC EMBL: X85653; CAA60346.1; -;
DR EMBL: U21985; AAA64703.1; -;
DR PIR: S58612; S58612.
DR MaltzDB: 107782; -;
DR InterPro: IPR003916; NADhub_oxred5.
DR InterPro: IPR001750; Oxidored_q1.
DR InterPro: IPR002128; Oxidored_q1_C.
DR InterPro: IPR001516; Oxidored_q1_N.
DR Pfam: PF00361; Oxidored_q1; 1.
DR Pfam: PF01010; Oxidored_q1_C; 1.
DR Pfam: PF00662; Oxidored_q1_N; 1.
DR PRINTS: PR01434; NADHGNASE5.
KW Oxidoreductase; NAD; NADP; Quinone; Plastoquinone; Chloroplast.

FT CONFLICT 268 268 MISSING (IN REF. 2).
FT CONFLICT 289 289 W -> L (IN REF. 2).
FT CONFLICT 570 570 R -> G (IN REF. 2).
FT CONFLICT 680 680 K -> R (IN REF. 2).
SQ SEQUENCE 738 AA; 82976 MW; F4E3EBDDDC91FA CRC64;

Query Match 72.9%; Score 35; DB 1; Length 738;
Best Local Similarity 75.0%; Pred. No. 64;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HOYLSWT 8
Db 69 YOYLSWT 76

RESULT 11
ID NUSC_WHEAT STANDARD; PRT; 739 AA.
AC Q95H46;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE NAD(P)H-quinone oxidoreductase chain 5, chloroplast (EC 1.6.5.-)
DE (NAD(P)H dehydrogenase, chain 5) (NADH-plastoquinone oxidoreductase chain 5).
GN NDHF.
OS Triticum aestivum (Wheat).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticaceae; Triticum.
OX NCBI_TaxID=4565;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Chinese Spring;
RA Ogihara Y., Isono K., Kojima T., Endo A., Hanaoka M., Shina T.,
RA Terachi T., Utsugi S., Murata M., Mori N., Takumi S., Ikeo K.,
RA Gojobori T., Murai R., Murai K., Matsuo Y., Ohnishi Y., Tajiri H.,
RA Tsunewaki K.;
RT "Chinese spring wheat (Triticum aestivum L.) chloroplast genome: complete sequence and config clones.";
RT Plant Mol. Biol. Rep. 18:243-253(2000).
RL Plant Mol. Biol. Rep. 18:243-253(2000).
CC -1- CATALYTIC ACTIVITY: NAD(P)H + plastoquinone = NAD(P)(+) + plastoquinol.
CC -----
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CC -----
CC EMBL: AB042240; BAB47082.1; -;
DR InterPro: IPR003916; NADhub_oxred5.
DR InterPro: IPR001750; Oxidored_q1.
DR InterPro: IPR002128; Oxidored_q1_C.
DR InterPro: IPR001516; Oxidored_q1_N.
DR Pfam: PF00361; Oxidored_q1; 1.
DR Pfam: PF01010; Oxidored_q1_C; 1.
DR Pfam: PF00662; Oxidored_q1_N; 1.
DR PRINTS: PR01434; NADHGNASE5.
KW Oxidoreductase; NAD; NADP; Quinone; Plastoquinone; Chloroplast.
SQ SEQUENCE 739 AA; 82860 MW; D22C29E699A3354F CRC64;

Query Match 72.9%; Score 35; DB 1; Length 739;
Best Local Similarity 75.0%; Pred. No. 64;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HOYLSWT 8
Db 69 YOYLSWT 76

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RESULT 12
N5C_SPIOL
ID N5C_SPIOL STANDARD: PRT: 742 AA.
AC 09M3J4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE (NAD(P)H-quinone oxidoreductase chain 5, chloroplast (RC 1.6.5.-)
DE (NAD(P)H dehydrogenase, chain 5) (NADH-plastoquinone oxidoreductase
DE chain 5).
GN NDHF.
OS Spinacia oleracea (Spinach).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Geant d'iver, and cv. Monatol;
RC MEDLINE=21187424; PubMed=11292076;
RA Schmitz-Lannebeber C., Maier R.M., Alcaraz J.-P., Cottet A.,
RA Hermann R.G., Mache R.;
RT "The plastid chromosome of spinach (Spinacia oleracea): complete
RT nucleotide sequence and gene organization."
RL Plant Mol. Biol. 45:307-315(2001).
CC -1- CATALYTIC ACTIVITY: NAD(P)H + plastoquinone -> NAD(P)(+) +
CC plastoquinol.
CC -----
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CC -----
DR EMBL: AJ400848; CAB88780.1; -
DR InterPro: IPR003916; NADHdb_oxred5.
DR InterPro: IPR001150; Oxidored_g1.
DR InterPro: IPR002128; Oxidored_g1_C.
DR InterPro: IPR001516; Oxidored_g1_N.
DR Pfam: PF00361; Oxidored_g1; 1.
DR Pfam: PF01010; Oxidored_g1_C; 1.
DR Pfam: PF00662; Oxidored_g1_N; 1.
DR PRINTS: PR01434; NADHGNAS5.
DR OXloreductase; NAD; NADP; Quinone; Plastoquinone; Chloroplast.
SQ SEQUENCE 742 AA; 84529 MW; AB84C8A15E185E7F CRC64;

Query Match
Best Local Similarity 72.9%; Score 35; DB 1; Length 742;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HOYLSWT 8
DB 69 YOYLSWT 76

RESULT 13
YCF2_OENHO
ID YCF2_OENHO STANDARD: PRT: 2280 AA.
AC 09MEF2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical 266.3 kDa protein ycf2.
GN YCF2-A AND YCF2-B.
OS Oenothera hookeri (Hooker's evening primrose).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Onagraceae; Oenothera.

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OX NCBI_TaxID=85636;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Johansen;
RC MEDLINE=20309318; PubMed=10852478;
RA Hupfer H., Swiatek M., Hornung S., Herrmann R.G., Maier R.M.,
RA Chlu W.-L., Sears B.;
RT "Complete nucleotide sequence of the Oenothera elata plastid
RT chromosome, representing plastome I of the five distinguishable
RT Euenothera plastomes."
RL Mol. Gen. Genet. 263:581-585(2000).
CC -1- SIMILARITY: BELONGS TO THE YCF2 FAMILY.
CC -----
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CC -----
DR EMBL: AJ271079; CAB67203.1; -
DR EMBL: AJ271079; CAB67242.1; -
DR InterPro: IPR003593; AAA_Artpase.
DR SMART: SM00382; AAA; 1.
KM Chloroplast, Hypothetical protein.
SQ SEQUENCE 2280 AA; 266257 MW; 0DC3FD2EF9358657 CRC64;

Query Match
Best Local Similarity 72.9%; Score 35; DB 1; Length 2280;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 HOYLSWT 8
DB 24 HHFLDSWT 31

RESULT 14
YCF2_TOBAC
ID YCF2_TOBAC STANDARD: PRT: 2280 AA.
AC P09977; P09977;
DT 01-MAR-1989 (Rel. 10, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 267 kDa protein ycf2 (ORF 2280).
GN YCF2.
OS Nicotiana tabacum (Common tobacco).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Bright Yellow 4;
RA Shinozaki K., Ohme M., Tanaka M., Wakasugi T., Hayashida N.,
RA Matsubayashi T., Zaita N., Chunwongse J., Obozaki J.,
RA Yamaguchi-Shinozaki K., Ohno C., Torazawa K., Meng B.-Y., Sugita M.,
RA Dene H., Kamogashira T., Yamada K., Kusuda J., Takaiwa F., Kato A.,
RA Tohoh N., Shimada H., Sugiyura M.;
RT "The complete nucleotide sequence of the tobacco chloroplast genome:
RT its gene organization and expression."
RL EMBO J. 5:2043-2049(1986).
RN 12
RP REVISIONS.
RA Sugiyura M.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: NOT YET KNOWN.
CC -1- SIMILARITY: BELONGS TO THE YCF2 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).

DR EMBL: Z00044: CAA77427.1; -
DR EMBL: Z00044: CAA77438.1; -
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR003959; AAA_ATPase_central.
DR Pfam: PF00004; AAA; 1.
DR SMART: SM00382; AAA; 1.
KM Chloroplast: Hypothetical protein.
SQ SEQUENCE 2280 AA; 266812 MW; E246D5F3D902C06D CRC64;

Query Match 72.9%; Score 35; DB 1; Length 2280;
Best Local Similarity 62.5%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYLSSWT 8
|:|:|
Db 24 HHFLDSWT 31

RESULT 15
Y825_CHLMU STANDARD; PRT; 238 AA.
ID Y825_CHLMU
AC Q9PJRK4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein TC0825.
GN TC0825.
OS Chlamydia muridarum.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MOPN / N199;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Uppback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwin M., Nelson W., Deboy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
CC -!- SIMILARITY: BELONGS TO THE CHLAMYDIAL CPN0658/CT538/TC0825
CC FAMILY.

CC -----
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CC or send an email to license@isb-sib.ch).

DR EMBL: AE002349; AAF39626.1; -
DR PIR: B81660; B81660.
DR TIGR: TC0825; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 238 AA; 27303 MW; 5FF62FD7D893D049 CRC64;

Query Match 70.8%; Score 34; DB 1; Length 238;
Best Local Similarity 57.1%; Pred. No. 30;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSSW 7
|:|:|
Db 227 HEYISQW 233

Search completed: October 7, 2003, 19:14:59
Job time : 2.62759 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 7, 2003, 19:04:06 ; Search time 7.97241 Seconds
(without alignments)
258.946 Million cell updates/sec

Title: US-09-988-013a-2_COPY_95_102

Perfect score: 48

Sequence: 1 HOYISSWT 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	41	85.4	658	8	09GDW8
2	39	81.2	686	8	P92299
3	39	81.2	705	8	08M9R0
4	39	81.2	730	8	08HTN9
5	39	81.2	3202	12	08QY01
6	38	79.2	610	8	09BB58
7	38	79.2	657	8	09GDV8
8	38	79.2	660	8	09GDV9
9	38	79.2	686	8	P92344
10	38	79.2	686	8	003646
11	38	79.2	686	8	P92329
12	38	79.2	688	8	095645
13	38	79.2	701	8	08HTM4
14	38	79.2	702	10	09SC10
15	38	79.2	704	8	08HTM2
16	38	79.2	704	8	08HTM1

17	38	79.2	726	8	08HTN2	08htn2 ranzania ja
18	38	79.2	726	8	08HTM9	08htm9 sinopodophy
19	38	79.2	726	8	08HTM8	08htm8 diphyllaia
20	38	79.2	726	8	08HTM7	08htm7 podophyllum
21	38	79.2	726	8	08HTM6	08htm6 dysosma ple
22	38	79.2	728	8	08HTN4	08htn4 nandina dom
23	38	79.2	728	8	08HTN3	08htn3 caulophyllu
24	38	79.2	728	8	08HTM5	08htm5 bongardia c
25	38	79.2	728	8	08HTL9	08htl9 eplinedium k
26	38	79.2	729	8	08HTN1	08htn1 jeffersonia
27	38	79.2	729	8	08HTN0	08htn0 jeffersonia
28	37	77.1	429	8	09GFR3	09gfr3 liriiodendro
29	37	77.1	731	8	095D45	095d45 liriiodendro
30	37	77.1	732	8	095D44	095d44 liriiodendro
31	37	77.1	732	8	09TL43	09tl43 liriiodendro
32	37	77.1	743	8	09GE24	09gez4 gilia rigid
33	37	77.1	853	16	092MT9	092mt9 rhizobium m
34	36	75.0	145	10	094DT5	094dt5 oryza sativ
35	36	75.0	409	16	08KC60	08kc60 chlorobium
36	36	75.0	426	16	08DI53	08di53 synchococc
37	36	75.0	737	12	08OM28	08om28 cowpox viru
38	36	75.0	737	12	08M371	08m371 variola maj
39	36	75.0	737	12	09PX52	09px52 variola vir
40	36	75.0	737	12	08ULG3	08ulg3 ectromelia
41	36	75.0	737	12	09QNK3	09qnk3 variola min
42	36	75.0	737	12	057185	057185 vaccinia vi
43	36	75.0	737	12	08Y2W3	08y2w3 camelpox vi
44	36	75.0	737	12	09JFD8	09jfd8 vaccinia vi
45	36	75.0	843	10	08H821	08h821 oryza sativ

ALIGNMENTS

RESULT 1

Q9GDW8 PRELIMINARY; PRT; 658 AA.
ID Q9GDW8;
AC Q9GDW8;
DT 01-MAR-2001 (TREMBL) 16, Created)
DT 01-MAR-2001 (TREMBL) 16, Last sequence update)
DT 01-OCT-2002 (TREMBL) 22, Last annotation update)
DE NADH dehydrogenase subunit F (Fragment).
GN NDHF.
OS Androcymbium ciliolatum.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Colchicaceae;
OC Androcymbium.
OX NCBI_TaxID=59023;
RN [1]
RP SEQUENCE FROM N.A.
RA Patterson T.B., Glynnish T.J.;
RT "Phylogeny, concerted convergence, and phylogenetic niche conservatism
in the core Liliales: Insights from rbcL and ndhF sequence data.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF276012; AAC25128.1; -
DR InterPro; IPR003916; NADhub_oxred5.
DR InterPro; IPR001750; Oxidored_g1.
DR InterPro; IPR002128; Oxidored_g1_C.
DR InterPro; IPR001516; Oxidored_g1_N.
DR Pfam; PF00361; Oxidored_g1; 1.
DR Pfam; PF01010; Oxidored_g1_C; 1.
DR Pfam; PF00662; Oxidored_g1_N; 1.
DR PRINTS; PR01434; NADHGNASE5.
KW NAD; Oxidoreductase; Plastiquinone; Chloroplast.
FT NON_TER 1
FT NON_TER 658
SQ SEQUENCE 658 AA; 74621 MW; CEEA0AB25AC81880 CRC64;

Query Match 85.4%; Score 41; DB 8; Length 658;
Best Local Similarity 87.5%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSWT 8
 DB 40 HOYLSWT 47

RESULT 2

ID P92299 PRELIMINARY; PRT: 686 AA.
 AC P92299;
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, last annotation update)
 DE NADH dehydrogenase (Fragment).
 GN NDHF.
 OS Gleichenia hederacea (Ground-ivy).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Lamiales; Lamiaceae; Nepetoideae; Menthaceae;
 OC Glechoma.
 OC NCBI_TaxID=28509;
 OX [1]
 RN N
 RP SEQUENCE FROM N.A.
 RA Wagstaff S.J., Hickerson L., Spangler R., Reeves P.A., Olmstead R.G.;
 RT "Phylogeny of Labiales s.l. inferred from cpDNA sequences.";
 RL Plant Syst. Evol. 0:0-0(1997).
 DR EMBL: U78691; AAB37144.1; -;
 DR InterPro: IPR001064; Crystal11n.
 DR InterPro: IPR003916; NADHb_oxred5.
 DR InterPro: IPR001750; Oxidored_q1_C.
 DR InterPro: IPR002128; Oxidored_q1_C.
 DR InterPro: IPR001516; Oxidored_q1_N.
 DR Pfam: PF00361; Oxidored_q1; 1.
 DR Pfam: PF01010; Oxidored_q1_C; 1.
 DR Pfam: PF00662; Oxidored_q1_N; 1.
 DR PRINTS: PR01434; NADHDCGNASE5.
 DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; 1.
 DR NAD: Oxidoreductase; Plastocyanone; Chloroplast.
 FT NON_TER 686
 FT SEQUENCE 686 AA; 77786 MW; BA6381A5DC0BAC32 CRC64;
 SQ

Query Match 81.2%; Score 39; DB 8; Length 686;
 Best Local Similarity 75.0%; Pred. No. 55;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSWT 8
 DB 50 HOYLSWT 57

RESULT 3

ID Q8M9R0 PRELIMINARY; PRT: 705 AA.
 AC Q8M9R0;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, last annotation update)
 DE NADH dehydrogenase subunit F (Fragment).
 GN NDHF.
 OS Eucommia ulmoides.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Lamiales; Garryales; Eucommiaceae; Eucommia.
 OC NCBI_TaxID=4392;
 OX [1]
 RN N
 RP SEQUENCE FROM N.A.
 RA Bremer B., Bremer K., Heldari N., Erikson P., Olmstead R.G.,
 RA Anderberg A.A., Kallersjo M., Barkhoradian E.;
 RT "Phylogenetics of asterids based on 3 coding and 3 non-coding
 RT chloroplast DNA markers and the utility of non-coding DNA at higher
 RT taxonomic levels.";
 RL Mol. Phylogenet. Evol. 24:273-300(2002).

DR EMBL: AJ429113; CAD23091.1; -;
 DR InterPro: IPR003916; NADHb_oxred5.
 DR InterPro: IPR001750; Oxidored_q1.
 DR InterPro: IPR002128; Oxidored_q1_C.
 DR InterPro: IPR001516; Oxidored_q1_N.
 DR Pfam: PF00361; Oxidored_q1; 1.
 DR Pfam: PF01010; Oxidored_q1_C; 1.
 DR Pfam: PF00662; Oxidored_q1_N; 1.
 DR PRINTS: PR01434; NADHDCGNASE5.
 DR NAD: Oxidoreductase; Plastocyanone; Chloroplast.
 FT NON_TER 705
 FT SEQUENCE 705 AA; 79613 MW; 7703F997E04543FF CRC64;
 SQ

Query Match 81.2%; Score 39; DB 8; Length 705;
 Best Local Similarity 75.0%; Pred. No. 56;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSWT 8
 DB 61 YOYVSSWT 68

RESULT 4

ID Q8HTN9 PRELIMINARY; PRT: 730 AA.
 AC Q8HTN9;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, last annotation update)
 DE NADH dehydrogenase subunit F (Fragment).
 GN NDHF.
 OS Akebia quinata (Five leaf akebia).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
 OC Lardizabalaceae; Akebia.
 OC NCBI_TaxID=13331;
 OX [1]
 RN N
 RP SEQUENCE FROM N.A.
 RA Kim Y.-D., Kim S.-H., Jansen R.K.;
 RT "Phylogeny of the Berberidaceae based on the sequences of the
 RT chloroplast gene ndhF.";
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY145143; AAN64386.1; -;
 DR Chloroplast.
 FT NON_TER 730
 FT SEQUENCE 730 AA; 81618 MW; CAPE1770BF1B3A75 CRC64;
 SQ

Query Match 81.2%; Score 39; DB 8; Length 730;
 Best Local Similarity 75.0%; Pred. No. 58;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSWT 8
 DB 69 YOYVSSWT 76

RESULT 5

ID Q8QY01 PRELIMINARY; PRT: 3202 AA.
 AC Q8QY01;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, last annotation update)
 DE Polyprotein.
 OS Bean common mosaic virus (strain NL-3 / Michigan) (BCMV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 OC Polyvirus.
 OC NCBI_TaxID=12196;
 OX [1]
 RN N
 RP SEQUENCE FROM N.A.
 RC STRAIN=blackeye cowpea mosaic;

RA Adams M.J.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-blackeye cowpea mosaic;
RA Zheng H.Y., Chen J., Chen J.P., Adams M.J., Hou M.S.;
RT "bean common mosaic virus isolates causing different symptoms in
RT asparagus bean in China differ greatly in the 5'-parts of their
RT genomes";
RL Arch. Virol. 147:0-0(2002).
CC -1- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
DR EMBL: AJ12437; CAC86160.1; -.
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR001650; Helicase_C.
DR InterPro: IPR001730; Peptidase_C4.
DR InterPro: IPR001456; Peptidase_C6.
DR InterPro: IPR001592; Poly-coat.
DR InterPro: IPR002540; Poly_P1.
DR InterPro: IPR007095; RNA_pol_DS_PS.
DR InterPro: IPR001205; RNA_pol_P3D.
DR InterPro: IPR007094; RNA_pol_PSVLR.
DR Pfam: PF00271; Helicase_C.1.
DR Pfam: PF00863; Peptidase_C4.1.
DR Pfam: PF00851; Peptidase_C6.1.
DR Pfam: PF00767; Poly-coat.1.
DR Pfam: PF01577; Poly_P1.1.
DR Pfam: PF00680; RNA_dep_RNA_pol.1.
DR SMART: SM00487; DEXDC.1.
DR SMART: SM00490; HELICC.1.
DR PROSITE: PSS0507; RDRP_POSITIVE.1.
DR PROSITE: PSS0521; RDRP_VIRAL.1.
KW AMP-binding; Coat protein; Helicase; Hydrolase.
FT CHAIN 1 423
FT CHAIN 424 880
FT CHAIN 881 1227
FT CHAIN 1228 1279
FT CHAIN 1280 1913
FT CHAIN 1914 1966
FT CHAIN 1967 2156
FT CHAIN 2157 2399
FT CHAIN 2400 2915
FT CHAIN 2916 3202
SQ SEQUENCE 3202 AA; 363915 MW; 2BA72C32BCD65548 CRC64;

Query Match 81.2%; Score 39; DB 12; Length 3202;
Best Local Similarity 75.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYLSWT 8
DB 1743 HOYTSWT 1750

RESULT 6
Q9BB58 PRELIMINARY; PRT; 610 AA.
AC Q9BB58;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE NADH dehydrogenase F (Fragment).
GN NDHF.
OS Maschalocephalus dinklagei.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Commelinidae incertae sedis;
OC Rapateaceae; Maschalocephalus.
OX NCBI_TaxID=142432;
RN [1]
RP SEQUENCE FROM N.A.
RA Givnish T.J., Evans T.M., Zjhra M.L., Patterson T.B., Berry P.E.,
RT Molecular evolution, adaptive radiation, and geographic

RT diversification in the amphiatlantic family Rapateaceae: evidence from
RT ndhf sequences and morphology";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF207628; AAK21836.1; -.
DR InterPro: IPR003916; NADHub_oxred5.
DR InterPro: IPR001750; Oxidored_q1.
DR InterPro: IPR002128; Oxidored_q1_C.
DR InterPro: IPR001516; Oxidored_q1_N.
DR Pfam: PF00361; Oxidored_q1.1.
DR Pfam: PF01010; Oxidored_q1_C.1.
DR Pfam: PF00662; Oxidored_q1_N.1.
DR PRINTS: PRO1434; NADHGNASE5.
KW NAD; Oxidoreductase; Plastoquinone; Chloroplast.
FT NON_TER 1 610
FT NON_TER 610 610
SQ SEQUENCE 610 AA; 68669 MW; 3AF1F9E61C086AD1 CRC64;

Query Match 79.2%; Score 38; DB 8; Length 610;
Best Local Similarity 75.0%; Pred. No. 74;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSWT 8
DB 7 YOYLSWT 14

RESULT 7
Q9GDV8 PRELIMINARY; PRT; 657 AA.
AC Q9GDV8;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE NADH dehydrogenase subunit F (Fragment).
GN NDHF.
OS Tricyrtis latifolia.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Colchicaceae;
OC Tricyrtis.
OX NCBI_TaxID=85291;
RN [1]
RP SEQUENCE FROM N.A.
RA Patterson T.B., Givnish T.J.;
RT "Phylogeny, concerted convergence, and phylogenetic niche conservatism
RT in the core Liliales: Insights from rbcL and ndhf sequence data";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF276022; AAC25138.1; -.
DR InterPro: IPR003916; NADHub_oxred5.
DR InterPro: IPR001750; Oxidored_q1.
DR InterPro: IPR002128; Oxidored_q1_C.
DR InterPro: IPR001516; Oxidored_q1_N.
DR Pfam: PF00361; Oxidored_q1.1.
DR Pfam: PF01010; Oxidored_q1_C.1.
DR Pfam: PF00662; Oxidored_q1_N.1.
DR PRINTS: PRO1434; NADHGNASE5.
KW NAD; Oxidoreductase; Plastoquinone; Chloroplast.
FT NON_TER 1 657
FT NON_TER 657 657
SQ SEQUENCE 657 AA; 73991 MW; 13DC69801A1C360A CRC64;

Query Match 79.2%; Score 38; DB 8; Length 657;
Best Local Similarity 75.0%; Pred. No. 80;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSWT 8
DB 40 YOYLSWT 47

RESULT 8
Q9GDV9 PRELIMINARY; PRT; 660 AA.
ID Q9GDV9

```

AC 09GDV9;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, last annotation update)
DE NADH dehydrogenase subunit F (Fragment).
GN NDHF..
OS Triclyrtis affinis.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Colchicaceae;
OC Triclyrtis.
OX NCBI_TaxID-34198;
RN [1]
RP SEQUENCE FROM N.A.
RA Paterson T.B., Givnish T.J.;
RT *Phylogeny, concerted convergence, and phylogenetic niche conservatism
in the core Liliales: insights from rbcL and ndhF sequence data.";
RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF276021; ANG25137.1; -
DR InterPro: IPR003916; NADhub_oxred5.
DR InterPro: IPR001750; Oxidored_g1_C.
DR InterPro: IPR002128; Oxidored_g1_C.
DR InterPro: IPR001516; Oxidored_g1_N.
DR Pfam: PF00361; oxidored_g1_1.
DR Pfam: PF01010; oxidored_g1_C; 1.
DR Pfam: PF00662; oxidored_g1_N; 1.
DR PRINTS: PR01434; NADHDGNAS5.
KW NAD; Oxidoreductase; Plastocquinone; Chloroplast.
FT NON_TER 1
FT SEQUENCE 660 AA; 74316 MW; 7E549CCAC6DD5CCB CRC64;

Query Match
Best Local Similarity 79.2%; Score 38; DB 8; Length 660;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSWT 8
Db 40 HOYLSWT 47

RESULT 9
P92344 PRELIMINARY; PRT; 686 AA.
AC P92344;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, last annotation update)
DE NADH dehydrogenase (Fragment).
GN NDHF.
OS Salvia divinorum (Maria pastora).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamiales; Lamiaceae; Nepetoideae; Menthae;
OC Salvia.
OX NCBI_TaxID-28513;
RN [1]
RP SEQUENCE FROM N.A.
RA Magataff S.J., Hickerson L., Spangler R., Reeves P.A., Olmstead R.G.;
RT "Phylogeny of Labiatae s.l. inferred from cpDNA sequences.";
RL Plant Syst. Evol. 0:0-0(1997).
DR EMBL: U78703; AAB37159.1; -
DR InterPro: IPR001064; Crystallin.
DR InterPro: IPR003916; NADhub_oxred5.
DR InterPro: IPR001750; Oxidored_g1_C.
DR InterPro: IPR002128; Oxidored_g1_C.
DR InterPro: IPR001516; Oxidored_g1_N.
DR Pfam: PF00361; oxidored_g1_1.
DR Pfam: PF01010; oxidored_g1_C; 1.
DR Pfam: PF00662; oxidored_g1_N; 1.
DR PRINTS: PR01434; NADHDGNAS5.
DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; 1.
KW NAD; Oxidoreductase; Plastocquinone; Chloroplast.
FT NON_TER 1
FT SEQUENCE 660 AA; 77675 MW; 72C799DB30C92020 CRC64;

Query Match
Best Local Similarity 79.2%; Score 38; DB 8; Length 686;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSWT 8
Db 50 HOYLSWT 57

RESULT 10
003646
ID 003646 PRELIMINARY; PRT; 686 AA.
AC 003646;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, last annotation update)
DE NADH dehydrogenase (Fragment).
GN NDHF.
OS Mentha x rotundifolia.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamiales; Lamiaceae; Nepetoideae; Menthae;
OC Mentha.
OX NCBI_TaxID-54461;
RN [1]
RP SEQUENCE FROM N.A.
RA Magataff S.J., Hickerson L., Spangler R., Reeves P.A., Olmstead R.G.;
RT "Phylogeny of Labiatae s.l. inferred from cpDNA sequences.";
RL Plant Syst. Evol. 0:0-0(1997).
DR EMBL: U78696; AAB37149.1; -
DR InterPro: IPR001064; Crystallin.
DR InterPro: IPR003916; NADhub_oxred5.
DR InterPro: IPR001750; Oxidored_g1_C.
DR InterPro: IPR002128; Oxidored_g1_C.
DR InterPro: IPR001516; Oxidored_g1_N.
DR Pfam: PF00361; oxidored_g1_1.
DR Pfam: PF01010; oxidored_g1_C; 1.
DR Pfam: PF00662; oxidored_g1_N; 1.
DR PRINTS: PR01434; NADHDGNAS5.
DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; 1.
KW NAD; Oxidoreductase; Plastocquinone; Chloroplast.
FT NON_TER 686
FT SEQUENCE 686 AA; 77675 MW; 72C799DB30C92020 CRC64;

Query Match
Best Local Similarity 79.2%; Score 38; DB 8; Length 686;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSWT 8
Db 50 HOYLSWT 57

RESULT 11
P92329 PRELIMINARY; PRT; 686 AA.
AC P92329;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, last annotation update)
DE NADH dehydrogenase (Fragment).
GN NDHF.
OS Plectranthus barbatus.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamiales; Lamiaceae; Nepetoideae; Ocimeae;
OC Plectranthus.

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KW NAD; Oxidoreductase; Plastocquinone; Chloroplast.
FT NON_TER 686
FT SEQUENCE 686 AA; 77863 MW; FBFD32F3A9336AB CRC64;

Query Match
Best Local Similarity 79.2%; Score 38; DB 8; Length 686;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSWT 8
Db 50 HOYLSWT 57

RESULT 10
003646
ID 003646 PRELIMINARY; PRT; 686 AA.
AC 003646;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, last annotation update)
DE NADH dehydrogenase (Fragment).
GN NDHF.
OS Mentha x rotundifolia.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamiales; Lamiaceae; Nepetoideae; Menthae;
OC Mentha.
OX NCBI_TaxID-54461;
RN [1]
RP SEQUENCE FROM N.A.
RA Magataff S.J., Hickerson L., Spangler R., Reeves P.A., Olmstead R.G.;
RT "Phylogeny of Labiatae s.l. inferred from cpDNA sequences.";
RL Plant Syst. Evol. 0:0-0(1997).
DR EMBL: U78696; AAB37149.1; -
DR InterPro: IPR001064; Crystallin.
DR InterPro: IPR003916; NADhub_oxred5.
DR InterPro: IPR001750; Oxidored_g1_C.
DR InterPro: IPR002128; Oxidored_g1_C.
DR InterPro: IPR001516; Oxidored_g1_N.
DR Pfam: PF00361; oxidored_g1_1.
DR Pfam: PF01010; oxidored_g1_C; 1.
DR Pfam: PF00662; oxidored_g1_N; 1.
DR PRINTS: PR01434; NADHDGNAS5.
DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; 1.
KW NAD; Oxidoreductase; Plastocquinone; Chloroplast.
FT NON_TER 686
FT SEQUENCE 686 AA; 77675 MW; 72C799DB30C92020 CRC64;

Query Match
Best Local Similarity 79.2%; Score 38; DB 8; Length 686;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSWT 8
Db 50 HOYLSWT 57

RESULT 11
P92329 PRELIMINARY; PRT; 686 AA.
AC P92329;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, last annotation update)
DE NADH dehydrogenase (Fragment).
GN NDHF.
OS Plectranthus barbatus.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamiales; Lamiaceae; Nepetoideae; Ocimeae;
OC Plectranthus.

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OX  NCBI_TaxID=41228;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Magstiff S.J., Hickerson L., Spangler R., Reeves P.A., Olmstead R.G.;
RT  "Phylogeny of Labiales s.l. inferred from cpDNA sequences.";
RL  Plant Syst. Evol. 0:0-0(1997).
DR  EMBL: U78698; AAB37152.1; -.
DR  InterPro: IPR003916; NADHdb_oxred5.
DR  InterPro: IPR001750; Oxidored_q1.
DR  InterPro: IPR002128; Oxidored_q1_C.
DR  InterPro: IPR001516; Oxidored_q1_N.
DR  Pfam: PF00361; Oxidored_q1_1.
DR  Pfam: PF01010; Oxidored_q1_C_1.
DR  PRINTS: PR01434; NADHGNASE5.
KM  NAD: Oxidoreductase; Plastocyanone; Chloroplast.
FT  NON_TER 686
SQ  SEQUENCE 686 AA; 77797 MW; 2B735E7A80FEA8CF CRC64;

Query Match
Best Local Similarity 79.2%; Score 38; DB 8; Length 686;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY  1 HOYISSWT 8
DB  50 HOYVSWT 57

RESULT 12
ID  095645 PRELIMINARY; PRT; 688 AA.
AC  095645;
DT  01-FEB-1997 (TREMBLrel. 02, Created)
DT  01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT  01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE  NADH dehydrogenase (Fragment).
OS  NDBF.
OS  Gossypium hirsutum (Upland cotton).
OG  Chloroplast.
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC  eurosids II; Malvales; Malvaceae; Malvaceae; Gossypium.
OX  NCBI_TaxID=3635;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Seelanan T., Wendel J.F., Schnabel A.;
RT  "Congruence and consensus in the cotton tribe: Evidence from the
RT  nuclear and plastid genomes.";
RL  Syst. Bot. 0:0-0(1996).
DR  EMBL: U5340; AAB17747.1; -.
DR  InterPro: IPR003916; NADHdb_oxred5.
DR  InterPro: IPR001750; Oxidored_q1.
DR  InterPro: IPR002128; Oxidored_q1_C.
DR  InterPro: IPR001516; Oxidored_q1_N.
DR  Pfam: PF00361; Oxidored_q1_1.
DR  Pfam: PF01010; Oxidored_q1_C_1.
DR  Pfam: PF00662; Oxidored_q1_N_1.
DR  PRINTS: PR01434; NADHGNASE5.
KM  NAD: Oxidoreductase; Plastocyanone; Chloroplast.
FT  NON_TER 1
FT  NON_TER 688
SQ  SEQUENCE 688 AA; 77857 MW; B1FE8BEA0A95DA57 CRC64;

Query Match
Best Local Similarity 79.2%; Score 38; DB 8; Length 688;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY  1 HOYISSWT 8
DB  57 HOYVSWT 64

RESULT 13

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O8HTM4
ID  O8HTM4 PRELIMINARY; PRT; 701 AA.
AC  O8HTM4;
DT  01-MAR-2003 (TREMBLrel. 23, Created)
DT  01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT  01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE  NADH dehydrogenase subunit F (Fragment).
GN  NDBF.
OS  Achlys triphylla (Vanilla leaf).
OS  Chloroplast.
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
OC  Berberidaceae; Achlys.
OX  NCBI_TaxID=63345;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Kim Y.-D., Kim S.-H., Jansen R.K.;
RT  "Phylogeny of the Berberidaceae based on the sequences of the
RT  chloroplast gene ndhF.";
RL  Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR  EMBL: AY145158; AAN64401.1; -.
KM  Chloroplast.
FT  NON_TER 701
SQ  SEQUENCE 701 AA; 78560 MW; 7DB5860E7F53389A CRC64;

Query Match
Best Local Similarity 79.2%; Score 38; DB 8; Length 701;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY  1 HOYISSWT 8
DB  69 HOYVSWT 76

RESULT 14
ID  09SC10 PRELIMINARY; PRT; 702 AA.
AC  09SC10;
DT  01-MAY-2000 (TREMBLrel. 13, Created)
DT  01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT  01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE  NADH dehydrogenase subunit F (Fragment).
GN  NDBF.
OS  Tetracera asiatica.
OS  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC  Dilleniaceae; Tetracera.
OX  NCBI_TaxID=85285;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Albach D.C., Solits P.S., Solits D.E., Olmstead G.;
RT  "Phylogeny of the Asteridae s.l. based on sequences from four
RT  different genes.";
RL  Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR  EMBL: AJ236277; CAB65467.1; -.
DR  InterPro: IPR003916; NADHdb_oxred5.
DR  InterPro: IPR001750; Oxidored_q1.
DR  InterPro: IPR002128; Oxidored_q1_C.
DR  InterPro: IPR001516; Oxidored_q1_N.
DR  Pfam: PF00361; Oxidored_q1_1.
DR  Pfam: PF01010; Oxidored_q1_C_1.
DR  Pfam: PF00662; Oxidored_q1_N_1.
DR  PRINTS: PR01434; NADHGNASE5.
KM  NAD: Oxidoreductase.
FT  NON_TER 1
FT  NON_TER 702
SQ  SEQUENCE 702 AA; 78999 MW; 1CB8A0F547FB76B2 CRC64;

Query Match
Best Local Similarity 79.2%; Score 38; DB 10; Length 702;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY  1 HOYISSWT 8

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DB 60 HOYVMSWT 67

RESULT 15

08HTM2
ID 08HTM2 PRELIMINARY; PRT; 704 AA.
AC 08HTM2;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE NADH dehydrogenase subunit F (Fragment).
GN NDHF.
OS Leontice evermannii.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
OC Berberidaceae; Leontice.
OX NCBI_TaxID=211973;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim Y.-D., Kim S.-H., Jansen R.K.;
RT "Phylogeny of the Berberidaceae based on the sequences of the
RT chloroplast gene ndhF."
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY145160; MAM64403.1; -.
KW Chloroplast.
FT NON_TER 704 704
SQ SEQUENCE 704 AA; 78783 MW; 8EFEB8AEFB3ECA44 CRC64;

Query Match 79.2%; Score 38; DB 8; Length 704;
Best Local Similarity 75.0%; Pred. NO. 86;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYVMSWT 8
DB 69 HOYVMSWT 76

Search completed: October 7, 2003, 19:19:59
Job time : 9.97241 secs


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XX 12-AUG-1994; 94US-0289576.
PR (IMMU-) IMMUNOMEDICS INC.
XX
XX Hansen H, Leung S;
XX WPI: 1996-139454/14.
XX N-PSDB; AAT13802.
XX
XX Chinese and humanised LL2 antibodies - used to produce conjugates
XX for the therapy and diagnosis of B-cell lymphoma(s) and
XX leukaemia(s).
XX
XX Claim 5; Page 36-37; 70pp; English.
XX
XX The complementarity determining regions (CDRs) of mouse monoclonal
XX antibody (Mab) LL2 VK (AAR92215) and VH (AAR92216) regions were
XX recombinantly linked to the framework sequences of human VK and VH
XX regions, respectively, to give humanised LL2 VK (AAR92217) and VH
XX (AAR92218). These were subsequently linked, respectively, to human
XX kappa and IgG1 constant regions. A humanised Mab was obtained that
XX retained the B-lymphoma and leukaemia cell targeting and
XX internalisation characteristics of the parental LL2 Mab, and which
XX exhibited a lowered HAMA reaction. It can be linked to e.g. a
XX cytostatic agent for therapeutic appln.
XX
XX Sequence 116 AA:
SQ
Query Match 100.0%; Score 620; DB 17; Length 116;
Best Local Similarity 100.0%; Pred. No. 6,1e-43;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVQLDSGAELEKPGASVVMKSCASGYTFTSYLHWIKRPGQGLEWIGYINPRNDYTEY 60
DB 1 QVQLDSGAELEKPGASVVMKSCASGYTFTSYLHWIKRPGQGLEWIGYINPRNDYTEY 60
QY 61 NONFKDKATLVLDKSSSTAYVMOLSLTSDSAVYYCARDDITTFYWGQGTTLTVSS 116
DB 61 NONFKDKATLVLDKSSSTAYVMOLSLTSDSAVYYCARDDITTFYWGQGTTLTVSS 116
RESULT 2
AAM27696
ID AAM27696 standard; Protein; 116 AA.
XX
XX AAM27696;
XX
XX 14-APR-1998 (first entry)
XX
XX Variable heavy chain of Mab LL2.
XX
XX Variable heavy chain; B cell; monoclonal antibody; Mab; LL2;
XX B cell lymphoma; lymphocytic leukaemia cell; murine;
XX diagnosis; treatment; B cell malignancy; non-Hodgkins lymphoma;
XX chronic lymphocytic leukaemia.
XX
XX Mus sp.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX 31..35
XX Region /note= "complementarity determining region 1"
XX Region 50..66 /note= "complementarity determining region 2"
XX Region 99..105 /note= "complementarity determining region 3"
XX
XX W09734632-A1.
XX
XX 25-SEP-1997.
XX
XX 19-MAR-1997; 97WO-US04196.
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XX 20-MAR-1996; 96US-0013709.
PR (IMMU-) IMMUNOMEDICS INC.
XX
XX Hansen H, Leung S, Qu Z;
XX WPI: 1996-479995/44.
XX N-PSDB; AAT98129.
XX
XX Monoclonal antibody engineered to contain glycosylation site - in
XX non-FC constant heavy or light chain region, useful to diagnose or
XX treat B cell malignancies, e.g. non-Hodgkins lymphoma
XX
XX Example 3; Fig 4B; 88pp; English.
XX
XX The present sequence is the variable heavy chain of the
XX B cell specific monoclonal antibody (Mab) LL2, which contains an
XX engineered tripeptide N-glycan acceptor sequence. LL2 is a highly
XX specific anti-B cell lymphoma and anti-lymphocytic leukaemia cell
XX murine Mab. The Mab can be used to diagnose or treat B
XX cell malignancies, e.g. non-Hodgkins lymphoma or chronic
XX lymphocytic leukaemia. The glycosylation site allows a label or
XX therapeutic agent of increased size to be conjugated to the
XX carbohydrate moiety, without affecting the Mab's binding affinity
XX or specificity.
XX
XX Sequence 116 AA:
SQ
Query Match 100.0%; Score 620; DB 18; Length 116;
Best Local Similarity 100.0%; Pred. No. 6,1e-43;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVQLDSGAELEKPGASVVMKSCASGYTFTSYLHWIKRPGQGLEWIGYINPRNDYTEY 60
DB 1 QVQLDSGAELEKPGASVVMKSCASGYTFTSYLHWIKRPGQGLEWIGYINPRNDYTEY 60
QY 61 NONFKDKATLVLDKSSSTAYVMOLSLTSDSAVYYCARDDITTFYWGQGTTLTVSS 116
DB 61 NONFKDKATLVLDKSSSTAYVMOLSLTSDSAVYYCARDDITTFYWGQGTTLTVSS 116
RESULT 3
AAR92219
ID AAR92219 standard; Protein; 116 AA.
XX
XX AAR92219;
XX
XX 28-MAY-1996 (first entry)
XX
XX Humanised LL2 Mab VH region (version hLL2-1).
XX
XX Humanised antibody; monoclonal antibody; Mab; LL2; B-cell lymphoma;
XX leukaemia; therapy; diagnosis; complementarity determining region;
XX CDR; antibody engineering.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX 31..35
XX Region /label= CDR1
XX Region 50..66 /label= CDR2
XX Region 99..105 /label= CDR3
XX
XX W09604925-A1.
XX
XX 22-FEB-1996.
XX
XX 11-AUG-1995; 95WO-US09641.
XX
XX 12-AUG-1994; 94US-0289576.
```

XX (IMMUT-) IMMUNOMEDICS INC.
 PA Hansen H, Leung S;
 XX WPI: 1996-139454/14.
 DR
 XX Chimeric and humanised LL2 antibodies - used to produce conjugates
 PT for the therapy and diagnosis of B-cell lymphoma(s) and
 PT leukaemia(s).
 XX
 PS Example 1: Page 40; 70pp; English.
 XX
 CC The complementarity determining regions (CDRs) of mouse monoclonal
 CC antibody (Mab) LL2 VK (AAR92215) and VH (AAR92216) regions were
 CC recombinantly linked to the framework sequences of human VK and VH
 CC regions, respectively, to give humanised LL2 VK (AAR92217) and VH
 CC (AAR92218). In an alternative version a glutamine was introduced
 CC at position 5 of the humanised VH (AAR92219) to include a PstI site
 CC useful for subcloning. The humanised VK and VH were subsequently
 CC linked, respectively, to human kappa and IgG1 constant regions. A
 CC humanised Mab was obtd. that retained the B-lymphoma and leukaemia
 CC cell targeting and internalisation characteristics of the parental
 CC LL2 Mab, and which exhibited a lowered HAMA reaction. It can be
 CC linked to a cytostatic agent for therapeutic appln.
 XX
 SQ Sequence 116 AA;
 Query Match 89.8%; Score 557; DB 17; Length 116;
 Best Local Similarity 84.5%; Pred. No. 7.5e-38;
 Matches 98; Conservative 14; Mismatches 4; Indels 0; Gaps 0;
 QY 1 QVQLQESGAEISKPGASVYKMSCKASGYFTSYWLHWIKRPGGLEWIGYINPRNDYTEY 60
 Db 1 QVQLVQSGAEVKKRQSSVKVSKCKASGYFTSYWLHWIRQAPGGGLEWIGYINPRNDYTEY 60
 QY 61 NONPKDKATITLADSSSTAYWQLSSLSSEDSAVYYCARDDITTYWGQGITLTVSS 116
 Db 61 NONPKDKATITLADSTNTAYWELSLRSEDTAFYFCARDITTYWGQGITVTVSS 116

RESULT 4
 AAR92218
 ID AAR92218 standard; Protein: 116 AA.
 AC AAR92218;
 XX
 DT 28-MAY-1996 (first entry)
 DE Humanised LL2 Mab VH region.
 XX
 KW Humanised antibody; monoclonal antibody; Mab; LL2; B-cell lymphoma;
 KW leukaemia; therapy; diagnosis; complementarity determining region;
 KW CDR; antibody engineering.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 31..35
 FT Region /label- CDR1
 FT Region 50..66
 FT Region /label- CDR2
 FT Region 99..105
 FT Region /label- CDR3
 XX
 PN WO9604925-A1.
 XX
 PD 22-FEB-1996.
 XX
 PF 11-AUG-1995; 95WO-US09641.
 XX
 PR 12-AUG-1994; 94US-0289576.
 XX

PA (IMMUT-) IMMUNOMEDICS INC.
 XX Hansen H, Leung S;
 XX WPI: 1996-139454/14.
 DR N-PSDB; AAT15804.
 XX
 XX Chimeric and humanised LL2 antibodies - used to produce conjugates
 PT for the therapy and diagnosis of B-cell lymphoma(s) and
 PT leukaemia(s).
 XX
 PS Claim 5; Page 39; 70pp; English.
 XX
 CC The complementarity determining regions (CDRs) of mouse monoclonal
 CC antibody (Mab) LL2 VK (AAR92215) and VH (AAR92216) regions were
 CC recombinantly linked to the framework sequences of human VK and VH
 CC regions, respectively, to give humanised LL2 VK (AAR92217) and VH
 CC (AAR92218). These were subsequently linked, respectively, to human
 CC kappa and IgG1 constant regions. A humanised Mab was obtd. that
 CC retained the B-lymphoma and leukaemia cell targeting and
 CC internalisation characteristics of the parental LL2 Mab, and which
 CC exhibited a lowered HAMA reaction. It can be linked to e.g. a
 CC cytostatic agent for therapeutic appln.
 XX
 SQ Sequence 116 AA;
 Query Match 88.7%; Score 550; DB 17; Length 116;
 Best Local Similarity 83.6%; Pred. No. 2.8e-37;
 Matches 97; Conservative 14; Mismatches 5; Indels 0; Gaps 0;
 QY 1 QVQLQESGAEISKPGASVYKMSCKASGYFTSYWLHWIKRPGGLEWIGYINPRNDYTEY 60
 Db 1 QVQLVQSGAEVKKRQSSVKVSKCKASGYFTSYWLHWIRQAPGGGLEWIGYINPRNDYTEY 60
 QY 61 NONPKDKATITLADSSSTAYWQLSSLSSEDSAVYYCARDDITTYWGQGITLTVSS 116
 Db 61 NONPKDKATITLADSTNTAYWELSLRSEDTAFYFCARDITTYWGQGITVTVSS 116

RESULT 5
 AAM27698
 ID AAM27698 standard; Protein: 116 AA.
 AC AAM27698;
 XX
 DT 14-APR-1998 (first entry)
 DE Variable heavy chain of Mab hLL2.
 XX
 KW Variable heavy chain; B cell; monoclonal antibody; Mab; hLL2;
 KW B cell lymphoma; lymphocytic leukaemia cell; murine; humanised;
 KW diagnosis; treatment; B cell malignancy; non-Hodgkins lymphoma;
 KW chronic lymphocytic leukaemia.
 XX
 OS Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 31..35
 FT Region /note= "complementarity determining region 1"
 FT Region 50..66
 FT Region /note= "complementarity determining region 2"
 FT Region 99..105
 FT Region /note= "complementarity determining region 3"
 XX
 PN WO9734632-A1.
 XX
 PD 25-SEP-1997.
 XX
 PF 19-MAR-1997; 97WO-US04196.
 XX
 PR 20-MAR-1996; 96US-0013709.
 XX


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XX 19-APR-1988; 88DE-3813023.
XX (BEHW) BEHRINGERWERKE AG.
XX Domdey H, Marget M, Vonspecht B;
XX WPI; 1989-310861/43.
XX DR N-PSDB; AAN91645.
XX Monoclonal antibody to Pseudomonas aeruginosa - and DNA coding for
PT variable antibody regions.
XX Claim 1; page 6; 7pp; german.
XX The peptide is encoded by the heavy chain of monoclonal antibody 6A4.
CC 6A4 reacts with the OMP-1 protein of all 19 known serotypes of
CC P.aeruginosa. It is used for therapy and diagnosis of infection, and as
CC a carrier for drugs. The antibody is IgG2a subclass.
CC (Updated on 31-OCT-2002 to add missing OS field.)
CC (Updated on 25-MAR-2003 to correct PA field.)
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 159 AA;
Query Match 85.3%; Score 529; DB 10; Length 159;
Best Local Similarity 82.5%; Pred. No. 1.9e-35;
Matches 99; Conservative 8; Mismatches 9; Indels 4; Gaps 1;
QY 1 QVOLOESGAELESRKPGASVKMSCKASGYTFSTYMWIKORRPGGLEWIGYINPNDYTEY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 20 QVOLOQSGAELADPGASVKMSCKASGYTFSTYMWIKORRPGGLEWIGYINPNDYTEY 79
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 NQNFKDKATLTADKSSSTAYVQSLTSEDSAVYYCAR---DITFYMGQGTLLTVSS 116
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 80 NQNFKDKATLTADKSSSTAYVQSLTSEDSAVYYCARSGNYSYNGANDYMGQGTSTVYSS 139
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
RESULT 8
AAW76127
ID AAW76127 standard; Protein; 138 AA.
XX
AC AAW76127;
XX
DT 20-NOV-1998 (first entry)
XX
DE Murine ICR-1.1 V-H region PCR product protein.
XX
KW Intercellular adhesion molecule; ICAM-R; modulator; 14.3.3 family;
KW HSI-beta; tubulin; inhibitor; stimulator; effector; immune response;
KW inflammation; disorder; T cell activation; macrophage; Crohn's disease;
KW adult respiratory distress syndrome; stroke; multiple sclerosis; asthma;
KW rheumatoid arthritis; tumour growth; human immune deficiency virus;
KW infection; diabetes; graft vs. host disease; passive immunisation.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT MISC-difference 2
FT MISC-difference 6 /label= unknown
FT MISC-difference 7 /label= unknown
FT MISC-difference 8 /label= unknown
FT MISC-difference 8 /label= unknown
XX
PN US5773218-A.
XX
PD 30-JUN-1998.
XX
PF 07-JUN-1995; 95US-0482882.
XX

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PR 05-AUG-1994; 94US-0286754.
PR 27-JAN-1992; 92US-0827689.
PR 26-MAY-1992; 92US-0889724.
PR 05-JUN-1992; 92US-0894061.
PR 22-JUN-1993; 93US-0009286.
PR 26-JAN-1993; 93WO-0500787.
PR 05-AUG-1993; 93US-0102852.
PR 07-JUN-1995; 95US-0482882.
XX
PA (ICOS-) ICOS CORP.
XX
PI Gallatin WM, Vazeux R;
XX
DR WPI; 1998-386989/33.
DR N-PSDB; AAV56413.
XX
PT Identifying compounds that modulate interaction of intercellular
PT adhesion molecule R - with ligands HSI-beta and tubulin using
PT two-hybrid assay, useful for treating inflammation, T cell
PT activation etc.
XX
PS Example 13; Column 125-128; 108pp; English.
XX
CC This sequence represents a murine ICR-1.1 V-H region amplified PCR
CC product. This sequence is used in the isolation of a novel human
CC intercellular adhesion molecule, ICAM-R. This sequence is used in a
CC method which investigates modulators of the interaction between ICAM-R
CC and the 14.3.3 family member HSI-beta and tubulin. An anti-ICAM-R
CC antibody optionally coupled to toxin or radionuclide, or an ICAM-R
CC peptide, can block, inhibit or stimulate ligand/receptor interactions
CC involving ICAM-R, particularly its effector functions involved in
CC (non)specific immune responses. ICAM-R related agents may be used to
CC treat or monitor inflammation, disorders involving T cell activation or
CC macrophages, e.g. adult respiratory distress syndrome, stroke, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis, asthma, tumour growth,
CC human immune deficiency virus infection, diabetes, graft vs. host disease
CC and many others. Antibodies may also be used for passive immunisation,
CC for purifying, detecting or quantifying ICAM-R and for identifying
CC ICAM-R expressing cells.
XX
SQ Sequence 138 AA;
Query Match 84.6%; Score 524.5; DB 19; Length 138;
Best Local Similarity 82.4%; Pred. No. 3.8e-35;
Matches 98; Conservative 9; Mismatches 9; Indels 3; Gaps 1;
QY 1 QVOLOESGAELESRKPGASVKMSCKASGYTFSTYMWIKORRPGGLEWIGYINPNDYTEY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 20 QVOLOQSGAELADPGASVKMSCKASGYTFSTYMWIKORRPGGLEWIGYINPNDYTEY 79
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 NQNFKDKATLTADKSSSTAYVQSLTSEDSAVYYCAR---DITFYMGQGTLLTVSS 116
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 80 NQNFKDKATLTADKSSSTAYVQSLTSEDSAVYYCARSGNYSYNGANDYMGQGTSTVYSS 138
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
RESULT 9
AAW71257
ID AAW71257 standard; Protein; 138 AA.
XX
AC AAW71257;
XX
DT 25-MAR-2003 (updated)
DT 18-NOV-1998 (first entry)
XX
DE Murine antibody ICR-1.1 heavy chain amino acid sequence.
XX
KW Human; ICAM-R; intercellular adhesion molecule; adhesion; treatment;
KW inflammatory condition; asthma; tumour growth; metastasis;
KW viral infection; antibody ICR-1.1.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers

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FT M1sc-difference 2 /note- "encoded by GRA"
FT M1sc-difference 6 /note- "encoded by RTC"
FT M1sc-difference 7 /note- "encoded by WTB"
FT M1sc-difference 8 /note- "encoded by HTC"
XX US5811517-A.
XX
XX 22-SEP-1998.
XX
XX 07-JUN-1995; 95US-0483389.
XX
XX 05-AUG-1994; 94US-0286754.
XX 26-JAN-1993; 93WO-US00787.
XX 27-JAN-1992; 92US-0827689.
XX 26-MAY-1992; 92US-0889724.
XX 05-JUN-1992; 92US-0894061.
XX 22-JAN-1993; 93US-0009266.
XX 03-AUG-1993; 93US-0102852.
XX
XX (ICOS-) ICOS CORP.
XX
XX Gallatin WM, Vazeux R;
XX
XX WPI; 1998-530940/45.
XX N-PSDB; AAV54863.
XX
XX DNA encoding mutant ICAM-R polypeptide(s) - useful for diagnosis
XX and treatment of cell adhesion based disease conditions e.g.
XX inflammation or asthma
XX
XX Example 13; Columns 125-126; 11pp; English.
XX
XX The present sequence represents the heavy chain of murine antibody
XX ICR-1.1. This antibody is specific for ICAM-R (intercellular adhesion
XX molecule-R). ICAM-R are polypeptides that are expressed on blood vessel
XX endothelial cell surfaces and are involved in the adhesion events in
XX various conditions. ICAM-R variants (see AAW1264-69) can be used to
XX treat or monitor inflammatory conditions involving specific or
XX non-specific immune responses, asthma, tumour growth and/or metastasis
XX and viral infections. The ICAM variants are produced recombinantly, from
XX expression libraries of mutated sequences, and the ones that are
XX claimed are the ones that have been found to be especially involved in
XX adhesion events. They can also be used to raise antibodies, also for
XX use as therapeutic or diagnostic agents.
XX (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 138 AA:
SQ
XX
XX Query Match 84.6%; Score 524.5; DB 19; Length 138;
XX Best Local Similarity 82.4%; Pred. No. 3.8e-35;
XX Matches 98; Conservative 9; Mismatches 9; Indels 3; Gaps 1;
XX
XX 1 OVOLOESGAEISFGASVMSCKASGYTFTYWMHMKRPGQGLEWIGYINPRNDYTEY 60
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 20 OVOLODSGAEIADPGASVMSCKASGYTFTYWMHMKRPGQGLEWIGYINPRNDYTEY 79
XX
XX 61 NONFKDQATLTADKSSSTAYMQLSLTSDSAVYVCARDITFT--YWGQGTTLTVSS 116
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 80 NORFDQATLTADKSSSTAYMQLSLTSDSAVYVCARDGNSYGLDYGQGTSTVSS 138
XX
XX RESULT 10
XX AAY00783
XX ID AAY00783 standard; Protein; 138 AA.
XX
XX AC AAY00783;
XX
XX DT 14-MAY-1999 (first entry)
XX

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DE Antibody against ICAM-R.
XX
XX ICAM; immunoglobulin-like loop; intercellular adhesion molecule receptor;
XX alpha d/CD18; antibody; immunisation; inflammatory response; asthma;
XX tumour growth; viral infection; therapy.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX M1sc-difference 1..138 /note- "Xaa- unspecified amino acid"
XX
XX US5880268-A.
XX
XX 09-MAR-1999.
XX
XX 07-JUN-1995; 95US-0483932.
XX
XX 05-AUG-1994; 94US-0286754.
XX 27-JAN-1992; 92US-0827689.
XX 26-MAY-1992; 92US-0889724.
XX 05-JUN-1992; 92US-0894061.
XX 22-JAN-1993; 93US-0009266.
XX 26-JAN-1993; 93WO-US00787.
XX 05-AUG-1993; 93US-0102852.
XX 07-JUN-1995; 95US-0483932.
XX
XX (ICOS-) ICOS CORP.
XX
XX Gallatin WM, Vazeux R;
XX
XX WPI; 1999-204041/17.
XX N-PSDB; AAX21879.
XX
XX New intercellular adhesion molecule receptor (ICAM-R) specific
XX antibodies - useful for modulating ligand/receptor binding and
XX biological activities involving ICAM-R, especially those of the
XX specific and non-specific immune systems
XX
XX Example 13; Column 125-126; 108pp; English.
XX
XX This sequence represents an antibody specific for ICAM-R.
XX The invention relates to antibodies (Ab) which bind specifically
XX to the intercellular adhesion molecule receptor (ICAM-R), inhibiting the
XX interaction between ICAM-R and alpha d/CD18. Abs with specific ICAM-R
XX binding are useful in compositions for immunisation, and for purifying
XX ICAM-R polypeptides and identifying cells expressing ICAM-R on their cell
XX surface, modulating ligand/receptor binding and biological activities
XX involving ICAM-R, especially inflammatory responses of the specific
XX immune system, the non-specific immune system, monitoring and treating
XX asthma, tumour growth, and/or metastasis, and viral infection (e.g. HIV
XX infection). In particular diseases involving an essential T cell
XX activation (e.g. asthma, psoriasis, diabetes, graft vs. host disease,
XX tissue transplant rejection, and multiple sclerosis) may be treated with
XX anti-ICAM-R antibodies. The Abs specifically bind to and identify ICAM-R
XX and disrupt ICAM-R to cell adhesion molecule, especially alpha d/CD18
XX binding.
XX
XX Sequence 138 AA:
SQ
XX
XX Query Match 84.6%; Score 524.5; DB 20; Length 138;
XX Best Local Similarity 82.4%; Pred. No. 3.8e-35;
XX Matches 98; Conservative 9; Mismatches 9; Indels 3; Gaps 1;
XX
XX 1 OVOLOESGAEISFGASVMSCKASGYTFTYWMHMKRPGQGLEWIGYINPRNDYTEY 60
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 20 OVOLODSGAEIADPGASVMSCKASGYTFTYWMHMKRPGQGLEWIGYINPRNDYTEY 79
XX
XX 61 NONFKDQATLTADKSSSTAYMQLSLTSDSAVYVCARDITFT--YWGQGTTLTVSS 116
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 80 NORFDQATLTADKSSSTAYMQLSLTSDSAVYVCARDGNSYGLDYGQGTSTVSS 138
XX

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Query Match	84.6%	Score 524.5	DB 20	Length 138
AAW81451	standard; Protein; 138 AA.			
AAW81451				
AAW81451				
17-FEB-1999	(first entry)			
Murine antibody ICR-1.1 Vh region.				
Intercellular adhesion molecule polypeptide; ICAM-R; humanised; ICR-1.1;				
ICR-8.1; monoclonal antibody; therapeutic; inflammatory; asthma; tumour;				
graft-versus-host disease; viral infection; toxin; radionuclide;				
neovascularisation site; murine.				
Mus sp.				
Key	Location/Qualifiers			
Misc-difference 2	/label= unknown			
Misc-difference 6	/note= "encoded by GRA"			
Misc-difference 7	/label= unknown			
Misc-difference 8	/note= "encoded by RTC"			
Misc-difference 32	/label= unknown			
Misc-difference 32	/note= "encoded by HTC"			
Misc-difference 32	/note= "encoded by AAA"			
US5837822-A.				
17-NOV-1998.				
07-JUN-1995;	95US-0487113.			
07-JUN-1995;	95US-0487113.			
27-JAN-1992;	92US-0827689.			
26-MAY-1992;	92US-0889724.			
05-JUN-1992;	92US-0894061.			
22-JAN-1993;	93US-0009266.			
26-JAN-1993;	93WO-US00787.			
26-AUG-1993;	93US-0102852.			
(ICOS-) ICOS CORP.				
Gallatin WM, Vazeux R;				
WPI; 1999-023535/02.				
N-PSDB; AAV69185.				
Humanised antibodies specific for intercellular adhesion molecule				
polypeptide - useful for therapeutic or diagnostic purposes				
Example 13; Columns 137-138; 110pp; English.				
The invention relates to humanised ICR-1.1 and ICR-8.1 antibodies				
targeted to the human intercellular adhesion molecule polypeptide				
(ICAM-R) polypeptide. Antibodies specific for ICAM-R's are potentially				
useful as therapeutic compounds, for treating e.g. immune-mediated				
inflammatory conditions (e.g. graft-versus-host disease), asthma,				
tumours or viral infections. Monoclonal antibodies specific for ICAM-R,				
or their conjugates formed with e.g. toxins or radionuclides are useful				
for therapeutically targeting or detecting neovascularisation sites.				
The present sequence represents the amino acid sequence of the Vh region				
of the murine antibody ICR-1.1.				

	Best Local Similarity	82.4%	Pred. No. 3.8e-35;	
	Matches	98;	Conservative	9; Mismatches 9; Indels 3; Gaps 1;
Oy	1	OVOLOESGAEILSKPGASYKMSCKASGYFTSYLWLMIKRPGGGLIEWIGYINPRNDYREY	60	
		: : : : : : : : : :		
Db	20	OVOLOQSSAEIADPGASVKMSCKASGYFTSYLWLMVNRPGGGLIEWIGYINPTDYREY	79	
Oy	61	NQNEFKAKTLTADKSSSTAYNQLSLTSEDSANVYVCARDITTF--YMGQTTLVSS	116	
		: : : : : : : : : :		
Db	80	NQRQDKATLTADKSSSTAYNQLSLTSEDSANVYVCARWGGSYGLDYMGGTSTVSS	138	
		: : : : : : : : :		
	RESULT 12			
ID	AAB13047	standard; Protein; 138 AA.		
XX	AAB13047;			
AC				
XX				
DT	19-DEC-2000	(first entry)		
XX				
DE				
XX				
Murine ICR-1.1 Vh protein sequence.				
KM	Anti-human immunodeficiency virus; HIV; cytostatic; ICAM-R; ARDS; stroke;			
KM	intercellular adhesion molecule; immunoglobulin heavy chain; septicemia;			
KM	inflammatory conditions; glomerulonephritis; arthritis; dermatosis;			
KM	haemodialysis; leukapheresis; ulcerative colitis; Crohn's disease;			
KW	neotising enterocolitis; atherosclerosis; psoriasis; asthma;			
KW	transplant rejection; diabetes; tumour.			
XX				
OS	Mus sp.			
XX				
PH	Key	Location/Qualifiers		
FT	Misc-difference 2	/label= Unknown		
FT	Misc-difference 6	/label= Unknown		
FT	Misc-difference 7	/label= Unknown		
FT	Misc-difference 8	/label= Unknown		
FT	Misc-difference 8	/label= Unknown		
XX				
XX	US6100383-A.			
XX				
PD	08-AUG-2000.			
XX				
PE	07-JUN-1995;	95US-0475680.		
XX				
PR	05-AUG-1994;	94US-0286754.		
PR	26-JAN-1993;	93WO-0500787.		
PR	27-JAN-1992;	92US-0827689.		
PR	26-MAY-1992;	92US-0889724.		
PR	05-JUN-1992;	92US-0894061.		
PR	22-JAN-1993;	93US-0009266.		
PR	05-AUG-1993;	93US-0102852.		
XX				
PA	(ICOS) ICOS CORP.			
XX				
PI	Gallatin WM, Vazeux R;			
XX				
DR	WPI; 2000-542449/49.			
XX	N-PSDB; AAA97155.			
PT	Hybrid fusion proteins comprising intercellular adhesion molecule or			
PT	its variants useful, for treating inflammatory conditions, Crohn's			
XX	disease, atherosclerosis and diabetes			
XX				
PS	Example 13; Column 127-128; 109pp; English.			
XX				
CC	This invention relates to a hybrid fusion protein comprising an			
CC	intercellular adhesion molecule (ICAM-R) amino acid fragment at its			
CC	amino terminus and a constant domain of an immunoglobulin heavy chain at			
CC	its carboxy terminus. ICAM-R polypeptides are useful for treating and			
CC	monitoring inflammatory conditions such as adult respiratory distress			

PD 23-NOV-1999.
 XX 27-SEP-1996; 9605-0720420.
 XX 27-JAN-1992; 9205-0827689.
 PR 26-MAY-1992; 9205-0889724.
 PR 05-JUN-1992; 9205-0894061.
 PR 22-JAN-1993; 9305-0009266.
 PR 26-JAN-1993; 9305-0500787.
 PR 05-AUG-1993; 9305-0102852.
 PR 07-JUN-1995; 9505-0487113.
 XX (ICOS-) ICOS CORP.
 XX Gallatin WM, Vazeux R;
 PI WPI: 2000-022778/02.
 DR N-PSDB; AA224327.
 XX Identifying modulators of protein kinase C phosphorylation of human
 PT intercellular adhesion molecule polypeptide -
 XX Example 14; Column 143-144; 122pp; English.
 CC This invention describes a novel method for identifying a compound that
 CC modulates phosphorylation of human intercellular adhesion molecule
 CC polypeptide (ICAM-R) by protein kinase C isoform. The method comprises:
 CC (a) exposing a purified peptide consisting of the cytoplasmic domain of
 CC ICAM-R to protein kinase C isoform and labeled adenosine triphosphate in
 CC the presence and absence of a test compound; (b) measuring labeled
 CC phosphate transferred to the peptide; and (c) identifying a test compound
 CC that affects transfer of the labeled phosphate as a modulator compound.
 CC The method is useful for identifying compounds that modulate the
 CC phosphorylation of human intercellular adhesion molecule polypeptide
 CC which might form the basis for the development of therapeutic and
 CC diagnostic agents. This sequence represents the murine ICR-1.1 antibody
 CC VH region which is used in the method of the invention.
 XX
 SQ Sequence 138 AA;
 Query Match 84.6%; Score 524.5; DB 21; Length 138;
 Best Local Similarity 82.4%; Pred. No. 3.8e-35;
 Matches 98; Conservative 9; Mismatches 9; Indels 3; Gaps 1;
 QY 1 QVOLOESGAELEKPGASVKNKSKASGYTFYTHWIKORPGGLEWIGYINPNDDYEX 60
 Db 20 QVOLOQSGAELEADPGASVKNKSKASGYTFYTHWIKORPGGLEWIGYINPNDDYEX 79
 QY 61 NONFKRATLTADKSSSTAYMQLSLTSEDSAVYYCARDDITP---YMGGTLTVSS 116
 Db 80 NORFQKATLTADKSSSTAYMQLSLTSEDSAVYYCARMGCGNSYGLDYGCGTSVTYSS 138

XX Mus sp.
 OS US2001029293-A1.
 XX 11-OCT-2001.
 PD 03-JAN-2001; 200105-0753436.
 XX 24-AUG-1999; 9905-0382289.
 PR 27-JAN-1992; 9205-0827689.
 PR 26-MAY-1992; 9205-0889724.
 PR 05-JUN-1992; 9205-0894061.
 PR 22-JAN-1993; 9305-0009266.
 PR 26-JAN-1993; 9305-0500787.
 PR 05-AUG-1993; 9305-0102852.
 PR 07-JUN-1995; 9505-0487113.
 XX (ICOS-) ICOS CORP.
 XX Gallatin WM, Vazeux R;
 PI WPI: 2002-009992/01.
 DR P-PSDB; AAU70939.
 XX Novel hybridoma cell line useful for producing monoclonal antibody for
 PT treating inflammatory conditions, immune system disorders and
 PT infectious diseases, is deposited under specified ATCC accession number
 XX -
 XX Page 78; Example 14; 126pp; English.
 CC The invention relates to a novel hybridoma cell line (I) ATCC HB 12190.
 CC (I) is useful for producing an intercellular adhesion molecule (ICAM)
 CC monoclonal antibody (II). (II) is useful for treating inflammatory
 CC conditions including adult respiratory distress syndrome, multiple organ
 CC injury syndrome, secondary to septicemia or trauma, tissue reperfusion
 CC injury, acute glomerulonephritis, reactive arthritis, dermatosis with
 CC acute inflammatory components, stroke, thermal injury, haemodialysis,
 CC leukoencephalitis, ulcerative colitis, Crohn's disease, necrotizing
 CC enterocolitis, granulocyte transfusion associated syndrome, diabetes,
 CC atherosclerosis, cytokine-induced toxicity, psoriasis, organ/tissue
 CC transplant rejection, autoimmune diseases including Raynaud's syndrome,
 CC autoimmune thyroiditis, multiple sclerosis, rheumatoid arthritis,
 CC lupus erythematosus, asthma, tumour growth and/or metastasis, viral
 CC infection, tissue transplant rejection, graft versus host disease and
 CC multiple sclerosis. (II) is also useful for immunisation, for purifying
 CC ICAM-R polypeptides and for identifying cells that display the
 CC polypeptides on their surfaces. AAU70928-AAU70946 represent ICAM
 CC amino acid sequences of the invention.
 XX
 SQ Sequence 138 AA;
 Query Match 84.6%; Score 524.5; DB 23; Length 138;
 Best Local Similarity 82.4%; Pred. No. 3.8e-35;
 Matches 98; Conservative 9; Mismatches 9; Indels 3; Gaps 1;
 QY 1 QVOLOESGAELEKPGASVKNKSKASGYTFYTHWIKORPGGLEWIGYINPNDDYEX 60
 Db 20 QVOLOQSGAELEADPGASVKNKSKASGYTFYTHWIKORPGGLEWIGYINPNDDYEX 79
 QY 61 NONFKRATLTADKSSSTAYMQLSLTSEDSAVYYCARDDITP---YMGGTLTVSS 116
 Db 80 NORFQKATLTADKSSSTAYMQLSLTSEDSAVYYCARMGCGNSYGLDYGCGTSVTYSS 138

Search completed: October 7, 2003, 19:13:55
 Job time : 147 secs

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OM protein - protein search, using sw model

Run on: October 7, 2003, 19:07:41 ; Search time 60 Seconds

(without alignments)
305,878 Million cell updates/sec

Title: US-09-988-013a-4

Perfect score: 620
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Gapop 10.0 , Gaepct 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications_AA:*

1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	620	100.0	116	10	US-09-741-843-4
2	620	100.0	116	11	US-09-894-839-4
3	620	100.0	116	11	US-09-988-013a-4
4	557	89.8	116	10	US-09-741-843-9
5	557	89.8	116	11	US-09-894-839-21
6	557	89.8	116	11	US-09-988-013a-9
7	550	88.7	116	10	US-09-741-843-8
8	550	88.7	116	11	US-09-894-839-8
9	550	88.7	116	11	US-09-988-013a-8
10	524.5	84.6	138	9	US-09-753-436-78
11	523	84.4	116	12	US-10-127-890-167
12	523	84.4	135	12	US-10-244-821-91
13	519	83.7	438	12	US-10-244-821-88
14	507	81.8	331	15	US-10-059-261-169
15	505.5	81.5	119	11	US-09-795-515-30

16	505.5	81.5	119	15	US-10-267-286A-10	Sequence 10, Appl
17	505.5	81.5	468	11	US-09-795-515-7	Sequence 7, Appl
18	501	80.8	116	12	US-10-127-890-168	Sequence 168, Appl
19	499	80.5	256	15	US-10-247-488-2	Sequence 2, Appl
20	499	80.5	258	15	US-10-247-488-4	Sequence 4, Appl
21	496	80.0	120	15	US-10-096-246-12	Sequence 12, Appl
22	491.5	79.3	500	12	US-10-168-809-22	Sequence 22, Appl
23	484	78.1	242	16	US-10-259-087A-18	Sequence 18, Appl
24	483	77.9	127	10	US-09-998-831-7	Sequence 7, Appl
25	483	77.9	127	12	US-10-373-561-7	Sequence 7, Appl
26	482.5	77.8	143	8	US-08-779-784-26	Sequence 26, Appl
27	482	77.7	122	15	US-10-096-246-10	Sequence 10, Appl
28	482	77.7	122	15	US-10-096-246-11	Sequence 11, Appl
29	480	77.4	242	16	US-10-259-087A-20	Sequence 20, Appl
30	478.5	77.2	119	15	US-10-233-996-39	Sequence 39, Appl
31	477.5	77.0	140	15	US-10-283-349-27	Sequence 27, Appl
32	476	76.8	122	8	US-08-779-784-28	Sequence 28, Appl
33	473.5	76.4	116	11	US-09-940-727B-17	Sequence 17, Appl
34	473.5	76.4	464	12	US-10-384-933-9	Sequence 9, Appl
35	473.5	76.4	464	11	US-10-216-484-9	Sequence 9, Appl
36	471	76.0	113	11	US-09-940-727B-118	Sequence 118, Appl
37	469.5	75.7	136	15	US-10-138-505-12	Sequence 12, Appl
38	469.5	75.7	245	15	US-10-138-505-40	Sequence 40, Appl
39	469.5	75.7	271	15	US-10-138-505-34	Sequence 34, Appl
40	469.5	75.7	274	15	US-10-138-505-32	Sequence 32, Appl
41	469	75.6	116	12	US-10-127-890-169	Sequence 169, Appl
42	464.5	74.9	123	9	US-09-753-436-86	Sequence 86, Appl
43	464.5	74.9	412	12	US-10-244-821-6	Sequence 6, Appl
44	464.5	74.9	412	15	US-10-013-173-6	Sequence 6, Appl
45	464.5	74.9	412	15	US-10-150-762-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1

US-09-741-843-4

Sequence 4, Application US/09741843

Patent No. US20020102254A1

GENERAL INFORMATION:

APPLICANT: LEUNG, Shui-on

INVENTOR: HANSEN, Hans

TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL

FILE REFERENCE: 018733/0996

CURRENT FILING DATE: 2000-12-22

PRIOR FILING DATE: 1998-08-03

PRIOR APPLICATION NUMBER: US 09/127,902

PRIOR FILING DATE: 1996-07-06

PRIOR APPLICATION NUMBER: US 08/690,102

PRIOR FILING DATE: 1994-08-12

PRIOR APPLICATION NUMBER: US 08/289,576

NUMBER OF SEQ ID NOS: 21

SOFTWARE: PatentIn version 3.1

SEQ ID NO 4

LENGTH: 116

TYPE: PRT

ORGANISM: Murinae gen. sp.

US-09-741-843-4

Query Match 100.0%; Score 620; DB 10; Length 116;

Best Local Similarity 100.0%; Pred. No. 1.1e-49;

Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVOLOESGAELEKPGASVKMGSGYTFISYMLHWIKORPGGLEWIGYINPRNDYEV 60

DB 1 QVOLOESGAELEKPGASVKMGSGYTFISYMLHWIKORPGGLEWIGYINPRNDYEV 60

QY 61 NONFRKATLTADSSSTAYVQSLTSEDSAVYYCARDDITFYWGQGTTLTVSS 116

DB 61 NONFRKATLTADSSSTAYVQSLTSEDSAVYYCARDDITFYWGQGTTLTVSS 116

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RESULT 2
US-09-894-839-4
; Sequence 4, Application US/09894839
; Publication No. US20030035800A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; APPLICANT: QU, Zhengxing
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/1049
; CURRENT APPLICATION NUMBER: US/09/894,839
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/155,107
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 60/013,709
; PRIOR FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-894-839-4

Query Match
Best Local Similarity 100.0%; Score 620; DB 11; Length 116;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OVOLOESGAELEKPGASVMSCKASGYTFTSYMLHWIKORPGGLEWIGYINPRNDYTY 60
DB 1 OVOLOESGAELEKPGASVMSCKASGYTFTSYMLHWIKORPGGLEWIGYINPRNDYTY 60

OY 61 NONFKDKATLTADKSSSTAYMQLSLTSDSAVYYCARDITTFYWGQTTLVSS 116
DB 61 NONFKDKATLTADKSSSTAYMQLSLTSDSAVYYCARDITTFYWGQTTLVSS 116

RESULT 3
US-09-988-013A-4
; Sequence 4, Application US/09988013A
; Publication No. US20030103979A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-
; FILE REFERENCE: 18733/1082
; CURRENT APPLICATION NUMBER: US/09/988,013A
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 09/741,843
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/127,902
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/690,102
; PRIOR FILING DATE: 1996-07-06
; PRIOR APPLICATION NUMBER: US 08/289,576
; PRIOR FILING DATE: 1994-08-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-988-013A-4

Query Match
Best Local Similarity 100.0%; Score 620; DB 11; Length 116;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OVOLOESGAELEKPGASVMSCKASGYTFTSYMLHWIKORPGGLEWIGYINPRNDYTY 60
DB 1 OVOLOESGAELEKPGASVMSCKASGYTFTSYMLHWIKORPGGLEWIGYINPRNDYTY 60

OY 61 NONFKDKATLTADKSSSTAYMQLSLTSDSAVYYCARDITTFYWGQTTLVSS 116
DB 61 NONFKDKATLTADKSSSTAYMQLSLTSDSAVYYCARDITTFYWGQTTLVSS 116
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Query Match
Best Local Similarity 100.0%; Score 620; DB 11; Length 116;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OVOLOESGAELEKPGASVMSCKASGYTFTSYMLHWIKORPGGLEWIGYINPRNDYTY 60
DB 1 OVOLOESGAELEKPGASVMSCKASGYTFTSYMLHWIKORPGGLEWIGYINPRNDYTY 60

OY 61 NONFKDKATLTADKSSSTAYMQLSLTSDSAVYYCARDITTFYWGQTTLVSS 116
DB 61 NONFKDKATLTADKSSSTAYMQLSLTSDSAVYYCARDITTFYWGQTTLVSS 116

RESULT 4
US-09-741-843-9
; Sequence 9, Application US/09741843
; Patent No. US20020102254A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; APPLICANT: QU, Zhengxing
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL
; FILE REFERENCE: 018733/0996
; CURRENT APPLICATION NUMBER: US/09/741,843
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/127,902
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/690,102
; PRIOR FILING DATE: 1996-07-06
; PRIOR APPLICATION NUMBER: US 08/289,576
; PRIOR FILING DATE: 1994-08-12
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-741-843-9

Query Match
Best Local Similarity 89.8%; Score 557; DB 10; Length 116;
Matches 98; Conservative 14; Mismatches 4; Indels 0; Gaps 0;

OY 1 OVOLOESGAELEKPGASVMSCKASGYTFTSYMLHWIKORPGGLEWIGYINPRNDYTY 60
DB 1 OVOLOESGAELEKPGASVMSCKASGYTFTSYMLHWIKORPGGLEWIGYINPRNDYTY 60

OY 61 NONFKDKATLTADKSSSTAYMQLSLTSDSAVYYCARDITTFYWGQTTLVSS 116
DB 61 NONFKDKATLTADKSSSTAYMQLSLTSDSAVYYCARDITTFYWGQTTLVSS 116

RESULT 5
US-09-894-839-21
; Sequence 21, Application US/09894839
; Publication No. US20030035800A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; APPLICANT: QU, Zhengxing
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/1049
; CURRENT APPLICATION NUMBER: US/09/894,839
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/155,107
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 60/013,709
; PRIOR FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-894-839-21

Query Match
Best Local Similarity 89.8%; Score 557; DB 11; Length 116;
Matches 98; Conservative 14; Mismatches 4; Indels 0; Gaps 0;
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[illegible]

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1      RESULT 6
2      US-09-988-013A-9
3      ; Sequence 9, Application US/09988013A
4      ; Publication No. US20030103979A1
5      ; GENERAL INFORMATION:
6      ; APPLICANT: HANSEN, Hans
7      ; APPLICANT: LEUNG, Shui-on
8      ; TITLE OF INVENTION: IMMUNOCONTIGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B
9      ; TITLE OF INVENTION: CELL LYMPHOMA AND LEUKEMIA CELLS
10     ; FILE REFERENCE: 18733/1082
11     ; CURRENT APPLICATION NUMBER: US/09/988,013A
12     ; CURRENT FILING DATE: 2002-10-29
13     ; PRIOR APPLICATION NUMBER: US 09/741,843
14     ; PRIOR FILING DATE: 2000-12-22
15     ; PRIOR APPLICATION NUMBER: US 09/127,902
16     ; PRIOR FILING DATE: 1998-08-03
17     ; PRIOR APPLICATION NUMBER: US 08/690,102
18     ; PRIOR FILING DATE: 1996-07-06
19     ; PRIOR APPLICATION NUMBER: US 08/289,576
20     ; PRIOR FILING DATE: 1994-08-12
21     ; NUMBER OF SEQ ID NOS: 25
22     ; SOFTWARE: PatentIn version 3.1
23     ; SEQ ID NO 9
24     ; LENGTH: 116
25     ; TYPE: PRT
26     ; ORGANISM: Homo sapiens
27     ; US-09-988-013A-9

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[illegible]

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? RESULT 7
? US-09-741-843-8
? Sequence 8, Application US/09741843
? Patent No. US20020102254A1
? GENERAL INFORMATION:
? APPLICANT: LEUNG, Shut-on
? APPLICANT: HANSEN, Hans
? TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA
? TITLE OF INVENTION: AND LEUKEMIA CELLS
? FILE REFERENCE: 018733/0996
? CURRENT APPLICATION NUMBER: US/09/741,843
? CURRENT FILING DATE: 2000-12-22
? PRIOR APPLICATION NUMBER: US 09/127,902
? PRIOR FILING DATE: 1998-08-03
? PRIOR APPLICATION NUMBER: US 08/690,102
? PRIOR FILING DATE: 1996-07-06
? PRIOR APPLICATION NUMBER: US 08/289,576
? PRIOR FILING DATE: 1994-08-12
? NUMBER OF SEQ ID NOS: 21
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 8
? LENGTH: 116
? TYPE: PRT

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[illegible]

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RESULT 8
US-09-894-839-8
; Sequence 8, Application US/09894839
; Publication No. US20030035800A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; APPLICANT: GU, Zhengxing
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/1049
; CURRENT APPLICATION NUMBER: US/09/894, 839
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/155,107
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 60/103,709
; PRIOR FILING DATE: 1996-03-20
; NUMBER OF SEQ. ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-894-839-8

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	Query Match	88.7%	Score 550	DB 11	Length 116
	Similarity	83.6%	Pred. No. 2.9e+3		
	Matches	Conservative 14	Mismatches 5	Indels 0	Gaps 0
Oy	1	QVQLSESAGELSKRGASVYKSCAKSGYFTSYMLHWIKRPGGGGLWETIGYINPRNDYEX	60		
		: : : : : : : : : : :			
Db	1	QVQLQSAGAEKKRGSSVYKSCAKSGYFTSYMLHWIQAQGGGLWETIGYINPRNDYEX	60		
Oy	61	NONFRDKRTLLPADKSSSPAYMQLSLTSEDSAVVYVCARDDITTFPMWGQTLTVYSS	116		
		: : : : : : : : : :			
Db	61	NONFRDKRTITADESTNFAIMELSSLSBEDPAEFICARDITTFPMWGQTLTVYSS	116		

RESULT 9
US-09-988-013A-8
; Sequence 8, Application US/09988013A
; Publication No. US20030103979A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-
; TITLE OF INVENTION: CELL LYMPHOMA AND LEUKEMIA CELLS
; FILE REFERENCE: 18733/1082
; CURRENT APPLICATION NUMBER: US/09/988, 013A
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 09/741,843
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/127,902
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/690,102
; PRIOR FILING DATE: 1996-07-06
; PRIOR APPLICATION NUMBER: US 08/289,576
; PRIOR FILING DATE: 1994-08-12

NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 116
TYPE: PRT
ORGANISM: Homo sapiens
US-09-988-013a-8

Query Match
Best Local Similarity 88.7%; Score 550; DB 11; Length 116;
Matches 97; Conservative 14; Mismatches 5; Indels 0; Gaps 0;

QY 1 QVQLOSGAELSPGASVMSCKASGYTFTSYLHWIKRPGGGLMIGYINPRNDYTY 60
DB 1 QVQLOSGAELSPGASVMSCKASGYTFTSYLHWIKRPGGGLMIGYINPRNDYTY 60

QY 61 NONFKDKATLTADKSSSTAYMOLSLTSDSAVYYCARRDITFTFYWGQTTLVSS 116
DB 61 NONFKDKATLTADKSSSTAYMOLSLTSDSAVYYCARRDITFTFYWGQTTLVSS 116

RESULT 10
US-09-753-436-78
Sequence 78, Application US/09753436
Patent No. US20010029293A1
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/753,436
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/382,289
FILING DATE:
APPLICATION NUMBER: US 08/487,113
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,754
FILING DATE: 05-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Joseph A., Jr.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 33282

TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-753-436-78

Query Match
Best Local Similarity 84.6%; Score 524.5; DB 9; Length 138;
Matches 98; Conservative 9; Mismatches 9; Indels 3; Gaps 1;

QY 1 QVQLOSGAELSPGASVMSCKASGYTFTSYLHWIKRPGGGLMIGYINPRNDYTY 60
DB 20 QVQLOSGAELADPGASVMSCKASGYTFTSYLHWIKRPGGGLMIGYINPRNDYTY 79

QY 61 NONFKDKATLTADKSSSTAYMOLSLTSDSAVYYCARRDITFTFYWGQTTLVSS 116
DB 80 NONFKDKATLTADKSSSTAYMOLSLTSDSAVYYCARRDITFTFYWGQTTLVSS 138

RESULT 11
US-10-127-890-167
Sequence 167, Application US/10127890
Publication No. US2003016196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroli, Stephen F.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70, P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-9155
TELEFAX: 312/707-9155
TELEX: 650 388-1248

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; INFORMATION FOR SEQ ID NO: 167:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 116 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 167:
US-10-127-890-167

Query Match      84.4%; Score 523; DB 12; Length 116;
Best Local Similarity 86.2%; Pred. No. 8.7e-41;
Matches 100; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

OY 1 OVOLOESGAEISKPGASVKMSCKASGYFTSYMLHWIKORPGGLEWIGYINPRNDYTEY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 OVOLOOSGAEIAKPGASVKMSCKASGYFTSYRMHWIKORPGGLEWIGYINPSTGYTEY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

OY 61 NONFKDKATLTADKSSSTAYWQLSLTSEDSAVYYCARDDITTFYWGQGTTLTVSS 116
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 NONFKDKATLTADKSSSTAYWQLSLTSEDSAVYYCARGGGVFDYWGQGTTLTVSS 116
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RESULT 12
US-10-244-821-91
; Sequence 91, Application US/10244821
; Publication No. US20030143233A1
; GENERAL INFORMATION:
;   APPLICANT: Goshorn, Stephen Charles
;   APPLICANT: Graves, Scott Stoll
;   APPLICANT: Schultz, Joanne Elaine
;   APPLICANT: Lin, Yukang
;   APPLICANT: Sanderson, James Allen
;   APPLICANT: Reno, John M.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 690022.547C3
; CURRENT APPLICATION NUMBER: US/10/244,821
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-244-821-91

Query Match      84.4%; Score 523; DB 12; Length 135;
Best Local Similarity 86.2%; Pred. No. 1e-40;
Matches 100; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

OY 1 OVOLOESGAEISKPGASVKMSCKASGYFTSYMLHWIKORPGGLEWIGYINPRNDYTEY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 20 OVOLOOSGAEIAKPGASVKMSCKASGYFTSYRMHWIKORPGGLEWIGYINPSTGYTEY 79
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

OY 61 NONFKDKATLTADKSSSTAYWQLSLTSEDSAVYYCARDDITTFYWGQGTTLTVSS 116
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 80 NONFKDKATLTADKSSSTAYWQLSLTSEDSAVYYCARGGGVFDYWGQGTTLTVSS 135
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 13
US-10-244-821-88
; Sequence 88, Application US/10244821
; Publication No. US20030143233A1
; GENERAL INFORMATION:
;   APPLICANT: Goshorn, Stephen Charles
;   APPLICANT: Graves, Scott Stoll
;   APPLICANT: Schultz, Joanne Elaine
;   APPLICANT: Lin, Yukang
;   APPLICANT: Sanderson, James Allen
;   APPLICANT: Reno, John M.
;   APPLICANT: Dearsteyne, Erica A.
```

```
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 690022.547C3
; CURRENT APPLICATION NUMBER: US/10/244,821
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-244-821-88

Query Match      83.7%; Score 519; DB 12; Length 438;
Best Local Similarity 86.1%; Pred. No. 8e-40;
Matches 99; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

OY 1 OVOLOESGAEISKPGASVKMSCKASGYFTSYMLHWIKORPGGLEWIGYINPRNDYTEY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 23 OVOLOOSGAEIAKPGASVKMSCKASGYFTSYRMHWIKORPGGLEWIGYINPSTGYTEY 82
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

OY 61 NONFKDKATLTADKSSSTAYWQLSLTSEDSAVYYCARDDITTFYWGQGTTLTVSS 115
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 83 NONFKDKATLTADKSSSTAYWQLSLTSEDSAVYYCARGGGVFDYWGQGTTLTVSS 137
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 14
US-10-059-261-169
; Sequence 169, Application US/10059261
; Publication No. US20030077826A1
; GENERAL INFORMATION:
;   APPLICANT: EDELMAN, LENA
;   APPLICANT: JACOTOT, ETIENNE DANIEL FRANCOIS
;   APPLICANT: BRIAND, JEAN-PAUL
; TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET
; TITLE OF INVENTION: FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX
; TITLE OF INVENTION: (PTPC)
; FILE REFERENCE: 03495.0216
; CURRENT APPLICATION NUMBER: US/10/059,261
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/265,594
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: vector pAcGp67-ScFv350
US-10-059-261-169

Query Match      81.8%; Score 507; DB 15; Length 331;
Best Local Similarity 82.2%; Pred. No. 7.5e-39;
Matches 97; Conservative 9; Mismatches 10; Indels 2; Gaps 2;

OY 1 OVOLOESGAEISKPGASVKMSCKASGYFTSYMLHWIKORPGGLEWIGYINPRNDYTEY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 86 OVOLOOSGAEIAKPGASVKMSCKASGYFTSYRMHWIKORPGGLEWIGYINLSSGYTRY 145
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

OY 61 NONFKDKATLTADKSSSTAYWQLSLTSEDSAVYYCAR-ROITTF-YWGQGTTLTVSS 116
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 146 NONFKDKATLTADKSSSTAYWQLSLTSEDSAVYYCARAAQATTFIDYWGQGTTLTVSS 203
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 15
US-09-795-515-30
; Sequence 30, Application US/09795515
; Publication No. US20030039645A1
; GENERAL INFORMATION:
;   APPLICANT: Adair, John R.
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 19:07:11 ; Search time 43.2 Seconds

(without alignments)
258.231 Million cell updates/sec

Title: US-09-988-013a-4

Perfect score: 620

Sequence: 1 QVQLQESGAEISKPGASVKM.....ARRDITFYWGCGTTLTVSS 116

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	529	85.3	139	2 PS0024	Ig heavy chain pre
2	511.5	82.5	117	2 JC2269	PL7-6 antibody hea
3	496	80.0	120	2 S41394	Ig heavy chain V r
4	494.5	79.8	120	2 S25175	Ig heavy chain V r
5	487	78.5	116	2 S53751	antibody Fab Jcl 1
6	487	78.5	141	2 JL0076	Ig heavy chain pre
7	486	78.4	120	2 B22769	Ig heavy chain V r
8	486	78.4	131	2 S66537	Ig heavy chain V r
9	482.5	77.8	123	2 S20646	Ig heavy chain V r
10	482	77.7	139	1 MHMS18	Ig heavy chain pre
11	482	77.7	287	4 PC4402	pelb leader/Ig hea
12	480.5	77.5	122	2 S20643	Ig heavy chain V r
13	478	77.1	118	2 S38717	Ig heavy chain V r
14	476	76.8	106	2 PH1005	Ig heavy chain V r
15	475	76.6	118	2 C30560	Ig gamma chain V r
16	475	76.6	126	2 S31930	Ig heavy chain pre
17	475	76.6	136	2 JL0077	Ig heavy chain pre
18	474.5	76.5	131	2 A27472	Ig heavy chain pre
19	474	76.5	139	2 A27609	Ig heavy chain pre
20	473.5	76.4	116	2 S55542	Ig heavy chain V r
21	473.5	76.4	118	2 S38565	Ig heavy chain V r
22	472.5	76.2	119	2 S20640	Ig heavy chain V r
23	470	75.8	122	2 S24287	Ig heavy chain V r
24	469.5	75.7	125	2 S20639	Ig heavy chain V r
25	469	75.6	114	2 PL0247	Ig heavy chain V r
26	468.5	75.6	138	2 S21810	Ig heavy chain V r
27	468	75.5	117	2 S25176	Ig heavy chain V r
28	467.5	75.4	136	2 B47159	Ig heavy chain V r
29	467.5	75.4	140	2 PH1482	Ig heavy chain V r

30	466.5	75.2	138	2 E32513	Ig heavy chain pre
31	464	74.8	115	2 C27563	Ig heavy chain V r
32	463.5	74.8	119	2 PL0089	Ig heavy chain V r
33	461	74.4	115	2 A54378	Ig heavy chain V r
34	461	74.4	141	2 A39276	Ig heavy chain pre
35	460	74.2	96	2 S17616	Ig heavy chain V r
36	460	74.2	120	2 G28195	Ig heavy chain V r
37	459	74.0	112	2 A30502	Ig heavy chain V r
38	458.5	74.0	117	2 G45722	anti-glycoprotein
39	458	73.9	135	2 A30577	Ig heavy chain pre
40	458	73.9	144	2 B30502	Ig heavy chain V r
41	457	73.7	474	1 G2MS11	Ig gamma-2b chain
42	456	73.5	123	2 S60067	Ig heavy chain V r
43	456	73.5	128	2 I37267	Ig heavy chain V r
44	456	73.5	137	1 G2MS43	Ig heavy chain pre
45	455.5	73.5	140	1 HVMSG7	Ig heavy chain pre

ALIGNMENTS

RESULT 1

PS0024 Ig heavy chain precursor V region (6A4) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 22-Nov-1996

C/Accession: PS0024

R/Margot, M.; Echhardt, A.; Ehret, W.; von Specht, B.U.; Duchene, M.; Dondey, H.

A/Title: Cloning and characterization of cDNAs coding for the heavy and light chains

A/Reference number: PS0023; MUID:89232725; PMID:3149944

A/Accession: PS0024

A/Molecule type: mRNA

A/Residues: 1-139 <MAR>

A/Experimental source: strain BALB/c

C/Comment: This chain is obtained from an IgG2a monoclonal antibody against Pseudomon

C/Superfamily: Immunoglobulin V region; Immunoglobulin homology

C/Keywords: heterotrimer; signal sequence; status predicted <SIG>

F/1-19/Domain: signal sequence #status predicted <SIG>

F/20-139/Domain: Ig heavy chain V region #status predicted <IGV>

F/34-117/Domain: Immunoglobulin homology <IMH>

F/20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predic

Query Match 85.3%; Score 529; DB 2; Length 139;

Best local similarity 82.5%; Pred. No. 2e-40;

Matches 99; Conservative 8; Mismatches 9; Indels 4; Gaps 1;

QY 1 QVQLQESGAEISKPGASVKSCASGTTFTSYLHWIKORPGGLEWIGTINRNDYTEY 60

Db 20 QVQLQESGAEISKPGASVKSCASGTTFTSYLHWIKORPGGLEWIGTINRNDYTEY 79

QY 61 NONFKDKATLTADKSSSTAYMOLSLTSEDSAYYYCAR---DITFYWGCGTTLTVSS 116

Db 80 NONFKDKATLTADKSSSTAYMOLSLTSEDSAYYYCTRSYNTYEGANDYWGCGTTLTVSS 139

RESULT 2

JC2269 PL7-6 antibody heavy chain - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 07-May-1999

C/Accession: JC2269; PC2186

R/Kurume, T.; Katayama, M.; Murakami, K.; Hashino, K.; Kamihagi, K.; Yasunoto, M.; Ka

J. Biochem. 115, 608-614, 1994

A/Title: Expression of recombinant mouse/human chimeric antibody specific to human GM

A/Reference number: JC2269; MUID:94334310; PMID:7520038

A/Accession: JC2269

A/Molecule type: mRNA

A/Residues: 1-117 <KUR>

A/Accession: PC2186

A/Molecule type: protein

A/Residues: 2-27 <KUR>

A/Experimental source: hybridoma cell

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 19:03:46 ; Search time 23.6 Seconds

(without alignments)
231.148 Million cell updates/sec

Title: US-09-988-013a-4

Perfect score: 620
Sequence: 1 QVQLQESGAELSKPGASVKM.....ARRDITTFYGGCTLTFFVSS 116

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	482	77.7	139	1	P01751 mus musculu
2	465.5	75.1	120	1	P01747 mus musculu
3	456	73.5	137	1	P01755 mus musculu
4	455.5	73.5	140	1	P01746 mus musculu
5	448.5	72.3	138	1	P03980 mus musculu
6	443	71.5	120	1	P06329 mus musculu
7	435.5	70.2	117	1	P01756 mus musculu
8	434.5	70.1	117	1	P01757 mus musculu
9	432	69.7	117	1	P01748 mus musculu
10	430	69.4	117	1	P01749 mus musculu
11	429	69.2	117	1	P01750 mus musculu
12	428.5	69.1	121	1	P01745 mus musculu
13	424	68.4	117	1	P01753 mus musculu
14	421	67.9	117	1	P06328 mus musculu
15	420	67.7	117	1	P01754 mus musculu
16	415	66.9	118	1	P06330 mus musculu
17	404	65.2	117	1	P06337 mus musculu
18	392	63.2	117	1	P01758 mus musculu
19	386.5	62.3	136	1	P01759 mus musculu
20	373	60.2	147	1	P01744 homo sapien
21	369	59.5	114	1	P01741 mus musculu
22	368	59.4	117	1	P01743 homo sapien
23	354	57.1	117	1	P23083 homo sapien
24	329	53.0	119	1	P01807 mus musculu
25	328.5	53.0	117	1	P01811 mus musculu
26	328	52.9	119	1	P01808 mus musculu
27	320	51.6	119	1	P01810 mus musculu
28	316.5	51.0	117	1	P01812 mus musculu
29	315.5	50.9	118	1	P01809 mus musculu
30	314.5	50.7	125	1	P06326 homo sapien
31	312.5	50.4	142	1	P01805 rattus norv
32	311	50.2	111	1	P01804 mus musculu
33	308	49.7	122	1	P01768 homo sapien

34	306.5	49.4	117	1	P01786 mus musculu
35	304	49.0	136	1	P01783 mus musculu
36	303.5	49.0	121	1	P01771 homo sapien
37	302.5	48.8	113	1	P01801 mus musculu
38	299.5	48.3	113	1	P01799 mus musculu
39	299	48.2	117	1	P01742 homo sapien
40	298.5	48.1	119	1	P01770 homo sapien
41	298	48.1	120	1	P80421 homo sapien
42	298	48.1	124	1	P01760 homo sapien
43	297	47.9	122	1	P01769 homo sapien
44	294.5	47.5	113	1	P01796 mus musculu
45	293.5	47.3	115	1	P01802 mus musculu

ALIGNMENTS

RESULT 1
ID HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region BI-8/186-2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; Pubmed=6788376;
RA Boltwell A.L.M., Pasikind M., Reih M., Imanishi-Kari T., Rajewsky K., Baltimore D.;
RT "heavy chain variable region contribution to the NPB family of antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE BI-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB ANTIBODIES).
CC CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00529; AAA38170.1; -
CC PIR; A90809; MHMS18.
CC PDB; 1A6U; 27-MAY-98.
CC PDB; 1A6W; 15-JUL-98.
CC InterPro: IPR007110; Ig-like.
CC InterPro: IPR003016; Ig_MHC.
CC InterPro: IPR003596; Ig_V.
CC Pfam; PFO0047; Ig; 1.
CC SMART; SM00406; IgV; 1.
CC PROSITE; PSS0835; IG_LIKE; 1.
CC Immunoglobulin V region; Signal; 3D-structure.
CC KW SIGNAL
CC FT CHAIN 1
CC FT CHAIN 20 139 IG HEAVY CHAIN V REGION BI-8/186-2.
CC FT DOMAIN 20 49 FRAMEWORK-1.
CC FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
CC FT DOMAIN 55 68 FRAMEWORK-2.
CC FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
CC FT DOMAIN 86 117 FRAMEWORK-3.
CC FT DOMAIN 118 124 D SEGMENT.
CC FT DOMAIN 125 139 JH2 SEGMENT.
CC FT DISULFID 41 115 BY SIMILARITY.
CC FT NON_TER 139 139
CC SQ SEQUENCE 139 AA; 13419 MW; 1B57DD4FD0C9F465 CRC64;

```

Query Match          77.7%; Score 482; DB 1; Length 139;
Best Local Similarity 77.5%; Pred. No. 8e-42;
Matches 93; Conservative 10; Mismatches 13; Indels 4; Gaps 2;

OY 1 OVLOESGAEISKPGASYKMSCKASGYGTTSTYWLHMVKORPGGLEWIGYINPRNDYTEX 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 20 OVLODOPGAEIVKPGASVKLSCKASGYGTTSTYWMHWKORPGRGLEWIGRIDPNSGGRKY 79
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 NONFKDKATLTADKSSSTAYMOLSLTSDSAVYVCARRDI---TTF-YMGCGTTLTVSS 116
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 80 NEKFKSKATLTVDKSSSTAYMOLSLTSDSAVYVCARDYGGSSYFDYMGCGTTLTVSS 139
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 2
HV03_MOUSE
ID HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
RN [1]
RX MEDLINE=831846; PubMed=6186498;
RA Slezewitz M., Gefter M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idotype response of the strain A mouse.";
RT Eur. J. Immunol. 12:1023-1032(1982).
CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC HSP; P01789; IMCP.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART; SM00406; Igv_1.
DR PROSITE; PS50835; Ig_LIKE; 1.
DR Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 111
FT NON_TER 120 120 IG-LIKE.
SQ SEQUENCE 120 AA; 13307 MW; FFO4EAA167B654AF CRC64;

Query Match          75.1%; Score 465.5; DB 1; Length 120;
Best Local Similarity 75.0%; Pred. No. 3.1e-40;
Matches 90; Conservative 9; Mismatches 16; Indels 5; Gaps 1;

OY 2 VOLOESGAEISKPGASYKMSCKASGYGTTSTYWLHMVKORPGGLEWIGYINPRNDYTEXN 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 VOLOSGAEIVKPGASVKMSCKASGYGTTSTYGMVWVKORPGGLEWIGYINPGNGYTRYN 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 62 ONFKKATLTADKSSSTAYMOLSLTSDSAVYVCARR----DITTFYMGCGTTLTVSS 116
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 EKFKKTTLTVDKSSSTAYMOLSLTSDSAVYVCARSYVYGGSSYFDYMGCGTTLTVSS 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
HV11_MOUSE
ID HV11_MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region S43 precursor.
OS Mus musculus (Mouse).

```

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
RN [1]
RX MEDLINE=81234548; PubMed=6708376;
RA Boltwell A.L.M., Paskind M., Reih M., Imanishi-Karl T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RT Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE GAMMA-2a CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@sib-sib.ch)
CC -----
CC EMBL; J00539; AAA38172.1; -.
CC PIR; A02038; G2MS43.
DR HSP; P01810; 2FBJ.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART; SM00406; Igv_1.
DR PROSITE; PS50835; Ig_LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFD 41 115 BY SIMILARITY.
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF448BEC9 CRC64;

Query Match          73.5%; Score 456; DB 1; Length 137;
Best Local Similarity 73.7%; Pred. No. 3.3e-39;
Matches 87; Conservative 12; Mismatches 17; Indels 2; Gaps 1;

OY 1 OVLOESGAEISKPGASYKMSCKASGYGTTSTYWLHMVKORPGGLEWIGYINPRNDYTEX 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 20 OVLODOPGAEIVKPGASVKLSCKASGYGTTSTYWLHMVKORPGRGLEWIGRIDPNSGGRKY 79
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 NONFKDKATLTADKSSSTAYMOLSLTSDSAVYVCARRDITTF---YMGCGTTLTVSS 116
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 80 NEKFKSKATLTVDKSSSTAYMOLSLTSDSAVYVCARDYRILGRYDYMGCGTTLTVSS 137
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
HV02_MOUSE
ID HV02_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 93G precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
RN [1]
RX MEDLINE=81234548; PubMed=6708376;
RA Boltwell A.L.M., Paskind M., Reih M., Imanishi-Karl T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RT Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE GAMMA-2a CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC -----
CC EMBL; J00539; AAA38172.1; -.
CC PIR; A02038; G2MS43.
DR HSP; P01810; 2FBJ.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART; SM00406; Igv_1.
DR PROSITE; PS50835; Ig_LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFD 41 115 BY SIMILARITY.
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF448BEC9 CRC64;

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RC STRAIN-A/1;
RA MEDLINE=62152818; PubMed=6801765;
RA Sims J., Rabbits T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "omatic mutation in genes for the variable portion of the
RT Immunoglobulin heavy chain.";
RT Science 216:309-311(1982).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J00493; AAA38128.1; -
DR PIR: A94264; HYMSG7.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igy; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Hybridoma; Signal.
FT CHAIN 1 19
FT SIGNAL 1 19
FT DOMAIN 20 140 IG HEAVY CHAIN V REGION 9367.
FT NON_TER 140 140 IG-LIKE.
FT SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match 73.5%; Score 455.5; DB 1; Length 140;
Best Local Similarity 72.7%; Pred. No. 3.8e-39;
Matches 88; Conservative 9; Mismatches 19; Indels 5; Gaps 1;

QY 1 QVQLQESGAELEKPGASVKMSCKASGTFSTYLMHWIKORPGGLEIGYINPRNDYTEY 60
DB 20 QVQLQSGAELEKPGASVKMSCKASGTFSTYLMHWIKORPGGLEIGYINPRNDYTEY 79
QY 61 NQFKKATLTADKSSSTAAMQLSLTSESAVYVCARD--ITTFYWGQGTITLVSS 115
DB 80 NQFKKATLTADKSSSTAAMQLSLTSESAVYFCARSHYGGSYDFYWGQGTITLVSS 139
QY 116 S 116
DB 140 S 140

RESULT 5
HY48_MOUSE STANDARD; PRT; 138 AA.
ID HY48_MOUSE
AC P03980;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region TEPC 1017 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
RT delta in an Igd-secreting plasmacytoma.";
RT Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR PIR: A02033; HVMST7.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR007110; Ig-like.

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DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igy; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1 20
FT SIGNAL 1 20
FT DOMAIN 21 138 IG HEAVY CHAIN V REGION TEPC 1017.
FT DOMAIN 21 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 128 138 FRAMEWORK-4.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 138 138
FT SEQUENCE 138 AA; 15576 MW; 748157E4C69078BE CRC64;

Query Match 72.3%; Score 448.5; DB 1; Length 138;
Best Local Similarity 70.6%; Pred. No. 1.9e-38;
Matches 84; Conservative 14; Mismatches 18; Indels 3; Gaps 1;

QY 1 QVQLQESGAELEKPGASVKMSCKASGTFSTYLMHWIKORPGGLEIGYINPRNDYTEY 60
DB 20 QVQLQSGAELEKPGASVKMSCKASGTFSTYLMHWIKORPGGLEIGYINPRNDYTEY 79
QY 61 NQFKKATLTADKSSSTAAMQLSLTSESAVYVCARD--ITTFYWGQGTITLVSS 116
DB 80 NQFKKATLTADKSSSTAAMQLSLTSESAVYFCARSDGYIDWFYWGQGTITLVSS 138
QY 116 S 116
DB 140 S 140

RESULT 6
HY50_MOUSE STANDARD; PRT; 120 AA.
ID HY50_MOUSE
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Stekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RT EMBO J. 3:517-523(1984).
DR PIR: A02037; MHMS15.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igy; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT CHAIN 1 98
FT DOMAIN 99 105 V SEGMENT.
FT DOMAIN 106 120 D SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 120 120
FT SEQUENCE 120 AA; 914453F426F09834 CRC64;

Query Match 71.5%; Score 443; DB 1; Length 120;
Best Local Similarity 71.7%; Pred. No. 5.8e-38;
Matches 86; Conservative 9; Mismatches 21; Indels 4; Gaps 2;

QY 1 QVQLQESGAELEKPGASVKMSCKASGTFSTYLMHWIKORPGGLEIGYINPRNDYTEY 60
DB 80 NQFKKATLTADKSSSTAAMQLSLTSESAVYFCARSDGYIDWFYWGQGTITLVSS 138

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Db      1 OVQLODPEGLVKGPGASVNLSCKASGYTFTSYMHMIRORPGGLEWIGINPNSNGTNY 60
QY      61 NONFKDKATLTADKSSSTAYVMQSLTSDSAVYVCARRDI--TTFY--WGOGTTLTVSS 116
       1: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      61 NEKFKSKATLTVDKSSSTAYVMQSLTSDSAVYVCARRDIYGDYFVWAGTGTTVTVSS 120
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 7
HV12_MOUSE
ID      HV12_MOUSE      STANDARD:      PRT;      117 AA.
AC      P01756;
DR      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DE      15-SEP-2003 (Rel. 42, Last annotation update)
OS      Ig heavy chain V region MOPC 104E.
OC      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN      NCBI_TaxID=10090;
RP      [1]
SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RX      MEDLINE=83075344; PubMed=6816276;
RA      Kehy M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
       Hood L.E.;
RT      "Complete amino acid sequence of a mouse mu chain: homology among
       heavy chain constant region domains."
RU      Biotechnology 21:5615-5424(1982).
CC      -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
       PROTEIN HAS ALSO BEEN DETERMINED.
CC      -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC      -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR      PIR: A02039; MMS4E.
DR      HSSP: P01789; 1MCP.
DR      InterPro: IPR007110; Ig-like.
DR      InterPro: IPR003006; Ig_MHC.
DR      InterPro: IPR003596; Ig_V.
DR      Pfam: PF00047; Ig; 1.
DR      SMART: SM00406; IGV; 1.
DR      PROSITE: PS50835; IG-LIKE; 1.
KW      Immunoglobulin V region; Glycoprotein.
FT      DOMAIN 1 116
FT      DISULFID 22 96
FT      CARBOHYD 55 55
FT      NON_TER 117 117
SO      SEQUENCE 117 AA; 12983 MW; 3CFBACE4BE447E41 CRC64;

Query Match
Best Local Similarity 70.2%; Score 435.5; DB 1; Length 117;
Matches 86; Conservative 10; Mismatches 19; Indels 3; Gaps 2;

QY      1 OVQLODPEGLVKGPGASVNLSCKASGYTFTSYMHMIRORPGGLEWIGINPNSNGTNY 60
       :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 EVQLODSEGLVKGPGASVNLSCKASGYTFTSYMHMIRORPGGLEWIGINPNSNGTNY 60
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY      61 NONFKDKATLTADKSSSTAYVMQSLTSDSAVYVCARRDIYF--WGOGTTLTVSS 116
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      61 NOKFKGKATLTVDKSSSTAYVMQSLTSDSAVYVCARRDIYFVWAGTGTTVTVSS 117
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 8
HV13_MOUSE
ID      HV13_MOUSE      STANDARD:      PRT;      117 AA.
AC      P01757;
DR      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DE      15-SEP-2003 (Rel. 42, Last annotation update)
OS      Ig heavy chain V region J558.
OC      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
SEQUENCE.

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RX      MEDLINE=80078170; PubMed=6765983;
RA      Schilling J., Clevinger B., Davie J.M., Hood L.;
RT      "Amino acid sequence of homogeneous antibodies to dextran and DNA
       rearrangements in heavy chain V-region gene segments."
RU      Nature 283:35-40(1980).
CC      -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
       BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
       WHICH OCCUR IN THE D AND J SEGMENTS.
CC      -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC      -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR      PIR: A26242; MMSJ5.
DR      HSSP: P01789; 1MCP.
DR      InterPro: IPR007110; Ig-like.
DR      InterPro: IPR003006; Ig_MHC.
DR      InterPro: IPR003596; Ig_V.
DR      Pfam: PF00047; Ig; 1.
DR      SMART: SM00406; IGV; 1.
DR      PROSITE: PS50835; IG-LIKE; 1.
KW      Immunoglobulin V region.
FT      DOMAIN 1 116
FT      DISULFID 22 96
FT      NON_TER 117 117
SO      SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match
Best Local Similarity 70.1%; Score 434.5; DB 1; Length 117;
Matches 86; Conservative 8; Mismatches 22; Indels 1; Gaps 1;

QY      1 OVQLODPEGLVKGPGASVNLSCKASGYTFTSYMHMIRORPGGLEWIGINPNSNGTNY 60
       :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 EVQLODSEGLVKGPGASVNLSCKASGYTFTSYMHMIRORPGGLEWIGINPNSNGTNY 60
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY      61 NONFKDKATLTADKSSSTAYVMQSLTSDSAVYVCARRDIYF--WGOGTTLTVSS 116
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      61 NOKFKGKATLTVDKSSSTAYVMQSLTSDSAVYVCARRDIYFVWAGTGTTVTVSS 117
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9
HV04_MOUSE
ID      HV04_MOUSE      STANDARD:      PRT;      117 AA.
AC      P01748;
DR      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DE      15-JUL-1993 (Rel. 38, Last annotation update)
OS      Ig heavy chain V region 23 precursor.
OC      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
SEQUENCE FROM N.A.
RP      STRAIN=C57BL/6;
RA      MEDLINE=81234548; PubMed=6788376;
RA      Baltimore D.;
RT      "Heavy chain variable region contribution to the NPb family of
       antibodies: somatic mutation evident in a gamma 2a variable region."
RT      Cell 24:625-637(1981).
CC      -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
       RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR      PIR: A02030; HVM523.
DR      HSSP: P01810; 2FBS.
DR      InterPro: IPR007110; Ig-like.
DR      InterPro: IPR003006; Ig_MHC.
DR      InterPro: IPR003596; Ig_V.
DR      Pfam: PF00047; Ig; 1.
DR      SMART: SM00406; IGV; 1.
DR      PROSITE: PS50835; IG-LIKE; 1.
KW      Immunoglobulin V region; Signal.
FT      SIGNAL 1 19
FT      CHAIN 20 117
FT      DOMAIN 20 49
FT      DOMAIN 50 54
SO      SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

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FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DISULFID 86 117 FRAMEWORK-3.
FT NON_TER 41 115 BY SIMILARITY.
SO SEQUENCE 117 AA; 12772 MM; C530F82C906F69B CRC64;
Query Match 69.7%; Score 432; DB 1; Length 117;
Best Local Similarity 81.6%; Pred. No. 7.3e-37;
Matches 80; Conservative 5; Mismatches 13; Indels 0; Gaps 0;
OY 1 QVOLOESGAEILSKPGASVYKSCASGYFTSYLWLMHKORPGGLEWIGYINPRNDYTEY 60
DB 20 QVOLOQPGAEILVPGASVYKSCASGYFTSYLWLMHKORPGGLEWIGYINPRNDYTEY 79
OY 61 NONFKDKATLTADKSSSTAYMOLSLTSEDSAVYYCAR 98
DB 80 NEKFKSKVTLTVDKSSSTAYTQSLTSEDSAVYYCAR 117
RESULT 10
HV05_MOUSE STANDARD; PRT; 117 AA.
AC P01749;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig heavy chain V region 3 precursor.
GN IGH-VJ558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -I- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
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CC -----
DR EMBL: J00536; AAA38605.1; -.
DR PIR: A02031; HVMS3.
DR HSSP: P01810; 2PBJ.
DR MGD: MGI:96486; Igh-VJ558.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; signal.
FT CHAIN 1 19
FT SIGNAL 19
FT DOMAIN 20 49 IG HEAVY CHAIN V REGION 3.
FT DOMAIN 50 54 FRAMEWORK-1.
FT DOMAIN 55 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DISULFID 86 117 FRAMEWORK-3.
FT NON_TER 41 115 BY SIMILARITY.
FT NON_TER 117 117

SO SEQUENCE 117 AA; 13016 MM; 427C861C53975EDC CRC64;
Query Match 69.4%; Score 430; DB 1; Length 117;
Best Local Similarity 81.6%; Pred. No. 1.2e-36;
Matches 80; Conservative 7; Mismatches 11; Indels 0; Gaps 0;
OY 1 QVOLOESGAEILSKPGASVYKSCASGYFTSYLWLMHKORPGGLEWIGYINPRNDYTEY 60
DB 20 QVOLOQPGAEILVPGASVYKSCASGYFTSYLWLMHKORPGGLEWIGYINPRNDYTEY 79
OY 61 NONFKDKATLTADKSSSTAYMOLSLTSEDSAVYYCAR 98
DB 80 NEKFKSKVTLTVDKSSSTAYTQSLTSEDSAVYYCAR 117
RESULT 11
HV06_MOUSE STANDARD; PRT; 117 AA.
AC P01750;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 102 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -I- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: J00536; AAA38605.1; -.
DR PIR: A02032; HVMS2.
DR HSSP: P01810; 2PBJ.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; signal.
FT CHAIN 1 19
FT SIGNAL 19
FT DOMAIN 20 49 IG HEAVY CHAIN V REGION 102.
FT DOMAIN 50 54 FRAMEWORK-1.
FT DOMAIN 55 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DISULFID 86 117 FRAMEWORK-3.
FT NON_TER 41 115 BY SIMILARITY.
FT NON_TER 117 117
SO SEQUENCE 117 AA; 12867 MM; 740A65DB851CABC CRC64;
Query Match 69.2%; Score 429; DB 1; Length 117;
Best Local Similarity 83.3%; Pred. No. 1.5e-36;
Matches 80; Conservative 6; Mismatches 10; Indels 0; Gaps 0;
OY 2 VOLOESGAEILSKPGASVYKSCASGYFTSYLWLMHKORPGGLEWIGYINPRNDYTEY 61
DB 21 VOLOQPGAEILVPGASVYKSCASGYFTSYLWLMHKORPGGLEWIGYINPRNDYTEY 80
OY 62 QNFADKATLTADKSSSTAYMOLSLTSEDSAVYYCA 97
DB 81 QNFADKATLTADKSSSTAYMOLSLTSEDSAVYYCA 116
RESULT 12
HV01_MOUSE


```

FT    DOKAIN      50     54   COMPLEMENTARITY-DETERMINING-1.
FT    DOKAIN      55     68   FRAMEWORK-2.
FT    DOKAIN      69     85   COMPLEMENTARITY-DETERMINING-2.
FT    DOKAIN      86    117   FRAMEWORK-3.
FT    NON_TER     117    117
SQ    SEQUENCE    117 AA; 12921 MM; D37DBEBA3F543E996 CRC64;

Query Match          67.7%; Score 420; DB 1; Length 117;
Best Local Similarity 79.6%; Pred. No. 1,2e-35;
Matches 78; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY    1 QVQLQESGAELISKCSASYVMKSCASGYTFSTYMLHWIKRPGOGGLEWIGYINPRNDYYEK 60
      ||||| : ||| ||||||| : ||||||||| : ||||||| : ||| : ||| : |||
Db    20 QVQLDQGCAELIYRKCGASAYKLSSKASGYTFSTYMHWHYKQRGRGLEWIGRIDPNSGGTIKY 79
      ||||| : ||| ||||||| : ||||||||| : ||||||| : ||| : ||| : |||

QY    61 NQNFEDKATLTADXSSTAYMQLSLTSSEDSAVYYCAR 98
      | : | ||||| | ||||||||| |||||||||
Db    80 NEKFESKATLTIVDKPSSTAYMQLSLTSSEDSAVYYCAR 117

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 19:04:06 ; Search time 115.6 Seconds
(without alignments)
258.946 Million cell updates/sec

Title: US-09-988-013a-4

Perfect score: 620
Sequence: 1 QVQLQESGAEISKPGASVKM.....ARRDITTFYWGQITLVSS 116

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_23: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mmc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriophage: *
17: sp_archaeal: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	491.5	79.3	142	11	092401 mus musculus
2	490	79.0	141	11	092404 mus musculus
3	489	78.9	145	11	092409 mus musculus
4	487	78.5	137	11	092406 mus musculus
5	485	78.2	145	11	092408 mus musculus
6	484.5	78.1	146	11	092407 mus musculus
7	483	77.9	145	11	092407 mus musculus
8	482	77.7	145	11	092407 mus musculus
9	480	77.4	143	11	092409 mus musculus
10	479	77.3	143	11	092406 mus musculus
11	479	77.3	145	11	092406 mus musculus
12	477.5	77.0	140	11	092408 mus musculus
13	477	76.9	145	11	092404 mus musculus
14	476.5	76.9	146	11	092408 mus musculus
15	476.5	76.9	146	11	092403 mus musculus
16	473.5	76.4	142	11	092402 mus musculus

17	469.5	75.7	140	11	092402 mus musculus
18	468	75.5	142	11	092405 mus musculus
19	467	75.3	143	11	092405 mus musculus
20	467	75.3	143	11	092405 mus musculus
21	466	75.2	143	11	092407 mus musculus
22	464.5	74.9	144	11	092405 mus musculus
23	464	74.8	143	11	092400 mus musculus
24	462	74.5	148	11	092404 mus musculus
25	462	74.5	139	11	092405 mus musculus
26	462	74.5	145	11	092403 mus musculus
27	461	74.4	143	11	092402 mus musculus
28	459	74.0	278	11	092401 mus musculus
29	458	73.9	109	11	092405 mus musculus
30	457	73.7	143	11	092406 mus musculus
31	454.5	73.3	117	11	092406 mus musculus
32	453.5	73.1	481	11	092403 mus musculus
33	452.5	73.0	473	11	092403 mus musculus
34	452	72.9	468	11	092404 mus musculus
35	450.5	72.7	481	11	092403 mus musculus
36	448	72.3	613	11	092403 mus musculus
37	444.5	71.7	117	11	092403 mus musculus
38	443	71.5	473	11	092403 mus musculus
39	436.5	70.4	119	5	092402 mus musculus
40	436	70.3	114	11	092401 mus musculus
41	435.5	70.2	489	11	092403 mus musculus
42	432.5	69.8	117	11	092403 mus musculus
43	431.5	69.6	168	11	092403 mus musculus
44	429.5	69.3	480	11	092403 mus musculus
45	425	68.5	463	11	092403 mus musculus

ALIGNMENTS

RESULT 1

092401 ID 092401 PRELIMINARY: PRT; 142 AA.
AC 092401: 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE V23-D-J-C mu protein (fragment).
GN V23-D-J-C MO.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Scleroglossa; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP)".
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069913; BAB63929.1; -
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 142
SQ SEQUENCE 142 AA; 15622 MW; 24A265CE4EA4318B CRC64;

Query Match 79.3%; Score 491.5; DB 11; Length 142;

Best local similarity 79.5%; Pred. No. 1.9e-44;

Matches 93; Conservative 7; Mismatches 16; Indels 1; Gaps 1;

QY 1 QVQLQESGAEISKPGASVKSCASGTTFTSYLHWIKRPGGGLIEWIGTINRNDYTEY 60
DB 1 QVQLQPGTELVKPGASVKISCRASGTTFTSYLHWIKRPGGGLIEWIGTINRNDYTEY 60

QY 61 NONFKDKATLTPADKSSSTAYVMQLSLTSEDSAVYYCARRDITTF-YMGOGTTLTVSS 116
 DB 61 NEKFSKATLTVDKSSSTAYVMQLSLTSEDSAVYYCARRGEMAMDYMGOGTSVTSS 117

RESULT 2

Q92404 PRELIMINARY; PRT; 141 AA.

AC 092404: 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
 DE 01-MAR-2003 (TREMBLrel. 23, last annotation update)
 DE VH186.2-D-J-C mu protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
 Affinity Maturation of B Cell Antigen Receptors in Response to (4-
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
 RL Submitted (Aug-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AB067796; BAB63281.1; -
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1 141
 FT NON_TER 1 141
 SQ SEQUENCE 141 AA; 15561 MW; DDD08482D66876A0 CRC64;

Query Match 79.0%; Score 490; DB 11; Length 141;
 Best Local Similarity 78.4%; Pred. No. 2.7e-44;
 Matches 91; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 QVQLDSGAEISKSPASVYKMSCKASGYTFSTYWLHMIRKORPGGLEWIGYINPRNDYTEY 60
 DB 1 QVQLDQPGAEELVKKPASVYKLSCKASGYTFSTYWMHVMVQRGRGLEWIGRIDPNSGGTKY 60
 QY 61 NONFKDKATLTPADKSSSTAYVMQLSLTSEDSAVYYCARRDITTFYMGOGTTLTVSS 116
 DB 61 NEKFSKATLTVDKSSSTAYVMQLSLTSEDSAVYYCARRDITTFYMGOGTTLTVSS 116

RESULT 3

Q92409 PRELIMINARY; PRT; 145 AA.

AC 092409: 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
 DE 01-MAR-2003 (TREMBLrel. 23, last annotation update)
 DE VH186.2-D-J-C mu protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
 Affinity Maturation of B Cell Antigen Receptors in Response to (4-
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
 RL Submitted (Aug-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AB067791; BAB63276.1; -
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003006; IG_MHC.

DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1 145
 FT NON_TER 1 145
 SQ SEQUENCE 145 AA; 16001 MW; 0F409EB09FA333D2 CRC64;

Query Match 78.9%; Score 489; DB 11; Length 145;
 Best Local Similarity 76.7%; Pred. No. 3.6e-44;
 Matches 92; Conservative 12; Mismatches 12; Indels 4; Gaps 1;

QY 1 QVQLDSGAEISKSPASVYKMSCKASGYTFSTYWLHMIRKORPGGLEWIGYINPRNDYTEY 60
 DB 1 QVQLDQPGAEELVKKPASVYKLSCKASGYTFSTYWMHVMVQRGRGLEWIGRIDPNSGGTKY 60
 QY 61 NONFKDKATLTPADKSSSTAYVMQLSLTSEDSAVYYCARRDITTF---YMGOGTTLTVSS 116
 DB 61 NEKFSKATLTVDKSSSTAYVMQLSLTSEDSAVYYCARRSLTTTYAMDYMGOGTSVTSS 120

RESULT 4

Q924R6 PRELIMINARY; PRT; 137 AA.

AC 0924R6: 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
 DE 01-MAR-2003 (TREMBLrel. 23, last annotation update)
 DE VH186.2-D-J-C mu protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
 Affinity Maturation of B Cell Antigen Receptors in Response to (4-
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
 RL Submitted (Aug-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AB067783; BAB63268.1; -
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1 137
 FT NON_TER 1 137
 SQ SEQUENCE 137 AA; 15171 MW; 5C38D966DC6A4124 CRC64;

Query Match 78.5%; Score 487; DB 11; Length 137;
 Best Local Similarity 79.3%; Pred. No. 5.5e-44;
 Matches 92; Conservative 9; Mismatches 11; Indels 4; Gaps 1;

QY 1 QVQLDSGAEISKSPASVYKMSCKASGYTFSTYWLHMIRKORPGGLEWIGYINPRNDYTEY 60
 DB 1 QVQLDQPGAEELVKKPASVYKLSCKASGYTFSTYWMHVMVQRGRGLEWIGRIDPNSGGTKY 60
 QY 61 NONFKDKATLTPADKSSSTAYVMQLSLTSEDSAVYYCARRDITTFYMGOGTTLTVSS 116
 DB 61 NEKFSKATLTVDKSSSTAYVMQLSLTSEDSAVYYCARRD---YMGOGTTLTVSS 112

RESULT 5

Q924R1 PRELIMINARY; PRT; 145 AA.

AC 0924R1: 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
 DE 01-MAR-2003 (TREMBLrel. 23, last annotation update)
 DE VH186.2-D-J-C mu protein (Fragment).


```
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
DR Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067793; BAB63278.1; -.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 145
SQ SEQUENCE 145 AA; 16141 MW; 55A59A7908B2CD6A CRC64;

Query Match
Best Local Similarity 77.7%; Score 482; DB 11; Length 145;
Matches 93; Conservative 10; Mismatches 13; Indels 4; Gaps 2;

OY 1 OVQLOESGAELSKPGASVYKSCASGYFTSYLWIMIKRPGGLEWIGYINPRNDYTEY 60
DB 1 OVQLOQPGALVKPGASVYKSCASGYFTSYLWIMIKRPGGLEWIGYINPRNDYTEY 60
OY 61 NONFKDKATLTADKSSSTAYMQLSLTSDSAVYVCARRDI--TTF-YWGQGTTLTVSS 116
DB 61 NEKFKSKATLTVDKPSSTAYMQLSLTSDSAVYVCARYDYGSSYFDYWGQGTTLTVSS 120

RESULT 9
OY24P9 PRELIMINARY; PRT; 143 AA.
AC O924P9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE V303-D-0-C mu protein (Fragment).
GN V303-D-0-C MU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069916; BAB63932.1; -.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 143
SQ SEQUENCE 143 AA; 15704 MW; 43CD8C72D52134F6 CRC64;

Query Match
Best Local Similarity 77.4%; Score 480; DB 11; Length 143;
Matches 92; Conservative 8; Mismatches 16; Indels 2; Gaps 1;

OY 1 OVQLOESGAELSKPGASVYKSCASGYFTSYLWIMIKRPGGLEWIGYINPRNDYTEY 60
DB 1 OVQLOQPGALVKPGASVYKSCASGYFTSYLWIMIKRPGGLEWIGYINPRNDYTEY 60
OY 61 NONFKDKATLTADKSSSTAYMQLSLTSDSAVYVCARR--DITTFYWGQGTTLTVSS 116
DB 61 NOKFKGKATLTVDKSSSTAYMQLSLTSDSAVYVCASHYGSSSDYWGQGTTLTVSS 118

RESULT 10
O924R0 PRELIMINARY; PRT; 143 AA.
```

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ID O924R0 PRELIMINARY; PRT; 143 AA.
AC O924R0;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE V186-2-D-0-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067790; BAB63275.1; -.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 143
SQ SEQUENCE 143 AA; 15868 MW; 139B2E96B81E07F CRC64;

Query Match
Best Local Similarity 76.3%; Score 479; DB 11; Length 143;
Matches 90; Conservative 11; Mismatches 15; Indels 2; Gaps 1;

OY 1 OVQLOESGAELSKPGASVYKSCASGYFTSYLWIMIKRPGGLEWIGYINPRNDYTEY 60
DB 1 OVQLOQPGALVKPGASVYKSCASGYFTSYLWIMIKRPGGLEWIGYINPRNDYTEY 60
OY 61 NONFKDKATLTADKSSSTAYMQLSLTSDSAVYVCARR--RDITTFYWGQGTTLTVSS 116
DB 61 NEKFKSKATLTVDKPSSTAYMQLSLTSDSAVYVCARWDEYDYWGQGTTLTVSS 118

RESULT 11
OY24O6 PRELIMINARY; PRT; 145 AA.
AC O924O6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE V186-2-D-0-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067794; BAB63279.1; -.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 145
SQ SEQUENCE 145 AA; 16011 MW; 9BC0846D40DF97EA CRC64;
```


Db 121 S 121

RESULT 15

Q924Q3

PRELIMINARY; PRT; 146 AA.

AC Q924Q3

DT	01-DEC-2001	(TREMBlere1. 19, Created)
DT	01-DEC-2001	(TREMBlere1. 19, Created)

DT	01-DEC-2001	(Tremblay, 19, last sequence update)
DT	01-MAR-2003	(Tremblay, 23, last annotation update)

DE VH186.2-D-T-C mu protein (Fragment)
DI 01-MAR-2003 (11EMBLER: 23, last annotation update)

mus musculus (Mouse).

Eukaryota; Metazo

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-C57BL/6;

RA Kozono Y., Kozono H., Azuma T.,
BT "Direct Estimation of Relative

RT Affinity Maturation of B Cell Antigen Receptors in Response to 4A

Hydroxy-3-Nitrophenyl)Acetyl (NP) :
RT 11.111min

Submitted (AUG-2001) to the EMBL/GenBank

DR EMBL; AB067797; BAB63282.1; -.

DR InterPro; IPR007110; Ig-like.

```
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003006; Ig_MHC.
```

```
DR InterPro: IPR003596; Ig_v.  
DR Pfam: PF00047; Ig: 1
```

```
DR      E1a11;  F100047;  1g;  1.
SMART:  SM00406;  TGV:  1
```

DR PROSITE; PS50835; IG_L

FT	NON_TER	1	1
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ET	NON_TER	146	146
----	---------	-----	-----

SQ SEQUENCE 146 AA; 16

Overall Weight

Query Match	70
Best Local Alignment	70

DEBU LOCAL
Matches 9

STATION	TIME	REMARKS	DATE
1	0800	ARRIVED	10/10/50
2	0830	DEPARTED	10/10/50
3	0900	ARRIVED	10/10/50
4	0930	DEPARTED	10/10/50
5	1000	ARRIVED	10/10/50
6	1030	DEPARTED	10/10/50
7	1100	ARRIVED	10/10/50
8	1130	DEPARTED	10/10/50
9	1200	ARRIVED	10/10/50
10	1230	DEPARTED	10/10/50
11	1300	ARRIVED	10/10/50
12	1330	DEPARTED	10/10/50
13	1400	ARRIVED	10/10/50
14	1430	DEPARTED	10/10/50
15	1500	ARRIVED	10/10/50
16	1530	DEPARTED	10/10/50
17	1600	ARRIVED	10/10/50
18	1630	DEPARTED	10/10/50
19	1700	ARRIVED	10/10/50
20	1730	DEPARTED	10/10/50
21	1800	ARRIVED	10/10/50
22	1830	DEPARTED	10/10/50
23	1900	ARRIVED	10/10/50
24	1930	DEPARTED	10/10/50
25	2000	ARRIVED	10/10/50
26	2030	DEPARTED	10/10/50
27	2100	ARRIVED	10/10/50
28	2130	DEPARTED	10/10/50
29	2200	ARRIVED	10/10/50
30	2230	DEPARTED	10/10/50
31	2300	ARRIVED	10/10/50
32	2330	DEPARTED	10/10/50
33	0000	ARRIVED	10/10/50
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36	0130	DEPARTED	10/10/50
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38	0230	DEPARTED	10/10/50
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42	0430	DEPARTED	10/10/50
43	0500	ARRIVED	10/10/50
44	0530	DEPARTED	10/10/50
45	0600	ARRIVED	10/10/50
46	0630	DEPARTED	10/10/50
47	0700	ARRIVED	10/10/50
48	0730	DEPARTED	10/10/50
49	0800	ARRIVED	10/10/50
50	0830	DEPARTED	10/10/50

QY 1 QVQLQESGAELSKPGASVKMSCKASGYTFTSYWLHWIKORPGGLEWIGYINPRNDYTEY 60

[illegible]

Db 1 QVQLQQPGAEIVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEINIGRIDPNSGCTKY 60

Q: How many times did you see the defendant on the night of the murder?

61 NONFKDKALITADKSSSTAYMQLSSLTSEDSAVYYCARR-----DITTFYWGQGTTLTVS 115

61 NEKER
1: 11
Db

DE
OF NEW

116 S 116 QY

—

Search completed: October 7, 2003, 19:20:00
Job time : 116.6 secs

Job time : 116.6 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 19:03:26 ; Search time 6.2931 Seconds
(without alignments)
126.112 Million cell updates/sec

Title: US-09-988-013a-4_COPY_31_35

Perfect score: 34
Sequence: 1 SWHLH 5

Scoring table: BLOSUMP62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	90	23	ABBS3833
2	34	100.0	96	22	AAU22660
3	34	100.0	96	22	AAW2666
4	34	100.0	112	21	AAW2666
5	34	100.0	116	17	AAW2666
6	34	100.0	116	17	AAW2666
7	34	100.0	116	17	AAW2666
8	34	100.0	116	17	AAW2666
9	34	100.0	116	18	AAW2666

10	34	100.0	230	18	AAW07529	Anti-HGF receptor
11	34	100.0	482	23	ABW48149	Listeria monocytogenes
12	34	100.0	951	21	AAW44993	DC8scfV-erbB2EC fu
13	32	94.1	5	16	AAW49923	H-COR-1 of anti-1d
14	32	94.1	5	19	AAW70923	CDRI of the heavy
15	32	94.1	5	21	AAW19754	Erythropoietin rec
16	32	94.1	5	21	AAW92158	Murine 15B8 heavy
17	32	94.1	5	23	AAW11163	Murine antibody Act
18	32	94.1	8	14	AAW35020	GMP-140 MAB CDR1H
19	32	94.1	10	22	AAW35295	Murine PSCA antibo
20	32	94.1	61	22	AAW63721	Prophionbacterium
21	32	94.1	83	23	ABW63879	Human ORF249. Hom
22	32	94.1	98	21	AAW40136	Anti-hiL12 antibod
23	32	94.1	98	21	AAW40137	Anti-hiL12 antibod
24	32	94.1	98	21	AAW40139	Anti-hiL12 antibod
25	32	94.1	98	23	ABW91900	Human antibody fra
26	32	94.1	98	23	ABW91925	Human antibody fra
27	32	94.1	98	23	ABW78209	Human Fv molecule
28	32	94.1	98	23	ABW78234	Human Fv molecule
29	32	94.1	106	17	AAW91365	Anti-proenkephalin
30	32	94.1	110	18	AAW04586	Heavy chain of mon
31	32	94.1	111	18	AAW04586	Anti-DNA antibody
32	32	94.1	111	18	AAW04588	Anti-DNA antibody
33	32	94.1	111	18	AAW04589	Anti-DNA antibody
34	32	94.1	112	12	AAW12272	Anti-human Rhd JAC
35	32	94.1	113	20	AAW95483	Mouse derived RT3
36	32	94.1	114	13	AAW21279	Murine VH group 1
37	32	94.1	117	13	AAW30014	Heavy chain variab
38	32	94.1	117	14	AAW30032	GMP-140 MAB heavy
39	32	94.1	118	18	AAW27122	Murine antibody he
40	32	94.1	118	21	AAW56681	Anti-erythropoietin
41	32	94.1	119	14	AAW39464	MAB BW 2128 heavy
42	32	94.1	119	16	AAW79861	Anti-EGFR antibody
43	32	94.1	119	16	AAW79863	Anti-EGFR antibody
44	32	94.1	119	16	AAW79863	Immunoglobulin hea
45	32	94.1	119	17	AAW04332	Heavy chain of mon

ALIGNMENTS

RESULT 1	ABBS3833	standard; Protein: 90 AA.
ID	ABBS3833	
XX	ABBS3833;	
AC	ABBS3833;	
XX	16-MAY-2002 (first entry)	
DE	Lactococcus lactis protein yfBG.	
XX		
KW	Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.	
XX		
OS	Lactococcus lactis IL1403.	
XX		
PN	FR2807446-A1.	
XX		
PD	12-OCT-2001.	
XX		
PF	11-APR-2000; 2000FR-0004630.	
XX		
PR	11-APR-2000; 2000FR-0004630.	
XX		
PA	(INRG) INRA INST NAT RECH AGRONOMIQUE.	
XX		
PI	Boiotline A, Sorokline A, Renault P, Ehrlich SD;	
XX		
DR	WPI; 2002-043418/06.	
XX		
PT	New nucleotide sequence useful in the identification or Lactococcus	
PT	lactis and related species -	
XX		
PS	Claim 6; SEQ ID NO 535; 2504bp; French.	

XX The present invention is related to a Lactococcus lactis nucleotide
CC sequence (AB490521) and related proteins (AB853300-AB855621). The
CC nucleic acid sequence is useful in the detection and/or amplification of
CC nucleic acid sequence, particularly to identify Lactococcus lactis or
CC related species. The proteins of the invention are useful for the
CC biosynthesis or biodegradation of a composition of interest. The
CC invention helps research in lactic bacteria, particularly useful in the
CC production of yogurt and cheese.
CC Note: The sequence data for this patent is based on equivalent patent
CC WO20017734 (published 18-OCT-2001) which is available in electronic
CC format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).
XX
SQ Sequence 90 AA:

Query Match 100.0%; Score 34; DB 23; Length 90;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWLH 5
DB 17 SYWLH 21

RESULT 2
AAU22660
ID AAU22660 standard; Protein; 96 AA.
XX
AC AAU22660;
XX
DT 17-DEC-2001 (first entry)
XX
DE Novel human colon associated polypeptide #193.
XX
XX Human; colon cancer; congenital abnormality; infection; colitis;
KW Inflammatory bowel disease; IBD; neoplastic disorder; gene therapy;
KW Intestinal inflammatory disorder; malabsorption syndrome; gastric;
KW sigmoid disease; antibacterial; antiviral; antiinflammatory;
KW cytostatic.
XX
OS Homo sapiens.
XX
PN WO200155302-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01240.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.

PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
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PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 22-AUG-2000; 2000US-0227182.
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PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
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PR 05-SEP-2000; 2000US-0229509.
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PR 06-SEP-2000; 2000US-0230438.
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PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
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PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234957.
PR 25-SEP-2000; 2000US-0234958.
PR 25-SEP-2000; 2000US-0234959.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235634.
PR 27-SEP-2000; 2000US-0235636.
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PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
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PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239335.
PR 13-OCT-2000; 2000US-0239337.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
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PR	17-NOV-2000;	2000US-0249297.
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PR	17-NOV-2000;	2000US-0249300.
PR	01-DEC-2000;	2000US-0250160.
PR	01-DEC-2000;	2000US-0250391.
PR	05-DEC-2000;	2000US-0251030.
PR	05-DEC-2000;	2000US-0251988.
PR	05-DEC-2000;	2000US-0256719.
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PR	08-DEC-2000;	2000US-0251856.
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PR	08-DEC-2000;	2000US-0251869.
PR	08-DEC-2000;	2000US-0251989.
PR	08-DEC-2000;	2000US-0251990.
PR	11-DEC-2000;	2000US-0254097.
PR	05-JAN-2001;	2001US-0259678.
XX	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Rosen CA, Barash SC, Ruben SM;	
XX	WPI; 2001-465567/50.	
DR	N-PSDB; AAS39540.	
XX		
PT	Isolated polypeptide for treating, preventing and/or prognosing	
PT	disorders related to the colon including colon cancers and also for	
PT	testing and detection e.g. diagnosis -	
XX		
XX	Claim 11; SEQ ID NO 437; 562pp; English.	
XX		
CC	The present invention relates to the isolation of novel human colon	
CC	associated polypeptides, and the cDNA (AAS39348-AAS39581) and genomic	
CC	sequences encoding for them. The sequences of the invention are useful	
CC	in the diagnosis, treatment, prevention and/or prognosis of disorders	
CC	of the colon including colon cancer, congenital abnormalities	
CC	(e.g. atresia and stenosis), bacterial and viral infections,	
CC	inflammatory bowel disease (IBD), neoplastic cell disorders,	
CC	(e.g. polyps and adenomas), intestinal inflammatory disorders, colitis,	
CC	celiac inflammation, diarrhoea and dysentery, malabsorption syndromes	
CC	(e.g. lactose intolerance), intestinal obstruction and sigmoid diseases.	
CC	The polynucleotide sequences of the invention can also be used in gene	
CC	therapy. AAI22468-AAU22701 represent the novel human colon associated	
CC	polypeptides of the invention.	
CC	Note: The sequence data for this patent did not form part of the printed	
CC	specification, but was obtained in electronic format directly from WIPO	
CC	at ftp.wipo.int/pub/published_pct_sequences .	
XX		
SO	Sequence	96 AA;
Query Match 100.0%; Score 34; DB 22; Length 96;		
Best Local Similarity 100.0%; Pred. No. 95;		

Matches	5:	Conservative	0:	Mismatches	0:	Indels	0:	Gaps	0:
Oy	1	SYWLH 5							
Db	32	SYWLH 36							
RESULT 3									
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XX	AAM92666 standard; Protein; 96 AA.								
AC	AAM92666;								
XX									
DT	05-NOV-2001 (first entry)								
XX									
DE	Human digestive system antigen SEQ ID NO: 2015.								
XX									
KW	Human; digestive system antigen; gene therapy; cancer; appendicitis;								
KW	ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;								
RV	digestive system disorder; Meckel's diverticulum.								
XX									
OS	Homo sapiens.								
XX									
PN	WO200155314-A2.								
XX									
PD	02-AUG-2001.								
XX									
PF	17-JAN-2001; 2001WO-US01324.								
XX									
PR	31-JAN-2000; 2000US-0179065.								
PR	04-FEB-2000; 2000US-0180628.								
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PR	22-AUG-2000; 2000US-0226281.								
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PR	01-SEP-2000; 2000US-0229343.								
PR	01-SEP-2000; 2000US-0229344.								
PR	01-SEP-2000; 2000US-0229345.								
PR	05-SEP-2000; 2000US-0229509.								
PR	05-SEP-2000; 2000US-0229513.								
PR	06-SEP-2000; 2000US-0230437.								
PR	06-SEP-2000; 2000US-0230438.								

XX 11-MAY-1998; 98EP-0108534.
XX (MICR-) MICROMET GMBH.
XX
XX Rieber EP;
XX WPI: 2000-062300/05.
XX N-PSDB: AA248614.
XX
XX New antibodies against dendritic cells, used to produce products for
XX treating, e.g. cancer -
XX
XX Claim 8; Fig 9; 121pp; English.
XX
XX This sequence represents the DC8 antibody heavy chain variable region
XX (DC8-VH). The invention relates to an antibody that reacts with an
XX epitope on dendritic cells (DCs) displaying features of immature and/or
XX mature DCs from peripheral blood mononuclear cells (PBMCs), but does not
XX react with other PBMCs. The antibodies can be used for identifying or
XX isolating DCs. The DCs can be used for preparing activated
XX antigen-specific T-cells, for identifying an antigen recognisable by
XX T-cells, for identifying T-cell activating or co-stimulation compounds,
XX for identifying compounds which suppress T-cell activation or stimulation
XX and for identifying molecules synthesised by DCs having enhancing
XX modulating or suppressing effect on the antigen-specific activation of
XX T-cells. The products can be used for e.g. treating cancers,
XX infectious diseases, or autoimmune disease. The products can also be
XX used for diagnosis and for production of transgenic animals.
XX
SQ Sequence 112 AA;
Query Match 100.0%; Score 34; DB 21; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 SYWLH 5
| | | | |
DB 31 SYWLH 35
RESULT 5
AAR92216
ID AAR92216 standard; Protein: 116 AA.
XX
XX AAR92216;
XX
XX 28-MAY-1996 (first entry)
XX
XX LL2 Mab VH region.
XX
XX Humanised antibody; monoclonal antibody; Mab; LL2; B-cell lymphoma;
XX leukaemia; therapy; diagnosis; complementarity determining region;
XX CDR; antibody engineering.
XX
XX Mus musculus.
XX
XX
XX Key Location/Qualifiers
XX FH 31..35
XX FT /label= CDR1
XX FT /note= "claim 9, page 44"
XX FT 50..66
XX FT /label= CDR2
XX FT /note= "claim 10, page 45"
XX FT 99..105
XX FT /label= CDR3
XX FT /note= "claim 11, page 45"
XX
XX WO9604925-A1.
XX
XX 22-FEB-1996.
XX
XX 11-AUG-1995; 95WO-US09641.

XX 12-AUG-1994; 94US-0289576.
XX (IMMU-) IMMUNOMEDICS INC.
XX
XX Hansen H, Leung S;
XX WPI: 1996-139454/14.
XX N-PSDB: AAT15802.
XX
XX Chimeric and humanised LL2 antibodies - used to produce conjugates
XX for the therapy and diagnosis of B-cell lymphoma(s) and
XX leukaemia(s).
XX
XX Claim 5; Page 36-37; 70pp; English.
XX
XX The complementarity determining regions (CDRs) of mouse monoclonal
XX antibody (Mab) LL2 VK (AAR92215) and VH (AAR92216) regions were
XX recombinantly linked to the framework sequences of human VK and VH
XX regions, respectively, to give humanised LL2 VK (AAR92217) and VH
XX (AAR92218). These were subsequently linked, respectively, to human
XX kappa and IgG1 constant regions. A humanised Mab was obtd. that
XX retained the B-lymphoma and leukaemia cell targeting and
XX internalisation characteristics of the parental LL2 Mab, and which
XX exhibited a lowered HAMA reaction. It can be linked to e.g. a
XX cytostatic agent for therapeutic applin.
XX
SQ Sequence 116 AA;
Query Match 100.0%; Score 34; DB 17; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 SYWLH 5
| | | | |
DB 31 SYWLH 35
RESULT 6
AAR92218
ID AAR92218 standard; Protein: 116 AA.
XX
XX AAR92218;
XX
XX 28-MAY-1996 (first entry)
XX
XX Humanised LL2 Mab VH region.
XX
XX Humanised antibody; monoclonal antibody; Mab; LL2; B-cell lymphoma;
XX leukaemia; therapy; diagnosis; complementarity determining region;
XX CDR; antibody engineering.
XX
XX Synthetic.
XX
XX
XX Key Location/Qualifiers
XX FH 31..35
XX FT /label= CDR1
XX FT 50..66
XX FT /label= CDR2
XX FT 99..105
XX FT /label= CDR3
XX
XX WO9604925-A1.
XX
XX 22-FEB-1996.
XX
XX 11-AUG-1995; 95WO-US09641.
XX
XX 12-AUG-1994; 94US-0289576.
XX
XX (IMMU-) IMMUNOMEDICS INC.
XX
XX Hansen H, Leung S;

```

XX WPI; 1996-139454/14.
DR N-PSDB; AAT15804.
XX
XX Chimeric and humanised IL2 antibodies - used to produce conjugates
PT for the therapy and diagnosis of B-cell Lymphoma(s) and
PT Leukemia(s).
XX
XX Claim 5; Page 39; 70pp; English.
XX
XX The complementarity determining regions (CDRs) of mouse monoclonal
CC antibody (Mab) IL2 VK (AAR92215) and VH (AAR92216) regions were
CC recombinantly linked to the framework sequences of human VK and VH
CC regions, respectively, to give humanised IL2 VK (AAR92217) and VH.
CC (AAR92218). These were subsequently linked, respectively, to human
CC kappa and IgG1 constant regions. A humanised Mab was obtd. that
CC retained the B-lymphoma and leukaemia cell targeting and
CC internalisation characteristics of the parental IL2 Mab, and which
CC exhibited a lowered HAMA reaction. It can be linked to e.g. a
CC cytostatic agent for therapeutic appln.
XX
SQ Sequence 116 AA;

Query Match 100.0%; Score 34; DB 17; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.le+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
   11111
Db 31 SYWLH 35

RESULT 7
AAR92219
ID AAR92219 standard; Protein; 116 AA.
XX
XX AAR92219;
XX
XX 28-MAY-1996 (first entry)
XX
XX Humanised IL2 Mab VH region (version hLL2-1).
XX
XX Humanised antibody; monoclonal antibody; Mab; IL2; B-cell lymphoma;
KW leukemia; therapy; diagnosis; complementarity determining region;
KM CDR; antibody engineering.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Region 31..35
FT /label= CDR1
FT 50..66
FT /label= CDR2
FT 99..105
FT /label= CDR3
XX
XX WO9604925-A1.
XX
XX 22-FEB-1996.
XX
XX 11-AUG-1995; 95WO-US09641.
XX
XX 12-AUG-1994; 94US-0289576.
XX
XX (IMMU-) IMMUNOMEDICS INC.
XX
XX Hansen H, Leung S;
XX
XX WPI; 1996-139454/14.
XX
XX Chimeric and humanised IL2 antibodies - used to produce conjugates
PT for the therapy and diagnosis of B-cell Lymphoma(s) and
PT Leukemia(s).
PT

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```

XX Example 1; Page 40; 70pp; English.
PS
XX
XX The complementarity determining regions (CDRs) of mouse monoclonal
CC antibody (Mab) IL2 VK (AAR92215) and VH (AAR92216) regions were
CC recombinantly linked to the framework sequences of human VK and VH
CC regions, respectively, to give humanised IL2 VK (AAR92217) and VH
CC (AAR92218). In an alternative version, a glutamine was introduced
CC at position 5 of the humanised VH (AAR92219) to include a PstI site
CC useful for subcloning. The humanised VK and VH were subsequently
CC linked, respectively, to human kappa and IgG1 constant regions. A
CC humanised Mab was obtd. that retained the B-lymphoma and leukaemia
CC cell targeting and internalisation characteristics of the parental
CC IL2 Mab, and which exhibited a lowered HAMA reaction. It can be
CC linked to a cytostatic agent for therapeutic appln.
XX
SQ Sequence 116 AA;

Query Match 100.0%; Score 34; DB 17; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.le+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
   11111
Db 31 SYWLH 35

RESULT 8
AAW27696
ID AAW27696 standard; Protein; 116 AA.
XX
XX AAW27696;
XX
XX 14-APR-1998 (first entry)
XX
XX Variable heavy chain of Mab IL2.
XX
XX Variable heavy chain; B cell; monoclonal antibody; Mab; IL2;
KW B cell lymphoma; lymphocytic leukemia cell; murine;
KM diagnosis; treatment; B cell malignancy; non-Hodgkins lymphoma;
KW chronic lymphocytic leukemia.
XX
XX Mus sp.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Region 31..35
FT /note= "complementarity determining region 1"
FT 50..66
FT /note= "complementarity determining region 2"
FT 99..105
FT /note= "complementarity determining region 3"
XX
XX WO9734632-A1.
XX
XX 25-SEP-1997.
XX
XX 19-MAR-1997; 97WO-US04196.
XX
XX 20-MAR-1996; 96US-0013709.
XX
XX (IMMU-) IMMUNOMEDICS INC.
XX
XX Hansen H, Leung S, Qu Z;
XX
XX WPI; 1997-479995/44.
XX
XX N-PSDB; AAT88129.
XX
XX Monoclonal antibody engineered to contain glycosylation site - in
PT non-Fc constant heavy or light chain region, useful to diagnose or
PT treat B cell malignancies, e.g. non-Hodgkins lymphoma
XX
XX Example 3; Fig 4B; 88pp; English.
PS

```

XX The present sequence is the variable heavy chain of the
CC B cell specific monoclonal antibody (Mab) IL2, which contains an
CC engineered tri-peptide N-glycan acceptor sequence. IL2 is a highly
CC specific anti-B cell lymphoma and anti-lymphocytic leukaemia cell
CC murine Mab. The Mab can be used to diagnose or treat B
CC cell malignancies, e.g. non-Hodgkins lymphoma or chronic
CC lymphocytic leukaemia. The glycosylation site allows a label or
CC therapeutic agent of increased size to be conjugated to the
CC carbohydrate moiety, without affecting the Mab's binding affinity
CC or specificity.
XX

SO Sequence 116 AA;
Query Match 100.0%; Score 34; DB 18; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
|||||
DB 31 SYWLH 35

RESULT 9
AAW27698
ID AAW27698 standard; Protein: 116 AA.
AC AAW27698;
XX
DT 14-APR-1998 (first entry)
XX
DE Variable heavy chain of Mab hLL2.
XX
KM Variable heavy chain; B cell; monoclonal antibody; Mab; hLL2;
KM B cell lymphoma; lymphocytic leukaemia cell; murine; humanised;
KM diagnosis; treatment; B cell malignancy; non-Hodgkins lymphoma;
KM chronic lymphocytic leukaemia.
XX
OS Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
XX

XX Key Location/Qualifiers
FH Region 31..35
FT /note= "complementarily determining region 1"
FT Region 50..66
FT /note= "complementarily determining region 2"
FT Region 99..105
FT /note= "complementarily determining region 3"
XX
XX WO9734632-A1.
XX
XX 25-SEP-1997.
XX
XX 19-MAR-1997; 97WO-US04196.
XX
XX 20-MAR-1996; 96US-0013709.
XX
XX (IMMU-) IMMUNOMEDICS INC.
XX
XX Hansen H, Leung S, Qu Z;
XX WPI: 1997-479995/44.
XX DR N-PSDB: AAT88131.
XX
XX Monoclonal antibody engineered to contain glycosylation site - in
PT non-Fc constant heavy or light chain region, useful to diagnose or
PT treat B cell malignancies, e.g. non-Hodgkins lymphoma
XX
XX Example 3; Fig 5B; 88pp; English.
XX
XX The present sequence is the variable heavy chain of the
CC B cell specific monoclonal antibody (Mab) hLL2. hLL2 is a highly
CC specific anti-B cell lymphoma and anti-lymphocytic leukaemia cell

CC humanised murine Mab. The Mab can be used to diagnose or treat B
CC cell malignancies, e.g. non-Hodgkins lymphoma or chronic
CC lymphocytic leukaemia.
XX

SO Sequence 116 AA;
Query Match 100.0%; Score 34; DB 18; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
|||||
DB 31 SYWLH 35

RESULT 10
AAW07529
ID AAW07529 standard; Protein: 230 AA.
AC AAW07529;
XX
DT 04-MAR-1997 (first entry)
XX
DE Anti-HGF receptor Mab 5D5 Fab heavy chain.
XX
KM Hepatocyte growth factor receptor; HGF; c-Met; antagonist;
KM monoclonal antibody; Mab; Fab; breast cancer; pancreas cancer;
KM colon cancer; lung cancer; therapy.
XX
OS Mus sp.
XX
XX Key Location/Qualifiers
FH MISC-difference 1
FT /label= Glu, Gln
XX
XX WO9638557-A1.
XX
XX 05-DEC-1996.
XX
XX 31-MAY-1996; 96WO-US08094.
XX
XX 02-JUN-1995; 95US-0460368.
XX
XX (GETH) GENENTECH INC.
XX
XX Schwall RH, Tabor KH;
XX WPI: 1997-034371/03.
XX DR N-PSDB: AAT43874.
XX
XX Hepatocyte growth factor receptor antagonist - specifically
PT anti-c-Met receptor monoclonal antibody 5D5 Fab, useful for
PT mammalian cancer treatment
XX
XX Claim 12; Fig 1B; 69pp; English.
XX
XX 5D5 Fab comprises a light chain (AAW07528) and heavy chain (AAW07529)
CC of monoclonal antibody (Mab) 5D5, a murine Mab raised against the
CC hepatocyte growth factor (HGF) receptor (c-Met). The Fab can be
CC obtd. by papain digestion of the Mab or by recombinant methods
CC utilising cDNA clones (AAT43873-74) coding for the light and heavy
CC chains. 5D5 Fab is an antagonist of the HGF receptor and is useful
CC for the diagnosis and treatment of breast, pancreas, colon and lung
CC cancer.
XX
XX

SO Sequence 230 AA;
Query Match 100.0%; Score 34; DB 18; Length 230;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
|||||

DB		31 SYWLH 35	
RESULT 11			
ID ABB48149			
XX ABB48149 standard; Protein; 482 AA.			
AC ABB48149;			
XX 05-FEB-2002 (first entry)			
DE Listeria monocytogenes protein #853.			
KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;			
KW vitamin B12; bacterial infection; disease.			
OS Listeria monocytogenes.			
PX WO200177335-A2.			
PD 18-OCT-2001.			
PE 11-APR-2001; 2001WO-FR01118.			
PR 11-APR-2000; 2000FR-0004629.			
PA (INSP) INST PASTEUR.			
PI Buchrieser C, Frangeul L, Couve E, Rusnock C, Fsihi H, Dehoux P;			
PI Duesurget O, Chetouiati F, Nedjari H, Glaser P, Kunst F, Coscart P;			
PI Daniels J, Gobel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;			
PI Dominguez-Bernal G, Garrido-Garcia P, Merrez-Martinez A, Amend A;			
PI Charriborty T, Doman E, Haln T, Berche P, Charbit A, Durant L;			
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;			
PI Madueno E, De Pablos B, Wehlund J, Keerst U, Entlan K, Hauf J;			
PI Rose M, Voss H;			
DR WP1: 2002-010914/01.			
XX Genomic sequence for Listeria monocytogenes, useful e.g. for treatment			
PT and prevention of Listeria and related bacterial infections, and			
PT related polypeptides -			
PS Claim 6; SEQ ID No 854; 192pp; French.			
CC The present invention relates to the genome sequence of Listeria			
CC monocytogenes EGD-e (see ABR03041). The genome sequence and fragments of			
CC it are useful for selecting probes and primers for detecting genes in L.			
CC monocytogenes and related organisms, and for studying genetic			
CC polymorphisms and other genomes. The present sequence is a protein			
CC encoded by the genome sequence of the present invention. Proteins			
CC expressed from the genome sequence are useful for raising specific			
CC antibodies, identification of L. monocytogenes and related organisms, and			
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin			
CC B12. The genome sequence and proteins encoded by it are also useful for			
CC selecting compounds that regulate gene expression and cell replication			
CC and modulate L. monocytogenes-related diseases. In addition, the genome			
CC sequence and proteins encoded by it are useful in pharmaceutical and			
CC vaccines compositions for the treatment or prevention of infections by L.			
CC monocytogenes and related organisms.			
CC Note: The sequence data for this patent did not form part of the printed			
CC specification, but was obtained in electronic format directly from WIPO			
CC at ftp.wipo.int/pub/published_pct_sequences.			
XX			
SQ Sequence 482 AA:			
Query Match 100.0%; Score 34; DB 23; Length 482;			
Best Local Similarity 100.0%; Pred. No. 4.4e+02;			
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0			
OY 1 SYWLH 5			
DB 314 SYWLH 318			

RESULT 12	
AA444993	
ID	AA444993 standard; Protein; 951 AA.
XX	
AC	AA444993;
XX	
DT	23-MAY-2000 (first entry)
XX	
DE	DC8scfv-erbB2EC fusion protein containing tetramerisation domain.
XX	
KW	DC8 scfv; single-chain variable fragment; erbB2EC; extracellular domain;
KW	human; fusion construct; tetramerisation domain; constant domain;
KW	heteroinhibitor; multifunctional antigen; antileukemia; diagnosis;
KW	immunoglobulin; cytosolic; immunostimulatory; antileukemia; diagnosis;
KW	antiproliferative; prevention; treatment; malignant; haematopoietic cell;
KW	lymphoma; leukemia; solid tumour; carcinoma; melanoma; sarcoma.
XX	
OS	Chimeric - Unidentified.
OS	Chimeric - Homo sapiens.
XX	
PH	Key
FT	Location/Qualifiers
FT	1..19
FT	/label= Leader_sequence
FT	20..127
FT	/label= DC8scfv_light_chain_variable_region
FT	128..142
FT	/label= Glycine-Serine-Linker
FT	143..254
FT	/label= DC8scfv_heavy_chain_variable_region
FT	255..266
FT	/note= '5' end of human IgG3 upper hinge region
FT	with additional residues"
FT	267..305
FT	/label= Human_p53_tetramerisation_domain
FT	306..312
FT	/label= Short_peptide_linker
FT	313..945
FT	/label= erbB2EC_domain
FT	946..951
FT	/label= His_tag
XX	
PN	WO200006605-A2.
XX	
PD	10-FEB-2000.
XX	
PF	28-JUL-1999; 99MO-EP05416.
XX	
PR	28-JUL-1998; 98EP-0114082.
XX	
PA	(MICR-) MICROMET GRS BIOMEDIZINISCHE FORSCHUNG.
XX	
PI	Kuifer P, Dreier T, Baeuerle PA, Borschert K, Zettl F;
XX	
DR	WPI: 2000-195265/17.
DR	N-PSDB; AA250586.
XX	
PT	New multifunctional compounds useful for preventing and/or treating
PT	malignant cell growth and for detection and diagnosis -
XX	
PS	Example 9; Fig 49; 166pp; English.
XX	
CC	The patent discloses heteroinhibitors which are multifunctional compounds
CC	productable in a mammalian host cell as a secretable and fully functional
CC	heterodimer of two polypeptide chains, where one of the polypeptide
CC	chains comprises, a CH1-domain (constant domain of an immunoglobulin
CC	heavy chain) and the other chain comprises CH2-domain (constant domain of
CC	an immunoglobulin light chain). The polypeptide chains further comprise,
CC	fused to the constant domains at least two (poly)peptides having
CC	different receptor or ligand functions, where further at least two of the
CC	different (poly)peptides lack an intrinsic affinity for one another and
CC	are linked via the constant domains. The heteroinhibitors have

CC cytostatic, immunostimulatory, antileukaemia and antiproliferative
CC activities. These compounds can be used for diagnosing, preventing and
CC treating malignant cell growth related to malignancies of haematopoietic
CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,
CC melanomas and sarcomas.
CC The present sequence is a fusion protein comprising DCR
CC single-chain Fv (scFv) fragment at the N-terminus, extracellular
CC domain of human erbB2 at the C-terminus and a tetramerisation
CC domain between them. This construct was prepared to find out whether
CC an oligomerisation domain characterised in bacterial expression system
CC is applicable for expression of fully functional and secretable
CC recombinant protein in mammalian host cells. This tetrameric construct
CC was not expressed as secretable and fully functional protein
CC in mammalian cells. Hence general applicability of the tetramerisation
CC domain for oligomerisation strategies in mammalian cells was ruled out.
CC
XX
SQ Sequence 951 AA;

Query Match 100.0%; Score 34; DB 21; Length 951;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
|||:|
DB 173 SYWLH 177

RESULT 13
AAW74929
ID AAW74929 standard; peptide: 5 AA.
AC AAW74929;
XX
DT 19-JAN-1996 (first entry)
XX
DE H-CDR-1 of anti-idiotype antibody against human anticancer antibody.
KM Anticancer; cancer; CDR; heavy chain; light chain; immunoglobulin;
KW Complementarity determining region.
XX
OS Mus sp.
XX JPO7101999-A.
PN
XX 18-APR-1995.
PD
XX 06-OCT-1993; 93JP-0272950.
PF
XX 06-OCT-1993; 93JP-0272950.
PR
PA (HAGI/) HAGIWARA Y.
XX
DR WPI; 1995-182987/24.
XX
PT Novel anti-idiotype antibody against an human anticancer monoclonal
PT antibody - and DNA sequences encoding the antibody, useful in
PT pharmacology, medicine and biochemical fields.
XX
PS Claim 1; Page 2; 28pp; Japanese.
XX
CC A new anti-idiotype antibody against a human anticancer monoclonal
CC antibody is claimed. This antibody contains in its heavy chain 3
CC complementarity determining regions CDR1 (AAW74929-R74931), CDR2
CC (AAW74932-R74935) and CDR3 (AAW74936-R74939), this is also true of the
CC light chain which has its own CDR1 (AAW74944-R74946 and AAW85774), CDR2
CC (AAW74947-R74949) and CDR3 (AAW74950-R74954). The antibody and DNA
CC encoding it are useful in pharmacological, medical and biochemical
CC fields.
XX
SQ Sequence 5 AA;

Query Match 94.1%; Score 32; DB 16; Length 5;
Best Local Similarity 80.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
|||:|
DB 1 SYWLH 5

RESULT 14
AAW70923
ID AAW70923 standard; peptide: 5 AA.
XX
AC AAW70923;
XX
DT 18-FEB-1999 (first entry)
XX
DE CDR1 of the heavy chain of monoclonal antibody RV-133.
XX
KM Pathogenic virus; tropism: mucosa; CDR region; monoclonal antibody;
KM respiratory syncytial virus; RSV; VP6 protein; rota virus; RV;
KM viral infection; inhibit; fusion; protection; transcription;
KM antiviral agent; prophylaxis; diagnosis; infection; contamination.
XX
OS Synthetic.
OS Mus sp.
XX FR2758331-A1.
PN
XX 17-JUL-1998.
PD
XX 14-JAN-1997; 97FR-0000300.
PF
XX 14-JAN-1997; 97FR-0000300.
PR
XX 14-JAN-1997; 97FR-0000300.
PA (UYBO-) UNIV BOURGOGNE.
XX
PI Bourgeois C, Kohl E, Pothier P;
XX WPI; 1998-390320/34.
DR
XX New peptide(s) recognising viral epitope with tropism to mucosa -
PT useful for, e.g. diagnosing, preventing and treating viral
PT infection(s)
XX
PS Claim 12; Page 30; 51pp; French.
XX
CC AAW70905-46 represent peptide sequences that can recognise, by
CC antigen-antibody type reactions, at least 1 epitope of a pathogenic
CC virus having tropism for the mucosa. AAW70905-16 and AAW70929-46 are
CC analogous to CDR regions of monoclonal antibodies specific for
CC respiratory syncytial virus (RSV). AAW70917-28 are analogous to CDR
CC regions of monoclonal antibodies specific for site III or IV of the
CC VP6 protein of rota virus (RV). The peptides can neutralise viral
CC infections and may also inhibit fusion between infected and uninfected
CC cells or cells and viruses. They provide passive or active protection
CC and/or inhibit transcription of the virus, so are useful as antiviral
CC agents or for prophylaxis, in human or veterinary medicine. The peptides
CC can be labelled and used to diagnose infection or contamination by the
CC virus. The peptides are particularly directed against RSV or RS but may
CC also be used against papilloma, adeno, entero, polio, influenza or
CC immune deficiency viruses.
XX
SQ Sequence 5 AA;

Query Match 94.1%; Score 32; DB 19; Length 5;
Best Local Similarity 80.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
|||:|
DB 1 SYWLH 5

RESULT 15

AAB19754
 ID AAB19754 standard; Peptide: 5 AA.
 AC AAB19754;
 XX
 DT 19-FEB-2001 (first entry)
 XX
 DE Erythropoietin receptor agonist Mab 3G9 VH region CDR1.
 XX
 KM Erythropoietin receptor; agonist; monoclonal antibody; Mab; mouse;
 KW heavy chain variable region; antibody engineering; erythropoiesis;
 KW anemia; cytopenia; acute renal failure; antianemic; therapy;
 KM complementarity determining region; CDR.
 XX
 OS Mus sp.
 XX
 PN WO200061637-A1.
 XX
 PD 19-OCT-2000.
 XX
 PF 14-APR-2000; 2000WO-US10284.
 XX
 PR 14-APR-1999; 99US-0129263.
 XX
 PA (SMK) SMITHKLINE BEECHAM CORP.
 XX
 PI Erickson-Miller CL, Holmes SD, Taylor AH, Young PR;
 XX
 DR WPI; 2000-679469/66.
 XX
 PT Novel erythropoietin receptor agonist antibody useful for enhancing
 PT erythropoiesis in the treatment of anemia, cytopenia or acute renal
 PT failure -
 XX
 PS Claim 28; Page 50; 70pp; English.
 XX
 CC The present sequence is that of complementarity determining region
 CC 1 (CDR1) of the heavy chain variable region (VH) (see AAB19745) of
 CC 3G9, a murine erythropoietin receptor (Epor) agonist monoclonal
 CC antibody. Claimed Epor agonist antibodies comprise a VH region
 CC that includes the 3G9 VH CDRs. These include humanised agonist
 CC antibodies in which the 3G9 VH CDRs are incorporated into a human
 CC framework. The Epor agonist antibodies are used in a claimed
 CC method for enhancing erythropoiesis, for the treatment of anaemia,
 CC cytopenia, acute renal failure, and other conditions with depressed
 CC erythrocyte production. Agonist antibodies of Epor have the same
 CC therapeutic utility as the natural ligand, but with the advantages
 CC of easier purification and longer half-life in vivo.
 CC
 XX
 SQ Sequence 5 AA:
 QY
 Best Local Similarity 94.1%; Score 32; DB 21; Length 5;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 DB 1 SYWMH 5
 1 SYWMH 5
 1 SYWMH 5
 1 SYWMH 5

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 Job time : 8.2931 secs

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OM protein - protein search, using sw model

Run on: October 7, 2003, 19:07:41 ; Search time 2.58621 Seconds
(without alignments)
305.878 Million cell updates/sec

Title: US-09-988-013a-4_COPY_31_35
Perfect score: 34
Sequence: 1 SYWLH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/pubppa/PCRTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubppa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubppa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubppa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubppa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubppa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	34	100.0	96	11	US-09-764-872-437
2	34	100.0	116	10	US-09-741-843-4
3	34	100.0	116	10	US-09-741-843-8
4	34	100.0	116	10	US-09-741-843-9
5	34	100.0	116	11	US-09-894-839-4
6	34	100.0	116	11	US-09-894-839-8
7	34	100.0	116	11	US-09-894-839-21
8	34	100.0	116	11	US-09-888-013A-4
9	34	100.0	116	11	US-09-988-013A-8
10	34	100.0	230	10	US-09-988-013A-9
11	34	100.0	230	10	US-09-995-693-2
12	34	100.0	230	15	US-10-232-408-2
13	32	94.1	5	9	US-09-748-960-12
14	32	94.1	32	15	US-10-233-996-53
15	32	94.1	83	9	US-09-867-550-498

16	32	94.1	98	15	US-10-194-975-33	Sequence 33, Appl
17	32	94.1	118	9	US-09-905-243-78	Sequence 78, Appl
18	32	94.1	119	9	US-09-905-243-79	Sequence 79, Appl
19	32	94.1	119	15	US-10-233-996-2	Sequence 2, Appl
20	32	94.1	119	15	US-10-233-996-4	Sequence 4, Appl
21	32	94.1	119	15	US-10-233-996-39	Sequence 39, Appl
22	32	94.1	120	15	US-10-096-246-12	Sequence 12, Appl
23	32	94.1	122	8	US-08-779-784-28	Sequence 28, Appl
24	32	94.1	122	15	US-10-096-246-10	Sequence 10, Appl
25	32	94.1	122	15	US-10-096-246-11	Sequence 11, Appl
26	32	94.1	140	9	US-09-748-960-4	Sequence 4, Appl
27	32	94.1	142	9	US-08-564-329A-13	Sequence 13, Appl
28	32	94.1	142	10	US-09-855-153-13	Sequence 13, Appl
29	32	94.1	142	10	US-09-854-811-13	Sequence 13, Appl
30	32	94.1	142	10	US-09-934-773-13	Sequence 13, Appl
31	32	94.1	142	10	US-09-963-620-13	Sequence 13, Appl
32	32	94.1	142	11	US-09-855-632-13	Sequence 13, Appl
33	32	94.1	142	12	US-10-224-720-13	Sequence 13, Appl
34	32	94.1	142	12	US-10-225-779-13	Sequence 13, Appl
35	32	94.1	142	15	US-10-225-784-13	Sequence 13, Appl
36	32	94.1	143	8	US-08-779-784-26	Sequence 26, Appl
37	32	94.1	180	9	US-09-748-960-6	Sequence 6, Appl
38	32	94.1	242	11	US-09-880-748-2084	Sequence 2084, Ap
39	32	94.1	331	15	US-10-059-261-169	Sequence 169, Ap
40	31	91.2	177	11	US-09-768-235B-20	Sequence 20, Appl
41	31	91.2	383	11	US-09-978-418-38	Sequence 38, Appl
42	31	91.2	384	11	US-09-764-891-4366	Sequence 4366, Ap
43	31	91.2	416	9	US-09-925-301-1046	Sequence 1046, Ap
44	30	88.2	61	15	US-10-083-357-856	Sequence 856, Ap
45	30	88.2	132	14	US-10-056-359-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-09-764-872-437
; Sequence 437, Application US/09764872
; Publication No. US20030050231A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA125
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 957
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 437
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-872-437

Query Match
Best Local Similarity 100.0%; Score 34; DB 11; Length 96;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	SYWLH	5
DB	32	SYWLH	36

RESULT 2
US-09-741-843-4
; Sequence 4, Application US/09741843
; Patent No. US20020102254A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL
; TITLE OF INVENTION: AND LEUKEMIA CELLS
; FILE REFERENCE: 018733/0996

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; CURRENT APPLICATION NUMBER: US/09/741,843
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/127,902
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/690,102
; PRIOR FILING DATE: 1996-07-06
; PRIOR APPLICATION NUMBER: US 08/289,576
; PRIOR FILING DATE: 1994-08-12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-741-843-4

Query Match
Best Local Similarity 100.0%; Score 34; DB 10; Length 116;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWLH 5
   |||||
Db 31 SYWLH 35

RESULT 3
US-09-741-843-8
; Sequence 8, Application US/09741843
; Patent No. US20020102254A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL LYM
; FILE REFERENCE: 018733/0996
; CURRENT APPLICATION NUMBER: US/09/741,843
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/127,902
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/690,102
; PRIOR FILING DATE: 1996-07-06
; PRIOR APPLICATION NUMBER: US 08/289,576
; PRIOR FILING DATE: 1994-08-12
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-741-843-8

Query Match
Best Local Similarity 100.0%; Score 34; DB 10; Length 116;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWLH 5
   |||||
Db 31 SYWLH 35

RESULT 4
US-09-741-843-9
; Sequence 9, Application US/09741843
; Patent No. US20020102254A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL LYM
; FILE REFERENCE: 018733/0996
; CURRENT APPLICATION NUMBER: US/09/741,843
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/127,902
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; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/690,102
; PRIOR FILING DATE: 1996-07-06
; PRIOR APPLICATION NUMBER: US 08/289,576
; PRIOR FILING DATE: 1994-08-12
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-741-843-9

Query Match
Best Local Similarity 100.0%; Score 34; DB 10; Length 116;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWLH 5
   |||||
Db 31 SYWLH 35

RESULT 5
US-09-894-839-4
; Sequence 4, Application US/09894839
; Publication No. US20030035800A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; APPLICANT: QU, Zhengxing
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/1049
; CURRENT APPLICATION NUMBER: US/09/894,839
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/155,107
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 60/013,709
; PRIOR FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-894-839-4

Query Match
Best Local Similarity 100.0%; Score 34; DB 11; Length 116;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWLH 5
   |||||
Db 31 SYWLH 35

RESULT 6
US-09-894-839-8
; Sequence 8, Application US/09894839
; Publication No. US20030035800A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; APPLICANT: QU, Zhengxing
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/1049
; CURRENT APPLICATION NUMBER: US/09/894,839
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/155,107
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 60/013,709
; PRIOR FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 8
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-894-839-8

Query Match
Best Local Similarity 100.0%; Score 34; DB 11; Length 116;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWLH 5
   |||||
Db 31 SYWLH 35

RESULT 7
US-09-894-839-21
; Sequence 21, Application US/09894839
; Publication No. US20030035800A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; APPLICANT: OU, Zhengxing
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/1049
; CURRENT APPLICATION NUMBER: US/09/894,839
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/155,107
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 60/013,709
; PRIOR FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-894-839-21

Query Match
Best Local Similarity 100.0%; Score 34; DB 11; Length 116;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWLH 5
   |||||
Db 31 SYWLH 35

RESULT 8
US-09-988-013A-4
; Sequence 4, Application US/09988013A
; Publication No. US20030103979A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-
; FILE REFERENCE: 18733/1082
; CURRENT APPLICATION NUMBER: US/09/988,013A
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 09/741,843
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/127,902
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/690,102
; PRIOR FILING DATE: 1996-07-06
; PRIOR APPLICATION NUMBER: US 08/289,576
; PRIOR FILING DATE: 1994-08-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
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; ORGANISM: Murinae gen. sp.
US-09-988-013A-4

Query Match
Best Local Similarity 100.0%; Score 34; DB 11; Length 116;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWLH 5
   |||||
Db 31 SYWLH 35

RESULT 9
US-09-988-013A-8
; Sequence 8, Application US/09988013A
; Publication No. US20030103979A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-
; FILE REFERENCE: 18733/1082
; CURRENT APPLICATION NUMBER: US/09/988,013A
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 09/741,843
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/127,902
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/690,102
; PRIOR FILING DATE: 1996-07-06
; PRIOR APPLICATION NUMBER: US 08/289,576
; PRIOR FILING DATE: 1994-08-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-988-013A-8

Query Match
Best Local Similarity 100.0%; Score 34; DB 11; Length 116;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWLH 5
   |||||
Db 31 SYWLH 35

RESULT 10
US-09-988-013A-9
; Sequence 9, Application US/09988013A
; Publication No. US20030103979A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-
; FILE REFERENCE: 18733/1082
; CURRENT APPLICATION NUMBER: US/09/988,013A
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 09/741,843
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/127,902
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/690,102
; PRIOR FILING DATE: 1996-07-06
; PRIOR APPLICATION NUMBER: US 08/289,576
; PRIOR FILING DATE: 1994-08-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 116
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TYPE: PRT
ORGANISM: Homo sapiens
US-09-988-013a-9

Query Match 100.0%; Score 34; DB 11; Length 116;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWLH 5
11111
DB 31 SYWLH 35

RESULT 11
US-09-995-693-2
Sequence 2, Application US/09995693
Patent No. US20020136721A1
GENERAL INFORMATION:
APPLICANT: Schwall, Ralph H.
Tabdor, Kelly H.

TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
Antagonists and Uses Thereof

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatlin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/995,693
FILING DATE: 29-Jun-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/952,235
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-995-693-2

Query Match 100.0%; Score 34; DB 10; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWLH 5
11111
DB 31 SYWLH 35

RESULT 12
US-10-232-408-2

Sequence 2, Application US/10232408
Publication No. US20030118587A1
GENERAL INFORMATION:
APPLICANT: Schwall, Ralph H.
Tabdor, Kelly H.

TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
Antagonists and Uses Thereof

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatlin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/232,408
FILING DATE: 03-Sep-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/669,971
FILING DATE: 05-Jul-2001

APPLICATION NUMBER: US/08/952,235
FILING DATE: 02-Jun-1995

ATTORNEY/AGENT INFORMATION:

NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600

REFERENCE/DOCKET NUMBER: P0938P1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-232-408-2

Query Match 100.0%; Score 34; DB 15; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWLH 5
11111
DB 31 SYWLH 35

RESULT 13
US-09-748-960-12

Sequence 12, Application US/09748960
Patent No. US20010046496A1

GENERAL INFORMATION:

APPLICANT: Bretman, Lee R.
APPLICANT: Fox, Judith A.

TITLE OF INVENTION: Method of Administering an Antibody
FILE REFERENCE: 1855.2007-001

CURRENT APPLICATION NUMBER: US/09/748,960
CURRENT FILING DATE: 2000-12-27

PRIOR APPLICATION NUMBER: US 09/550,082
PRIOR FILING DATE: 2000-04-14

NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 12

LENGTH: 5
TYPE: PRT
ORGANISM: Mus musculus

FEATURE:
NAME/KEY: SITE

LOCATION: (1)...(5)

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; OTHER INFORMATION: CDRL of the heavy chain of antibodies Act-1 and
; OTHER INFORMATION: LDP-02
US-09-748-960-12

Query Match          94.1%; Score 32; DB 9; Length 5;
Best Local Similarity 80.0%; Pred. No. 5.2e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      1 SYWLH 5
        |||:|
Db       1 SYWMH 5

RESULT 14
US-10-233-996-53
; Sequence 53, Application US/10233996
; Publication No. US20030096976A1
; GENERAL INFORMATION:
; APPLICANT: HONG, HYO JEONG
; APPLICANT: PARK, SUNG SUP
; APPLICANT: KANG, YOUNG JUN
; APPLICANT: KANG, CHANG-YUL
; APPLICANT: YOON, SUNG KWAN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES LB-00503 AND LB-00506 SPECIFIC FOR HUMAN 4-1
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING SAID HUMANIZED ANTIBODIES
; FILE REFERENCE: 4363-0102P
; CURRENT APPLICATION NUMBER: US/10/233,996
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 32
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: Humanized antibody heavy chain directed against a human 4-1BB
; FEATURE:
; OTHER INFORMATION: molecule
; NAME/KEY: MISC_FEATURE
; LOCATION: (17)..(18)
; OTHER INFORMATION: X - any amino acid, unknown or other
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (21)..(22)
; OTHER INFORMATION: X - any amino acid, unknown or other
US-10-233-996-53

Query Match          94.1%; Score 32; DB 15; Length 32;
Best Local Similarity 80.0%; Pred. No. 75;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      1 SYWLH 5
        |||:|
Db       1 SYWMH 5

RESULT 15
US-09-867-550-498
; Sequence 498, Application US/09867550
; Patent No. US20020082206A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Mehraban, Fuad,
; APPLICANT: Conley, Pamela
; APPLICANT: Law, Debbie
; APPLICANT: Topper, James
; TITLE OF INVENTION: No. US20020082206A1 Polynucleotides from Atherogenic Cells and
; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 21402-013 (Cura-313)
; CURRENT APPLICATION NUMBER: US/09/867,550
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: USSN 60/208,427
; PRIOR FILING DATE: 2000-05-30
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; NUMBER OF SEQ ID NOS: 2125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 498
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (57)
; OTHER INFORMATION: wherein Xaa may be any one of
US-09-867-550-498

Query Match          94.1%; Score 32; DB 9; Length 83;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      1 SYWLH 5
        |||:|
Db       69 SYWMH 73

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Job time : 3.58621 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 19:07:11 ; Search time 1.86207 Seconds

(without alignments)
258.231 Million cell updates/sec

Title: US-09-988-013a-4_COPY_31_35

Perfect score: 34

Sequence: 1 SYWLH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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1: PIR_76:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	90	2 D86690	hypothetical prote
2	34	100.0	196	2 T01982	tumor related prot
3	34	100.0	317	2 E86264	protein R3F19.7 [i
4	34	100.0	482	2 AF1120	conserved hypotnet
5	34	100.0	494	2 A11480	protein T08G11.4 [
6	34	100.0	495	2 B87869	hypothetical prote
7	34	100.0	566	2 T24696	probable peptide s
8	34	100.0	4924	2 T50176	ig heavy chain v r
9	32	94.1	35	2 S46472	ig heavy chain v r
10	32	94.1	50	2 S26941	ig heavy chain v r
11	32	94.1	56	2 E49038	ig heavy chain v r
12	32	94.1	58	2 D49038	ig heavy chain v r
13	32	94.1	69	2 D25150	ig heavy chain v r
14	32	94.1	71	2 PH1136	ig heavy chain v r
15	32	94.1	76	2 PH1153	ig heavy chain v r
16	32	94.1	80	2 F28833	ig heavy chain v r
17	32	94.1	86	2 A25150	ig heavy chain v r
18	32	94.1	90	2 PH1152	ig heavy chain v r
19	32	94.1	94	2 J10078	ig heavy chain v r
20	32	94.1	94	2 PH1142	ig heavy chain v r
21	32	94.1	94	2 S42185	ig gamma chain v r
22	32	94.1	96	2 S17616	ig heavy chain v r
23	32	94.1	97	2 PH1137	ig heavy chain v r
24	32	94.1	98	2 P10121	ig heavy chain v r
25	32	94.1	98	2 PH1128	ig heavy chain v r
26	32	94.1	98	2 PH1129	ig heavy chain v r
27	32	94.1	98	2 PH1131	ig heavy chain v r
28	32	94.1	98	2 PH1134	ig heavy chain v r
29	32	94.1	98	2 PH1138	ig heavy chain v r

30	32	94.1	98	2 PH1139	ig heavy chain v r
31	32	94.1	98	2 PH1141	ig heavy chain v r
32	32	94.1	98	2 PH1147	ig heavy chain v r
33	32	94.1	98	2 PH1149	ig heavy chain v r
34	32	94.1	98	2 PH1150	ig heavy chain v r
35	32	94.1	98	2 PH1154	ig heavy chain v r
36	32	94.1	98	2 PH1156	ig heavy chain v r
37	32	94.1	98	2 PH1157	ig heavy chain v r
38	32	94.1	98	2 PH1164	ig heavy chain v r
39	32	94.1	98	2 PH1105	ig heavy chain v r
40	32	94.1	98	2 PH1108	ig heavy chain v r
41	32	94.1	98	2 PH1111	ig heavy chain v r
42	32	94.1	98	2 PH1114	ig heavy chain v r
43	32	94.1	98	2 PH1118	ig heavy chain v r
44	32	94.1	98	2 PH1119	ig heavy chain v r
45	32	94.1	98	2 PH1122	ig heavy chain v r

ALIGNMENTS

RESULT 1

D86690
hypothetical protein yfbc [imported] - Lactococcus lactis subsp. lactis (strain IL140
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C:Accession: D86690
R:Bohlin, A.; Winkler, P.; Manger, S.; Jallion, O.; Malame, K.; Weissenbach, J.; Eh
Genome Res. 11, 731-753, 2001
A>Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: D86690
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <STO>
A:Cross-references: GB:A005176; PID:g12723408; PIDN:AAK04622.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: yfbc

Query Match 100.0%; Score 34; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
DB 17 SYWLH 21

RESULT 2

T01982
tumor related protein HR4 - (common tobacco)
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 19-May-2000
C:Accession: T01982
R:Nakamura, C.; Nishimura, N.; Mishima, M.; Ueda, T.; Onaka, T.; Tsvetanov, S.; Takum
submitted to the EMBL Data Library, January 1998
A:Description: Molecular cloning and characterization of cDNAs preferentially express
A:Reference number: Z14477
A:Accession: T01982
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-196 <NAK>
A:Cross-references: EMBL:AF043554; NID:g2852376; PID:g2852377
A:Experimental source: tissue-type hairy root tumor; crown gall tumor
C:Genetics:
A:Gene: HR4
C:Superfamily: hydroxyproline-rich glycoprotein

Query Match 100.0%; Score 34; DB 2; Length 196;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
|||||
Db 153 SYWLH 157

RESULT 3

E86264
protein F3F19.7 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C/Accession: E86264
R/Neologs: A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Cln, C.W.; Chung, M.K.; Comp, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
anen, N.F.; Hughes, B.; Hutzler, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, J.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Martelli,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A86141; MUID:21016719; PMID:11130712
A/Accession: E86264
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-317 <STO>
A/Cross-references: GB:AE005172; NID:g4850388; PIDN:AAD31058.1; GSPDB:GN00141
C/Genetics:
A:Gene: F3F19.7
A:Map position: 1

Query Match 100.0%; Score 34; DB 2; Length 317;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
|||||
Db 289 SYWLH 293

RESULT 4

AF1120
conserved hypothetical protein homolog lmo0365 [imported] - Listeria monocytogenes (str
C/Species: Listeria monocytogenes
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C/Accession: AF1120
R/Glaeser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlian, K.D.; Fsihl, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A/Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkak, G.; Madueno, E.; Maltournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A/Title: Comparative genomics of Listeria species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669
A/Accession: AF1120
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-482 <GLA>
A/Cross-references: GB:NC_003210; PIDN:CAC98444.1; PID:g16409743; GSPDB:GN00177
A/Experimental source: strain EGD-e
C/Genetics:
A:Gene: lmo0365
C/Superfamily: conserved hypothetical protein ywbl

Query Match 100.0%; Score 34; DB 2; Length 482;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
|||||
Db 314 SYWLH 318

RESULT 5

A11480
conserved hypothetical protein homolog lln0384 [imported] - Listeria innocua (strain
C/Species: Listeria innocua
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C/Accession: A11480
R/Glaeser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlian, K.D.; Fsihl,
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A/Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkak, G.; Madueno, E.; Maltournam, A.;
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
A/Title: Comparative genomics of Listeria species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669
A/Accession: A11480
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-494 <GLA>
A/Cross-references: GB:AL592022; PIDN:CAC95617.1; PID:g16412813; GSPDB:GN00178
A/Experimental source: strain Clp11262
C/Genetics:
A:Gene: lln0384
C/Superfamily: conserved hypothetical protein ywbl

Query Match 100.0%; Score 34; DB 2; Length 494;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
|||||
Db 314 SYWLH 318

RESULT 6

B87869
protein T08G11.4 [imported] - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C/Accession: B87869
R/anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A/Title: Genome sequence of the nematode C. elegans: a platform for investigating blo
A/Reference number: A75000; MUID:99069613; PMID:9851916
A/Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C-
A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
A/Accession: B87869
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-495 <STO>
A/Cross-references: GB:chr_1; PIDN:CAB02307.1; PID:g3879758; GSPDB:GN00019; CESP:T08G
C/Genetics:
A:Gene: T08G11.4
A:Map position: 1

Query Match 100.0%; Score 34; DB 2; Length 495;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
|||||
Db 62 SYWLH 66

RESULT 7

T24696
hypothetical protein T08G11.4 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T24696
R/Dobson, R.
submitted to the EMBL Data Library, September 1996
A/Reference number: Z19925
A/Accession: T24696

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-566 <WID>
A:Cross-references: EMBL:Z80220; PIDN:CA802307.2; GSPDB:GN00019; CESP:T08G11.4
A:Experimental source: clone T08G11
C:Genetics:
A:Gene: CESP:T08G11.4
A:Map position: 1
A:introns: 47/2; 86/1; 177/3; 235/3; 282/2; 415/1; 521/3

Query Match 100.0%; Score 34; DB 2; Length 566;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
|||||
Db 133 SYWLH 137

RESULT 8

T50176
probable peptide synthetase [imported] - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 01-Dec-2000
C:Accession: T50176
R:Badcock, K.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, February 2000
A:Reference number: Z25044
A:Accession: T50176
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4924 <BAD>
A:Cross-references: EMBL:AL138854; PIDN:CA872227.1; GSPDB:GN00066; SPDB:SPAC23G3.02c
A:Experimental source: strain 972h(-); cosmid c23G3
C:Genetics:
A:Gene: SPDB:SPAC23G3.02c
A:Map position: 1
A:introns: 2125/1
C:Superfamily: acetate-CoA ligase homology; acyl carrier protein homology
C:Keywords: carrier protein; phosphopantetheine; phosphoprotein
F:260-697/Domain: acetate-CoA ligase homology <ACLI>
F:2772-3226/Domain: acetate-CoA ligase homology <ACLI2>
F:4405-4474/Domain: acyl carrier protein homology <ACP>
F:2206-3288/Binding site: phosphopantetheine (Ser) (covalent) #status predicted

Query Match 100.0%; Score 34; DB 2; Length 4924;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
|||||
Db 1794 SYWLH 1798

RESULT 9

S46472
Ig heavy chain V region (DA-8) - human
C:Species: Homo sapiens (man)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C:Accession: S46472
R:Cook, G.P.; Tomlinson, I.M.; Walter, G.; Rietman, H.; Carter, N.P.; Bulwela, L.; Wit
Nature Genet. 7, 162-168, 1994
A:Title: A map of the human immunoglobulin V(H) locus completed by analysis of the telom
A:Reference number: S46460; MUID:95004581; PMID:7920635
A:Accession: S46472
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-35 <COO>
A:Cross-references: EMBL:Z30082; NID:9505468; PIDN:CAA82900.1; PID:91335183
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 94.1%; Score 32; DB 2; Length 35;

Best Local Similarity 80.0%; Pred. No. 15;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
|||||
Db 4 SYWLH 8

RESULT 10

S26941
Ig heavy chain V region (DP-80) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 17-Mar-1999
C:Accession: S26941
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups o
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26941
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-50 <TOX>
A:Cross-references: EMBL:Z14076
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 94.1%; Score 32; DB 2; Length 50;
Best Local Similarity 80.0%; Pred. No. 21;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
|||||
Db 1 SYWLH 5

RESULT 11

E49038
Ig lambda chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: E49038
R:Weiss, U.; Zobelet, R.; Rajewsky, K.
Eur. J. Immunol. 22, 511-517, 1992
A:Title: Accumulation of somatic mutants in the B cell compartment after primary immu
A:Reference number: A49038; MUID:92164733; PMID:1537385
A:Accession: E49038
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-56 <WEI>
A:Cross-references: GB:S85736; NID:g246322; PIDN:AAB21563.1; PID:g246323
A:Experimental source: spleen
A:Note: sequence extracted from NCBI backbone (NCBIN:85736, NCBI:P:85804)
C:Keywords: heterotetramer; immunoglobulin

Query Match 94.1%; Score 32; DB 2; Length 56;
Best Local Similarity 80.0%; Pred. No. 23;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
|||||
Db 10 SYWLH 14

RESULT 12

D49038
Ig lambda chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: D49038
R:Weiss, U.; Zobelet, R.; Rajewsky, K.
Eur. J. Immunol. 22, 511-517, 1992
A:Title: Accumulation of somatic mutants in the B cell compartment after primary immu

A:Reference number: A49038; MUID:92164733; PMID:1537385
 A:Accession: D49038
 A>Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-58 <ME1>
 A:Cross-references: GB:S85735; NID:9246320; PIDN:AA821562.1; PID:9246321
 A:Experimental source: spleen
 A>Note: sequence extracted from NCBI backbone (NCBIN:85735, NCBIPI:85802)
 C:Keywords: heterotetramer; immunoglobulin

Query Match 94.1%; Score 32; DB 2; Length 58;
 Best Local Similarity 80.0%; Pred. No. 24;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
 |||:|
 DB 12 SYWMH 16

RESULT 13

D25150
 Ig heavy chain V region (AC38 260.2) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 16-Aug-1996
 C:Accession: D25150
 R:Didrop, R.; Boyens, J.; Stekevitz, M.; Beyreuther, K.; Rajewsky, K.
 EMBL J. 3, 517-523, 1984
 A:Title: A V region determinant (idiotope) expressed at high frequency in B lymphocytes
 A:Reference number: A91000; MUID:84182519; PMID:6201362
 A:Accession: D25150
 A:Molecule type: protein
 A:Residues: 1-69 <DIL>
 A:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 94.1%; Score 32; DB 2; Length 69;
 Best Local Similarity 80.0%; Pred. No. 28;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
 |||:|
 DB 19 SYWMH 23

RESULT 14

PH1136
 Ig heavy chain V region (clone V2075.1) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PH1136
 R:Schlitz, B.; Rajewsky, K.
 J. Exp. Med. 176, 427-438, 1992
 A:Title: Natural occurrence and origin of somatically mutated memory B cells in mice.
 A:Reference number: PH1105; MUID:92364545; PMID:1500855
 A:Accession: PH1136
 A:Molecule type: DNA
 A:Residues: 1-71 <SCH>
 A:Experimental source: B cell
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 94.1%; Score 32; DB 2; Length 71;
 Best Local Similarity 80.0%; Pred. No. 29;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
 |||:|
 DB 4 SYWMH 8

RESULT 15

PH1153
 Ig heavy chain V region (clone 43F.1) - mouse (fragment)

C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PH1153
 R:Schlitz, B.; Rajewsky, K.
 J. Exp. Med. 176, 427-438, 1992
 A:Title: Natural occurrence and origin of somatically mutated memory B cells in mice.
 A:Reference number: PH1105; MUID:92364545; PMID:1500855
 A:Accession: PH1153
 A:Molecule type: DNA
 A:Residues: 1-76 <SCH>
 A:Experimental source: B cell
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 94.1%; Score 32; DB 2; Length 76;
 Best Local Similarity 80.0%; Pred. No. 31;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
 |||:|
 DB 9 SYWMH 13

Search completed: October 7, 2003, 19:21:50
 Job time : 2.86207 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 19:03:46 ; Search time 1.01724 Seconds

(without alignments)
231.148 Million cell updates/sec

Title: US-09-988-013a-4_COPY_31_35.

Perfect score: 34

Sequence: 1 SYWLH 5

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SwIsProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	94.1	117	1 HV04_MOUSE	P01748 mus musculus
2	32	94.1	117	1 HV06_MOUSE	P01750 mus musculus
3	32	94.1	117	1 HV09_MOUSE	P01753 mus musculus
4	32	94.1	117	1 HV10_MOUSE	P01754 mus musculus
5	32	94.1	117	1 HV10_MOUSE	P06328 mus musculus
6	32	94.1	120	1 HV50_MOUSE	P06329 mus musculus
7	32	94.1	139	1 HV07_MOUSE	P01751 mus musculus
8	32	94.1	449	1 VNSS_INSVN	O01811 impatiens n
9	32	94.1	464	1 VNSS_TSMV1	P26002 tomato spot
10	32	94.1	467	1 VNSS_TSMV1	P26003 tomato spot
11	32	94.1	3080	1 POLG_ZYMYC	P18479 z genome po
12	32	94.1	3083	1 POLG_ZYMYR	O089330 z genome po
13	32	94.1	3083	1 POLG_ZYMYR	O36979 z genome po
14	31	91.2	309	1 YESP_BACSU	O31519 bacillus su
15	31	91.2	370	1 TAM2_HUMAN	O15035 homo sapien
16	31	91.2	373	1 TAM1_HUMAN	O15629 homo sapien
17	31	91.2	466	1 SYC_BACHD	Q48841 bacillus ha
18	31	91.2	473	1 PEPD_LACSK	Q48841 lactobacilli
19	30	88.2	137	1 BFR_NITWI	P13570 nitrobacter
20	30	88.2	137	1 YH97_MERTH	O37825 methanobact
21	30	88.2	161	1 BFR_BROME	P49944 brucella me
22	30	88.2	166	1 OV22_ONCVO	P29779 onchocerca
23	30	88.2	174	1 OV21_ONCVO	P29778 onchocerca
24	30	88.2	175	1 VIRR_AGRTR	O52278 agrobacteri
25	30	88.2	247	1 Y125_RICPR	P41087 rickettsia
26	30	88.2	264	1 FLIR_SALTY	P54702 salmonella
27	30	88.2	287	1 YISR_BACSU	P40331 bacillus su
28	30	88.2	301	1 MTAL_SORFI	O13596 sordaria fi
29	30	88.2	304	1 TRUB_PSEAE	P72154 pseudomonas
30	30	88.2	306	1 MTAL_SORMA	O42837 sordaria ma
31	30	88.2	372	1 B4G2_HUMAN	O60909 h beta-1.4-
32	30	88.2	372	1 G391_DROME	P58956 drosophila
33	30	88.2	400	1 SCW_DROME	P44631 drosophila

34	30	88.2	414	1 YAFI_SALTY	P37722 salmonella
35	30	88.2	466	1 SYC_BACSU	O06752 bacillus su
36	30	88.2	466	1 SYC_CLOPE	O6xh52 clostridium
37	30	88.2	469	1 SYC1_MYCTU	P56862 mycobacteri
38	30	88.2	473	1 SYC1_MYCLE	P57990 mycobacteri
39	30	88.2	473	1 SYC1_NEIMB	O9jx66 neisseria m
40	30	88.2	474	1 SYC1_CHLPR	O92634 chlamydia p
41	30	88.2	475	1 SYC1_AERPE	O9ybk6 aeropyrum p
42	30	88.2	475	1 SYC1_CHLMU	O9ple0 chlamydia m
43	30	88.2	476	1 SYC1_PYRHO	O58370 pyrococcus
44	30	88.2	477	1 SYC1_CHLPR	O84787 chlamydia t
45	30	88.2	477	1 SYC1_PYRAB	O9uyv2 pyrococcus

ALIGNMENTS

RESULT 1				
HV04_MOUSE	STANDARD;	PRT;	117 AA.	
ID HV04_MOUSE				
AC P01748;				
DT 21-JUL-1986 (Rel. 01, Created)				
DT 21-JUL-1986 (Rel. 01, last sequence update)				
DE 15-JUL-1999 (Rel. 38, last annotation update)				
DE Ig heavy chain V region 23 precursor.				
OS Mus musculus (Mouse).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX NCBI_TaxID:10090;				
RN [1]				
RP SEQUENCE FROM N.A.				
RC STRAIN=C57BL/6;				
RX MEDLINE=81234548; PubMed=6788376;				
RA Bothwell A.L.M., Paskind M., Reih M., Imanishi-Kari T., Rajewsky K.,				
RA Baltimore D.;				
RT "Heavy chain variable region contribution to the NPb family of				
RT antibodies: somatic mutation evident in a gamma 2a variable region."				
RL Cell 24:625-637(1981).				
CC -1- MISCELLANEOUS: THIS GERM LINE GENE BELONGS TO A SET OF CLOSELY				
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.				
DR PIR: A02030; HWS23.				
DR HSSP: P01810; 2REJ.				
DR CHAIN				
DR InterPro: IPR007110; Ig-like.				
DR InterPro: IPR003006; Ig_MHC.				
DR InterPro: IPR003596; Ig_V.				
DR Pfam: PF00047; Ig; 1.				
DR SMART: SM00406; IgV; 1.				
DR PROSITE: PS50835; IG_LIKE; 1.				
KW Immunoglobulin V region; Signal.				
FT SIGNAL	1	19		
FT CHAIN	20	117	IG HEAVY CHAIN V REGION 23.	
FT DOMAIN	20	49	FRAMEWORK-1.	
FT DOMAIN	50	54	COMPLEMENTARITY-DETERMINING-1.	
FT DOMAIN	55	68	FRAMEWORK-2.	
FT DOMAIN	69	85	COMPLEMENTARITY-DETERMINING-2.	
FT DOMAIN	86	117	FRAMEWORK-3.	
FT DISULFID	41	115	BY SIMILARITY.	
FT NON_TER	117	117		
SQ SEQUENCE	117 AA;	12772 MM;	C530F829C906F69B CRC64;	
Query Match		94.1%;	Score 32; DB 1; Length 117;	
Best Local Similarity		80.0%;	Pred. No. 22;	
Matches	4; Conservative	1; Mismatches	0; Indels	0; Gaps
QY	1 SYWLN 5	-		
DB	50 SYWMH 54			
RESULT 2				
HV06_MOUSE	STANDARD;	PRT;	117 AA.	
ID HV06_MOUSE				
AC P01750;				

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DR 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 102 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR PIR: A02032; HVMS02.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR007110; Ig_1like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 102.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117
SO SEQUENCE 117 AA; 12867 MW; 740A65DD851FCA8C CRC64;

Query Match
Best Local Similarity 94.1%; Score 32; DB 1; Length 117;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
DB 50 SYWLH 54

RESULT 3
HY09_MOUSE STANDARD; PRT; 117 AA.
AC P01753; P11271;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 186-1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR PIR: D90809; HVMS61.
DR HSSP: P01810; 2FBJ.

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DR InterPro: IPR007110; Ig_1like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117
SO SEQUENCE 117 AA; 12890 MW; 16191A08CB17F5A CRC64;

Query Match
Best Local Similarity 94.1%; Score 32; DB 1; Length 117;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
DB 50 SYWLH 54

RESULT 4
HY10_MOUSE STANDARD; PRT; 117 AA.
AC P01754; P11270;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig heavy chain V region 145 precursor.
GN IGH-VJ558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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CC -----
DR EMBL: J00533; AAA38602.1; -.
DR PIR: G90809; HVMS45.
DR HSSP: P01810; 2FBJ.
DR MGD: MGI:96486; Igh-VJ558.
DR InterPro: IPR007110; Ig_1like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 145.

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FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT NON_TER 117 117
 SO SEQUENCE 117 AA; 12921 MW; D37DE8AF543E996 CRC64;

Query Match 94.1%; Score 32; DB 1; Length 117;
 Best Local Similarity 80.0%; Pred. No. 22;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
 DB 50 SYWLH 54

RESULT 5
 HV49_MOUSE
 ID HV49_MOUSE STANDARD; PRT; 117 AA.
 AC P06328;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DE 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region VH558 B4 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8509340; PubMed=2578321;
 RA Yancopoulos G.D., Alt F.W.;
 RT "developmentally controlled and tissue-specific expression of
 RT unarranged VH gene segments.";
 RL Cell 40:371-281(1985).
 CC -----
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 CC -----
 CC EMBL; M13788; AAA38506.1; -.
 DR PIR; A02035; MEMSB4.
 DR HSSP; P01810; 2PBJ.
 DR InterPro: IPR007110; Ig_Like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 B4.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 86 117 COMPLEMENTARITY-DETERMINING-2.
 FT DISULFID 41 115 FRAMEWORK-3.
 FT NON_TER 117 117 BY SIMILARITY.
 SO SEQUENCE 117 AA; 12834 MW; B8862FAC67ABD345 CRC64;

Query Match 94.1%; Score 32; DB 1; Length 117;
 Best Local Similarity 80.0%; Pred. No. 22;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 SYWLH 5
 DB 50 SYWLH 54

RESULT 6
 HV50_MOUSE
 ID HV50_MOUSE STANDARD; PRT; 120 AA.
 AC P06329;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region AC38 15.3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=84182519; PubMed=6201362;
 RA Dildrop R., Bovens J., Stekevitz M., Beyreuther K., Rajewsky K.;
 RT "A V region determinant (idiotope) expressed at high frequency in B
 RT lymphocytes is encoded by a large set of antibody structural genes.";
 RL EMBO J. 3:517-523(1984).
 DR PIR; A02037; MEMS15.
 DR HSSP; P01810; 2PBJ.
 DR InterPro: IPR007110; Ig_Like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 98 D SEGMENT.
 FT DOMAIN 99 105 V SEGMENT.
 FT DOMAIN 106 120 J SEGMENT.
 FT DISULFID 22 96 BY SIMILARITY.
 FT NON_TER 120 120
 SO SEQUENCE 120 AA; 13311 MW; 914453F426F09834 CRC64;

Query Match 94.1%; Score 32; DB 1; Length 120;
 Best Local Similarity 80.0%; Pred. No. 22;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 SYWLH 5
 DB 31 SYWLH 35

RESULT 7
 HV07_MOUSE
 ID HV07_MOUSE STANDARD; PRT; 139 AA.
 AC P01751; P01752;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region BI-8/186-2 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=C57BL/6;
 RX MEDLINE=81234548; PubMed=6788376;
 RA Bochtell A.L.M., Paekind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.;
 RT "Heavy chain variable region contribution to the NPB family of
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";
 RL Cell 24:625-637(1981).
 CC -1- MISCELLANEOUS: THE BI-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
 CC MAKING ANTIBODIES TO THE HAPPEN (4-HYDROXY-3-NITROPHENYL)ACETYL
 CC (NPB ANTIBODIES).
 CC -----
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CC EMBL: J00529; AAA38170.1; -

DR PIR: A90809; MHMS18.

DR PDB: 1AGU; 27-MAY-98.

DR PDB: 1AGW; 15-JUL-98.

DR InterPro: IPR007110; Ig-1like.

DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003596; Ig_v.

DR Pfam: PF00047; Ig_1.

DR SMART: SM00406; IGV; 1.

DR PROSITE: PS50835; IG_LIKE; 1.

KW Immunoglobulin V region; Signal; 3D-structure.

FT SIGNAL 1 19 IG HEAVY CHAIN V REGION BI-8/186-2.

FT CHAIN 20 139 FRAMEWORK-1.

FT DOMAIN 20 49 FRAMEWORK-1.

FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 55 68 FRAMEWORK-2.

FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 86 117 FRAMEWORK-3.

FT DOMAIN 118 134 D SEGMENT.

FT DOMAIN 125 139 H2 SEGMENT.

FT DISULFID 41 115 BY SIMILARITY.

FT NON_TER 139 139

SEQUENCE 139 AA; 15419 MW; 1B57DD4FDC9F465 CRC64;

Query Match 94.1%; Score 32; DB 1; Length 139;

Best Local Similarity 80.0%; Pred. No. 26;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5

Db 50 SYWMH 54

RESULT 8

VNSS_INSVN STANDARD; PRT; 449 AA.

ID VNSS_INSVN 01811;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 01-JUN-1994 (Rel. 29, Last annotation update)

DE Nonstructural protein NS-S.

GN NSS.

OS Impatiens necrotic spot virus (strain NL-07) (INSV).

OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Tosopovirus.

OX NCBI_TaxID-31622;

RN RN

RP SEQUENCE FROM N.A.

RX MEDLINE-92331780; PubMed-1385787;

RA de Haan P., de Avila A.C., Kormelink R., Westerbroek A.,

RA Giesen J.J., Peters D., Goldbach R.;

RT "The nucleotide sequence of the S RNA of Impatiens necrotic spot

RT virus, a novel tospovirus."

RL FEBS Lett. 306:27-32(1992).

CC -1- FUNCTION: FORMS FILAMENTOUS INCLUSION BODIES.

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CC EMBL: X66972; CAA47382.1; -

DR PIR: S23158; S23158.

DR InterPro: IPR004915; Bunya_NS-S-2.

DR Pfam: PF03231; Bunya_NS-S-2; 1.

KW Nonstructural protein.

SQ SEQUENCE 449 AA; 51197 MW; C46AC1372B11ACAS CRC64;

Query Match 94.1%; Score 32; DB 1; Length 449;

Best Local Similarity 80.0%; Pred. No. 79;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5

Db 29 SYWMH 33

RESULT 9

VNSS_TSWVL STANDARD; PRT; 464 AA.

ID VNSS_TSWVL 26002;

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 01-JUN-1994 (Rel. 29, Last annotation update)

DE Nonstructural protein NS-S.

GN NSS.

OS Tomato spotted wilt virus (strain Brazilian Br-01) (TSWV).

OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Tosopovirus.

OX NCBI_TaxID-36413;

RN RN

RP SEQUENCE FROM N.A.

RX MEDLINE-90264829; PubMed-1693160;

RA de Haan P., Wagemakers L., Peters D., Goldbach R.;

RT "The S RNA segment of tomato spotted wilt virus has an ambisense

RT character".

RL J. Gen. Virol. 71:1001-1007(1990).

CC -1- FUNCTION: FORMS FILAMENTOUS INCLUSION BODIES.

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CC EMBL: D00645; BAA00540.1; -

DR PIR: J00547; MNYTWC.

DR InterPro: IPR004915; Bunya_NS-S-2.

DR Pfam: PF03231; Bunya_NS-S-2; 1.

KW Nonstructural protein.

SQ SEQUENCE 464 AA; 52448 MW; AE5519179F9EF377 CRC64;

Query Match 94.1%; Score 32; DB 1; Length 464;

Best Local Similarity 80.0%; Pred. No. 82;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5

Db 29 SYWMH 33

RESULT 10

VNSS_TSWVL STANDARD; PRT; 467 AA.

ID VNSS_TSWVL 26003;

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 01-JUN-1994 (Rel. 29, Last annotation update)

DE Nonstructural protein NS-S.

GN NSS.

OS Tomato spotted wilt virus (strain Bulgarian L3) (TSWV).

OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Tosopovirus.

OX NCBI_TaxID-36415;

RN RN

RP SEQUENCE FROM N.A.

RX MEDLINE-91132150; PubMed-1993884;

RA Mais E., Ivanova L., Breyel E., Adam G.;

RT "Cloning and sequencing of the S RNA from a Bulgarian isolate of
RT tomato spotted wilt virus.";
RT J. Gen. Virol. 72:461-464(1991).
CC -1- FUNCTION: FORMS FILAMENTOUS INCLUSION BODIES.
CC -----
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CC -----
CC EMBL: D13926; BAA03024.1; -.
DR PIR: J00954; MNVWL.
DR InterPro: IPR004915; Bunya_NS-S_2.
DR Pfam: PF03231; Bunya_NS-S_2; 1.
KM Nonstructural protein.
SQ SEQUENCE 467 AA; 52413 MW; 38E5CA4E802DB6DC CRC64;

Query Match 94.1%; Score 32; DB 1; Length 467;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWLH 5
Db 29 SYWLH 33
|||||

RESULT 11
POLG_ZYMVC STANDARD; PRT; 3080 AA.
ID POLG_ZYMVC
AC P18479; Q89334;
DT 01-NOV-1990 (Rel. 16, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Genome polypeptide [contains: N-terminal protein (PI); Helper
DE component proteinase (EC 3.4.22.45) (HC-Pro); protein P3; 6 kDa
DE protein 1 (P1); Cytoplasmic inclusion protein (CI); 6 kDa protein 2
DE (6K2); Genome-linked protein (VP6); Nuclear inclusion protein A (NI-A)
DE (NIA) (EC 3.4.22.44) (49 kDa proteinase) (49 kDa-Pro); Nuclear
DE inclusion protein B (NI-B) (NIB) (RNA-directed RNA polymerase)
DE (EC 2.7.7.48); Coat protein (CP)].
OS Zucchini yellow mosaic virus (Strain California) (ZYMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Polyviridae;
OC Polyviruses.
OX NCBI_TaxID=117128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9514658; PubMed=7844540;
RA Wisler G.C., Purcifull D.E., Hiebert E.;
RT "Characterization of the PI protein and coding region of the zucchini
RT yellow mosaic virus.";
RL J. Gen. Virol. 76:37-45(1995).
RN [2]
RP SEQUENCE OF 2694-3080 FROM N.A.
RX MEDLINE=90236320; PubMed=2185142;
RA Gal-On A., Antignus Y., Rosner A., Raccach B.;
RT "Nucleotide sequence of the zucchini yellow mosaic virus
RT capsid-encoding gene and its expression in Escherichia coli.";
RL Gene 87:273-277(1990).
CC -1- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHID
CC TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.
CC -1- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT
CC MAY BE INVOLVED IN REPLICATION.
CC -1- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
CC further restricted by preferences for glutamyl bonds, and activity is
CC that vary with the species of polyviruses, e.g. Glu-Xaa-Xaa-Tyr-Xaa-
CC Gln(Ser or Gly) for the enzyme from tobacco etch virus. The
CC natural substrate is the viral polypeptide, but other proteins and
CC oligopeptides containing the appropriate consensus sequence are
CC also cleaved.

CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate +
CC (RNA)(N).
CC -1- CATALYTIC ACTIVITY: Hydrolyzes a gly-l-gly bond at its own C-
CC terminus, commonly in the sequence -Tyr-Xaa-Val-Gly-l-gly, in the
CC processing of the polyviral polypeptide.
CC -1- PFM: VP6 IS COVALENTLY LINKED TO THE GENOMIC RNA
CC POLYPEPTIDE WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
CC INDIVIDUAL PROTEINS.
CC -1- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
CC -1- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.
CC -1- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPEPTIDE FAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L31350; AAA65559.1; -.
DR PIR: M35095; AAA48511.1; -.
DR HSSP: P27958; 1HE1.
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR001650; Helicase_C.
DR InterPro: IPR001730; Peptidase_C4.
DR InterPro: IPR001456; Peptidase_C6.
DR InterPro: IPR001592; Poly_coat.
DR InterPro: IPR002540; Poly_P1.
DR InterPro: IPR007095; RNA_pol_DS_PS.
DR InterPro: IPR001205; RNA_pol_P3D.
DR InterPro: IPR007094; RNA_pol_PSVLr.
DR Pfm: PR00271; helicase_C_1.
DR Pfm: PF00863; Peptidase_C4; 1.
DR Pfm: PF00851; Peptidase_C6; 1.
DR Pfm: PF00767; Poly_coat; 1.
DR Pfm: PF01577; Poly_P1; 1.
DR Pfm: PF00680; RNA_dep_RNA_pol; 1.
DR PRINTS: PR00966; NTPOTPYRASE.
DR SMART: SM00487; DEXDC; 1.
DR SMART: SM00490; HELICG; 1.
KM Hydrolyase; Transferase; Thiol protease; RNA-directed RNA polymerase;
KM Coat protein; Polypeptide; Covalent protein-RNA linkage; Helicase;
KM ATP-binding.
FT CHAIN 1 304 N-TERMINAL PROTEIN.
FT CHAIN 305 766 HELPER COMPONENT PROTEINASE.
FT CHAIN 767 ? PROTEIN P3.
FT CHAIN ? 1164 6 KDA PROTEIN 1.
FT CHAIN 1165 1798 CYTOPLASMIC INCLUSION PROTEIN.
FT CHAIN 1799 1851 6 KDA PROTEIN 2.
FT CHAIN 1852 2041 GENOME-LINKED PROTEIN.
FT CHAIN 2042 2284 NUCLEAR INCLUSION PROTEIN A.
FT CHAIN 2285 2801 NUCLEAR INCLUSION PROTEIN B.
FT CHAIN 2802 3080 COAT PROTEIN.
FT NP_BIND 1249 1256 ATP (POTENTIAL).
FT CONFLICT 2694 2695 LE -> ST (IN REF. 2).
FT CONFLICT 2699 2701 IVS -> LFP (IN REF. 2).
FT CONFLICT 2811 2811 A -> T (IN REF. 2).
FT CONFLICT 2811 2811 G -> S (IN REF. 2).
FT CONFLICT 2834 2834
SQ SEQUENCE 3080 AA; 350624 MW; 2A1E501DEA6B9F73 CRC64;

Query Match 94.1%; Score 32; DB 1; Length 3080;
Best Local Similarity 80.0%; Pred. No. 5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWLH 5
Db 2179 SYWLH 2183
|||||

```

RESULT 12
POLG_ZYMVR          STANDARD:          PRT: 3083 AA.
ID POLG_ZYMVR
AC 089330;
DT 15-DEC-1998 (rel. 37, Created)
DT 15-DEC-1998 (rel. 37, Last sequence update)
DT 28-FEB-2003 (rel. 41, Last annotation update)
DE Genome polypeptide [contains: N-terminal protein (P1); Helper
component proteinase (EC 3.4.22.45) (HC-Pro); Protein P3; 6 kDa
protein 1 (6K1); Cytoplasmic inclusion protein (CI); 6 kDa protein 2
(6K2); Genome-linked protein (VPG); Nuclear inclusion protein A (NI-A)
(NIA) (EC 3.4.22.44) (49 kDa proteinase) (49 kDa-Pro); Nuclear
inclusion protein B (NI-B) (NIB) (RNA-directed RNA polymerase)
(EC 2.7.7.48); Coat protein (CP)].
DE Zucchini yellow mosaic virus (strain Reunion Island) (ZYMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Polyviridae;
OC Potyviruses.
OX NCBI_TaxID-117129;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-95146958; PubMed-7844540;
RA Wisler G.C., Purcell D.E., Hiebert E.;
RT *Characterization of the P1 protein and coding region of the zucchini
RT yellow mosaic virus*;
RL J. Gen. Virol. 76:37-45(1995).
CC -1- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHID
CC TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.
CC -1- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT
CC MAY BE INVOLVED IN REPLICATION.
CC -1- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
CC -1- CATALYTIC ACTIVITY: Hydrolyzes glutamyl bonds, and activity is
CC further restricted by preferences for the amino acids in p6 - p1'
CC that vary with the species of polyvirus, e.g. Glu-Xaa-Xaa-Tyr-Xaa-
CC Glu+(Ser or Gly) for the enzyme from tobacco etch virus. The
CC natural substrate is the viral polypeptide, but other proteins and
CC oligopeptides containing the appropriate consensus sequence are
CC also cleaved.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
CC (RNA)(N).
CC -1- CATALYTIC ACTIVITY: Hydrolyzes a Gly-I-Gly bond at its own C-
CC terminus, commonly in the sequence -Tyr-Xaa-Val-Gly-I-Gly, in the
CC processing of the polyviral polypeptide.
CC -1- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.
CC -1- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
CC POLYPEPTIDE WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
CC INDIVIDUAL PROTEINS.
CC -1- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
CC -1- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.
CC -1- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPEPTIDE FAMILY.
CC -----
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: L29569; AAA65558.1;
CC DR HESP; P27958; 1HEI.
CC DR MERO; C04.003; -.
CC DR InterPro: IPR001410; DEAD.
CC DR InterPro: IPR001650; Helicase_C.
CC DR InterPro: IPR001730; Peptidase_C4.
CC DR InterPro: IPR001456; Peptidase_C6.
CC DR InterPro: IPR001592; Poly-coat.
CC DR InterPro: IPR002540; Poly_p1.
CC DR InterPro: IPR007095; RNA_pol_DS_PS.
CC DR InterPro: IPR001205; RNA_pol_P3D.
CC DR InterPro: IPR007094; RNA_pol_PSVIR.
CC DR Pfam: PF00271; Helicase_C.1.
CC DR Pfam: PF00663; Peptidase_C4.1.

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DR Pfam: PF00851; Peptidase_C6.1.
DR Pfam: PF00767; Poly-coat.1.
DR Pfam: PF01577; Poly_p1.1.
DR Pfam: PF00680; RNA_dep_RNA_pol.1.
DR PRINTS: PR00966; NIAPOTYPTASE.
DR SMART: SM00487; DEXDC.1.
DR SMART: SM00490; HELIC_C.1.
KW Hydrolyase; Transferase; Thiol protease; RNA-directed RNA polymerase;
KW Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase;
KW ATP-binding.
FT CHAIN 1 307 N-TERMINAL PROTEIN.
FT CHAIN 308 769 HELPER COMPONENT PROTEINASE.
FT CHAIN 770 1115 PROTEIN P3.
FT CHAIN 1116 1167 6 kDa PROTEIN 1.
FT CHAIN 1168 1801 CYTOPLASMIC INCLUSION PROTEIN.
FT CHAIN 1802 1854 6 kDa PROTEIN 2.
FT CHAIN 1855 2044 GENOME-LINKED PROTEIN.
FT CHAIN 2045 2287 NUCLEAR INCLUSION PROTEIN A.
FT CHAIN 2288 2804 NUCLEAR INCLUSION PROTEIN B.
FT CHAIN 2805 3083 COAT PROTEIN.
FT CHAIN 1252 1259 ATP (POTENTIAL).
SQ SEQUENCE 3083 AA; 351156 MW; 55E51B455C20C537 CRC64;

Query Match          94.1%; Score 32; DB 1; Length 3083;
Best Local Similarity 80.0%; Pred. No. 5; 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYMLH 5
DB 2182 SYMH 2186

RESULT 13
POLG_ZYMVS          STANDARD:          PRT: 3083 AA.
ID POLG_ZYMVS
AC 036979;
DT 15-JUL-1999 (rel. 38, Created)
DT 28-FEB-2003 (rel. 41, Last sequence update)
DE Genome polypeptide [contains: N-terminal protein (P1); Helper
component proteinase (EC 3.4.22.45) (HC-Pro); Protein P3; 6 kDa
protein 1 (6K1); Cytoplasmic inclusion protein (CI); 6 kDa protein 2
(6K2); Genome-linked protein (VPG); Nuclear inclusion protein A (NI-A)
(NIA) (EC 3.4.22.44) (49 kDa proteinase) (49 kDa-Pro); Nuclear
inclusion protein B (NI-B) (NIB) (RNA-directed RNA polymerase)
(EC 2.7.7.48); Coat protein (CP)].
DE Zucchini yellow mosaic virus (strain Singapore) (ZYMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Polyviridae;
OC Potyviruses.
OX NCBI_TaxID-117130;
RN [1]
RP SEQUENCE FROM N.A.
RX Lee K.C., Wong S.M.;
RT Submitted (MAY-2001) to the EMBL/Genbank/DBD databases.
CC -1- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHID
CC TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.
CC -1- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT
CC MAY BE INVOLVED IN REPLICATION.
CC -1- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
CC -1- CATALYTIC ACTIVITY: Hydrolyzes glutamyl bonds, and activity is
CC further restricted by preferences for the amino acids in p6 - p1'
CC that vary with the species of polyvirus, e.g. Glu-Xaa-Xaa-Tyr-Xaa-
CC Glu+(Ser or Gly) for the enzyme from tobacco etch virus. The
CC natural substrate is the viral polypeptide, but other proteins and
CC oligopeptides containing the appropriate consensus sequence are
CC also cleaved.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
CC (RNA)(N).
CC -1- CATALYTIC ACTIVITY: Hydrolyzes a Gly-I-Gly bond at its own C-
CC terminus, commonly in the sequence -Tyr-Xaa-Val-Gly-I-Gly, in the
CC processing of the polyviral polypeptide.
CC -1- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.
CC -1- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE

```

POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT INDIVIDUAL PROTEINS.

-1- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.

-1- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.

-1- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.

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DR EMBL; AF014811; AAB72004.2; -

DR HSSP; P27958; 1HEI.

DR MEROPS; C04.003; -

DR MEROPS; C06.001; -

DR MEROPS; S30.001; -

DR InterPro; IPR001410; DEAD.

DR InterPro; IPR001650; Helicase_C.

DR InterPro; IPR001730; Peptidase_C4.

DR InterPro; IPR001456; Peptidase_C6.

DR InterPro; IPR001592; Pcty_coat.

DR InterPro; IPR002540; Pcty_P1.

DR InterPro; IPR007095; RNA_pol_DS_PS.

DR InterPro; IPR001205; RNA_pol_P3D.

DR InterPro; IPR007094; RNA_pol_PSVLr.

DR Pfam; PF00271; helicase_C.1.

DR Pfam; PF00863; peptidase_C4.1.

DR Pfam; PF00851; peptidase_C6.1.

DR Pfam; PF00767; Pcty_P1.1.

DR Pfam; PF01577; Pcty_P1.1.

DR Pfam; PF00680; RNA_dep_RNA_pol.1.

DR PRINTS; PR00966; NIAPOTYPRASE.

DR SMART; SM00487; DEXDC.1.

DR SMART; SM00480; HELICC.1.

DR HydroLase; TransErase; 1.

KW Coat protein; Polypeptide; Covalent protein-RNA linkage; Helicase;

KW ATP-binding.

FT CHAIN 1 307 N-TERMINAL PROTEIN.

FT CHAIN 308 769 HELPER COMPONENT PROTEINASE.

FT CHAIN 770 1115 PROTEIN P3.

FT CHAIN 1116 1167 6 kDa PROTEIN 1.

FT CHAIN 1168 1801 CYTOPLASMIC INCLUSION PROTEIN.

FT CHAIN 1802 1854 6 kDa PROTEIN 2.

FT CHAIN 1855 2044 GENOME-LINKED PROTEIN.

FT CHAIN 2045 2287 NUCLEAR INCLUSION PROTEIN A.

FT CHAIN 2288 2804 NUCLEAR INCLUSION PROTEIN B.

FT CHAIN 2805 3083 COAT PROTEIN.

FT NP_BIND 1252 1259 ATP (POTENTIAL).

SEQUENCE 3083 AA; 351028 MW; B4B6C53C14524A8 CRC64;

Query Match Score 32; DB 1; Length 3083;

Best Local Similarity 80.0%; Pred. No. 5.1e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=1423;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=168;

RA MEDLINE=98044033; PubMed=9384377;

RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Borries R., Bourcier L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A., Denzot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T., Enlitan K.D., Errington J., Fabret C., Ferrati E., Foulger D., Fritz C., Fujita M., Fujita Y., Fuma S., Gallizzi A., Galleron N., Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grand G., Gutseppel G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A., Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Klaerr-Blandhard M., Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Manuel C., Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H., Parro V., Pohl T.M., Portecelle D., Porwollik S., Prescott A.M., Prescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivoletta C., Rochelle E., Roche B., Rose M., Sadate Y., Sato T., Scanlan E., Schleich S., Schroeder R., Scoffone F., Sekiguchi J., Sekowala A., Seror S.J., Serro P., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H., Weltzenegger T., Winters P., Wipat A., Yamamoto H., Yamae K., Yasunoto K., Yata K., Yoshida K., Yoshikawa H.F., Zunsstein E., Yoshikawa H., Danchin A.;

RT "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis".

RL Nature 390:249-256(1997).

CC -1- FUNCTION: PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM. PROBABLY RESPONSIBLE FOR THE TRANSLLOCATION OF THE SUBSTRATE ACROSS THE MEMBRANE (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).

CC -1- SIMILARITY: BELONGS TO THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM PERMEASE FAMILY. MALFG SUBFAMILY.

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DR EMBL; Z99107; CAB12517.1; -

DR PIR; G69796; G69796.

DR Subtilist; BG12850; yesp.

DR InterPro; IPR000515; BPD_transp.

DR Pfam; PF00528; BPD_transp.1.

DR PROSITE; PS00402; BPD_TRANSP_INN_MEMBER.1.

CC Hypothetical protein; Transport; Transmembrane; Complete proteome.

FT TRANSMEM 29 49 POTENTIAL.

FT TRANSMEM 84 104 POTENTIAL.

FT TRANSMEM 114 134 POTENTIAL.

FT TRANSMEM 167 187 POTENTIAL.

FT TRANSMEM 217 237 POTENTIAL.

FT TRANSMEM 275 295 POTENTIAL.

SEQUENCE 309 AA; 34614 MW; 971DE02DA4F9153B CRC64;

Query Match Score 31; DB 1; Length 309;

Best Local Similarity 80.0%; Pred. No. 83;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 299 SYWVH 303

RESULT 15

TRANSLOC_HUMAN STANDARD; PRT; 370 AA.

ID TBM2_HUMAN

AC 015035;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE Translocation associated membrane protein 2.

GN TBM2 OR KIAA0057.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_TaxID=9606;

ON [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Bone marrow;

RX MEDLINE=96051398; PubMed=7584044;

RA Nomura N., Nagase T., Miyajima N., Sazuka T., Tanaka A., Sato S., Seki N., Kawarabayashi Y., Ishikawa K.-I., Tabata S.;

RT *Prediction of the coding sequences of unidentified human genes. II. The coding sequences of 40 new genes (KIAA0041-KIAA0080) deduced by analysis of cDNA clones from human cell line KG-1.;

RT DNA Res. 1:223-229(1994).

RM [2]

RP SEQUENCE FROM N.A.

RA Tracey A.;

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=2388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K., Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Dadin T.B., Toshylyuk S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.A., Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT *Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.;

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -1- SIMILARITY: BELONGS TO THE LASSI FAMILY.

CC -----

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CC -----

DR EMBL: D31762; BAA06540.1; -

DR EMBL: AL049611; CAB71119.1; -

DR EMBL: BC028121; AAH28121.1; -

DR GenBank: U000000000; TBM2.

DR InterPro: IPR005547; LAG1.

DR InterPro: IPR006634; LAG1.

DR Pfam: PF03798; LAG1; 1.

DR SMART: SM00724; TBC; 1.

KW Transmembrane; Glycoprotein; Translocation.

FT TRANSMEM 23 43 POTENTIAL.

FT TRANSMEM 76 96 POTENTIAL.

FT TRANSMEM 120 140 POTENTIAL.

FT TRANSMEM 160 180 POTENTIAL.

FT TRANSMEM 199 219 POTENTIAL.

FT TRANSMEM 251 271 POTENTIAL.

FT TRANSMEM 288 308 POTENTIAL.

FT CARBOHYD 35 55 POTENTIAL.

SQ SEQUENCE 370 AA; 43327 MW; 9B5183F1A3D45366 CRC64; N-LINKED (GLCNAC...) (POTENTIAL).

Query Match 91.2%; Score 31; DB 1; Length 370;

Best Local Similarity 80.0%; Pred. No. 99;

Matches 4; Conservative 1; Mismatches 0; Gaps 0;

Job time : 2.01724 secs

Search completed: October 7, 2003, 19:15:01

Db 169 AYLWH 173

QY 1 SYWLH 5

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 19:04:06 ; Search time 4.98276 Seconds
(without alignments)
258.946 Million cell updates/sec

Title: US-09-988-013a-4_COPY_31_35

Perfect score: 34
Sequence: 1 STWLH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rv1rus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	90	16	09c142
2	34	100.0	105	10	08w0f7
3	34	100.0	196	10	04g198
4	34	100.0	224	11	09d561
5	34	100.0	250	10	09xev8
6	34	100.0	302	11	09d592
7	34	100.0	317	10	09sae0
8	34	100.0	430	5	026424
9	34	100.0	482	16	08ya02
10	34	100.0	494	16	092es4
11	34	100.0	537	16	08x070
12	34	100.0	566	5	094013
13	34	100.0	675	17	08rnp4
14	34	100.0	4924	3	09p7t1
15	34	94.1	114	11	09j181
16	32	94.1	117	11	09z1c6

17	32	94.1	137	11	0924r6	0924r6 mus musculus
18	32	94.1	139	11	0924r5	0924r5 mus musculus
19	32	94.1	140	11	0924p8	0924p8 mus musculus
20	32	94.1	140	11	0924r2	0924r2 mus musculus
21	32	94.1	141	11	0924o4	0924o4 mus musculus
22	32	94.1	142	11	0924o1	0924o1 mus musculus
23	32	94.1	143	11	091va2	091va2 mus musculus
24	32	94.1	143	11	0924o5	0924o5 mus musculus
25	32	94.1	143	11	091v67	091v67 mus musculus
26	32	94.1	143	11	0924r7	0924r7 mus musculus
27	32	94.1	143	11	0924p6	0924p6 mus musculus
28	32	94.1	143	11	0924r0	0924r0 mus musculus
29	32	94.1	144	11	0924p5	0924p5 mus musculus
30	32	94.1	145	11	0924o6	0924o6 mus musculus
31	32	94.1	145	11	0924o9	0924o9 mus musculus
32	32	94.1	145	11	0924r3	0924r3 mus musculus
33	32	94.1	145	11	0924o7	0924o7 mus musculus
34	32	94.1	145	11	0924p7	0924p7 mus musculus
35	32	94.1	145	11	0924r1	0924r1 mus musculus
36	32	94.1	145	11	0924r4	0924r4 mus musculus
37	32	94.1	146	11	0924r8	0924r8 mus musculus
38	32	94.1	146	11	0924o3	0924o3 mus musculus
39	32	94.1	189	5	046120	046120 fasciola he
40	32	94.1	278	11	0921k1	0921k1 mus musculus
41	32	94.1	371	5	0903p5	0903p5 caenorhabdi
42	32	94.1	373	5	09xxk7	09xxk7 caenorhabdi
43	32	94.1	434	8	09gg28	09gg28 naies minor
44	32	94.1	466	12	08jxj9	08jxj9 tomato spot
45	32	94.1	466	12	08jxk0	08jxk0 tomato spot

ALIGNMENTS

RESULT 1

09c142 ID 09c142 PRELIMINARY; PRT; 90 AA.
AC 09c142;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Unknown protein.
GN YRBG OR L0524.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471;
RA Bolotin A., Wincker P., Manger S., Jallion O., Malarne K.,
RT Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
lactis ssp. lactis IL1403";
RL Genome Res. 11:731-753(2001).
DR EMBL; AF006287; AAK04622.1; -.
KW Complete Proteome.
SQ SEQUENCE 90 AA; 10209 MW; 1D4A61B0F3FF84P9 CRC64;

Query Match 100.0%; Score 34; DB 16; Length 90;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STWLH 5
Db 17 STWLH 21

RESULT 2
08w0f7 ID 08w0f7 PRELIMINARY; PRT; 105 AA.
AC 08w0f7;
DT 01-MAR-2002 (Tremblrel. 20, Created)

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DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE P0529E05.22 protein.
GN P0529E05.22.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriacridaceae; Oryzaceae; Oryza.
OC NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Saeki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nippobare(Gs3) genomic DNA, chromosome 1, PAC
RT clone:P0529E05.22"
RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AP003279; BAB84406.1; -.
DR Gramene; O8W0E7; -.
SQ SEQUENCE 105 AA; 12386 MW; 2BA42D3A6D61620F CRC64;

Query Match 100.0%; Score 34; DB 10; Length 105;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
DB 50 SYWLH 54

RESULT 3
ID 049198 PRELIMINARY; PRT; 196 AA.
AC 049198;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Hairy root 4.
GN HRA4
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Hairy root tumor;
RA Nakamura C., Nishimura N., Mishima M., Ueda T., Onaka T.,
RA Tsvetanov S., Takumi S., Mori N.;
RT "Molecular cloning and characterization of cDNAs preferentially
RT expressed during the development of hairy roots and normal roots in
RT tobacco (Nicotiana tabacum L.)."
RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF043554; AAC02087.1; -.
DR HSSP; P24337; IHRP.
DR InterPro; IPR003612; AAI.
DR Pfam; PF00234; tryf_alpha_amy1.1.
DR SMART; SM00499; AAI; 1.
SQ SEQUENCE 196 AA; 19904 MW; 7225COBBA1BEFB5 CRC64;

Query Match 100.0%; Score 34; DB 10; Length 196;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
DB 153 SYWLH 157

RESULT 4
ID 09D561 PRELIMINARY; PRT; 224 AA.
AC 09D561;
DT 01-JUN-2001 (TREMBLrel. 17, Created)

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DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE 493051MIRIK protein.
GN 493051MIRIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE-Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Aachii J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochika H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.W., Staahl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Wittaker C., Wilming L.,
RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK015761; BAB29963.1; -.
DR MGI; MGI:1922305; 493051MIRIK.
DR InterPro; IPR006214; UPF00005.
DR Pfam; PF01027; UPF00005.1.
SQ SEQUENCE 224 AA; 25646 MW; 6367E0BBE8BD93C CRC64;

Query Match 100.0%; Score 34; DB 11; Length 224;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
DB 160 SYWLH 164

RESULT 5
ID 09XEV8 PRELIMINARY; PRT; 290 AA.
AC 09XEV8;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE CCAT-binding transcription factor subunit B.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC Mundree S.G., Singh N.P., Singh N.K.;
RT "Cloning of two novel tobacco cDNA clones by functional sufficiency
RT for salt tolerance in Escherichia coli."
RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF120092; AAD28439.1; -.
DR InterPro; IPR01289; TF_CBBF.
DR Pfam; PF02045; CBBF_NFYA; 1.
DR PRINTS; PR00616; CCAATSUBUNT.
DR Prodom; PD003860; TF_CBBF; 1.
DR SMART; SM00521; CBBF; 1.
SQ SEQUENCE 290 AA; 33949 MW; 5F275974A10AF931 CRC64;

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Query Match 100.0%; Score 34; DB 10; Length 290;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
 |||||
 DB 183 SYWLH 187

RESULT 6

Q9D592 PRELIMINARY; PRT; 302 AA.
 ID Q9D592
 AC Q9D592;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE 4930500J03RLK protein.
 GN 4930500J03RLK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh J., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirral L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Oikido T., Furuno M., Iono H., Baldarelli R., Barsh G.,
 RA Blake J., Bonfelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gstaal J., Hill D., Hofmann M., Hume D.A., Kamliya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL: AK015666; BAB29920.1; -
 DR MGD: MGI:1922260; 4930500J03RLK.
 DR InterPro: IPR006214; DPF0005.
 DR Pfam: PF01027; UPF0005; 1.
 SQ SEQUENCE 302 AA; 34184 MW; CFE5E4B90891554C CRC64;

Query Match 100.0%; Score 34; DB 11; Length 302;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
 |||||
 DB 238 SYWLH 242

RESULT 7

Q9SAE0 PRELIMINARY; PRT; 317 AA.
 ID Q9SAE0
 AC Q9SAE0;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE F3F19.7.
 GN F3F19.7.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Vysotskaya V.S., Schwartz J.R., Yu G., Toriumi M., Lee J.M., Lanz C.,
 RA Liu S., Li J., Kremenetskaia I., Lucos J., Ngan I., Gonzalez A.,
 RA Altafi H., Araujo R., Chao Q., Conn L., Conway A.B., Dunn P.,
 RA Hansen N., Huizar L., Kim C., Palm C., Rowley D., Shinn P., Walker M.,
 RA Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
 RT "Arabidopsis thaliana chromosome 1 BAC F3F19 sequence.";
 RL Submitted (APR-1999) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Theologis A.;
 RL Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AC007357; AAD31058.1; -
 SQ SEQUENCE 317 AA; 35809 MW; 17972E206698CCD8 CRC64;

Query Match 100.0%; Score 34; DB 10; Length 317;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
 |||||
 DB 289 SYWLH 293

RESULT 8

Q26424 PRELIMINARY; PRT; 430 AA.
 ID Q26424
 AC Q26424;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE C-myc proto-oncogene homolog protein (Fragment).
 OS Crassostrea virginica (Eastern oyster).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;
 OC Ostreidae; Ostreidae; Crassostrea.
 OX NCBI_TaxID=6565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=95291374; PubMed=7773336;
 RA Marsh A.G., Chen T.T.;
 RT "A divergent cDNA homologue of the c-myc proto-oncogene in the eastern
 RT oyster Crassostrea virginica: Implications for Myc evolution.";
 RL Mol. Mar. Biol. Biotechnol. 4:185-192(1995).
 DR EMBL: S77334; AAB34577.1; -
 DR InterPro: IPR003582; SHKT.
 DR InterPro: IPR001007; VWF_C.
 DR Pfam: PF01549; SHKT; 2.
 DR Pfam: PF00093; VWC; 1.
 DR SMART: SM00254; SHKT; 2.
 DR SMART: SM00214; VWC; 1.
 FT NON TER 1
 SQ SEQUENCE 430 AA; 47896 MW; DPAFCF3A9B32E5DA3 CRC64;

Query Match 100.0%; Score 34; DB 5; Length 430;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
 |||||
 DB 240 SYWLH 244

RESULT 9

O8YA02 PRELIMINARY; PRT; 482 AA.
 ID O8YA02
 AC O8YA02;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)

DT 01-MAR-2002 (TReMBLrel. 20, last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, last annotation update)
 DE Hypothetical protein lmo0365.
 GN LMO0365.
 OS *Listeria monocytogenes*.
 OC Bacteria; Firmicutes; Bacilliales; Listeriaceae; Listeria.
 NC NCBL_TaxID=1639;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BGD-e / Serovar 1/2a;
 RX MEDLINE=21537279; PubMed=11679669;
 RA Glaeser P., Frangeul L., Buchrieser C., Rusnlok C., Amend A.,
 Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
 Charbit A., Chetouani F., Couve E., de Darvar A., Dehoux P.,
 Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
 Entlan K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapat G.,
 RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
 Nordtek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
 Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
 RA Vazquez-Boland J.-A., Voss H., Weiland J., Cossart P.,
 RT "Comparative genomics of *Listeria species*."
 RL Science 294:849-852(2001).
 DR EMBL: AL591975; CAC98444.1; -.
 DR ListList; LMO00365; -.
 DR InterPro: IPR003439; ABC_transporter.
 DR InterPro: IPR004923; FTFL.
 DR Pfam: PF03239; FTFL; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
 KM Hypothetical protein; Complete proteome.
 SQ SEQUENCE 482 AA; 53669 MW; D8ADD08062990EDF CRC64;

 Query Match 100.0%; Score 34; DB 16; Length 482;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 OY 1 SYWLH 5
 Db 314 SYWLH 318

 RESULT 10
 092ES4 PRELIMINARY; PRT; 494 AA.
 AC 092ES4;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, last annotation update)
 DE Hypothetical protein lln0384.
 GN Lln0384.
 OS *Listeria innocua*.
 OC Bacteria; Firmicutes; Bacilliales; Listeriaceae; Listeria.
 NC NCBL_TaxID=1642;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CUP 11262 / Serovar 6a;
 RX PubMed=11679669;
 RA Glaeser P., Frangeul L., Buchrieser C., Rusnlok C., Amend A.,
 Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
 Charbit A., Chetouani F., Couve E., de Darvar A., Dehoux P.,
 Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
 Entlan K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapat G.,
 RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
 Nordtek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
 Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
 RA Vazquez-Boland J.-A., Voss H., Weiland J., Cossart P.,
 RT "Comparative genomics of *Listeria species*."
 RL Science 294:849-852(2001).
 DR EMBL: AL596164; CAC95617.1; -.
 DR ListList; Lln00384; -.

DR InterPro: IPR004923; FTFL.
 DR Pfam: PF03239; FTFL; 1.
 KM Hypothetical protein; Complete proteome.
 SQ SEQUENCE 494 AA; 55050 MW; 882E6F1BF688E32 CRC64;

 Query Match 100.0%; Score 34; DB 16; Length 494;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 OY 1 SYWLH 5
 Db 314 SYWLH 318

 RESULT 11
 08X070 PRELIMINARY; PRT; 537 AA.
 ID 08X070;
 AC 08X070;
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, last sequence update)
 DE 01-MAR-2002 (TReMBLrel. 20, last annotation update)
 DE Probable transmembrane protein.
 GN RSP1416 OR RS03125.
 OS *Ralstonia solanacearum* (Pseudomonas solanacearum).
 OC Plasmid megaplasmid.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Ralstoniaceae; Ralstonia.
 NC NCBL_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CMI1000;
 RX MEDLINE=21681879; PubMed=11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 RA Arlat M., Billault A., Brotlier P., Camus J.-C., Catolico L.,
 RA Chandler M., Choise N., Claudel-Renard C., Cunac S., Demange N.,
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
 RA Siguer P., Thebaud P., Whalen M., Wincker P., Levy M.,
 RA Weisenbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen *Ralstonia solanacearum*."
 RL Nature 415:497-502(2002).
 DR EMBL: AL646084; CAD18567.1; -.
 KM Plasmid; Complete proteome.
 SQ SEQUENCE 537 AA; 57305 MW; FFF20EDA334ABE3D CRC64;

 Query Match 100.0%; Score 34; DB 16; Length 537;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 OY 1 SYWLH 5
 Db 41 SYWLH 45

 RESULT 12
 094013 PRELIMINARY; PRT; 566 AA.
 ID 094013;
 AC 094013;
 DT 01-FEB-1997 (TReMBLrel. 02, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, last annotation update)
 DE T08G11.4 protein.
 GN T08G11.4.
 OS *Caenorhabditis elegans*.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 NC NCBL_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Dobson R.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;

RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL: Z80220; CAB02307.2; -.
DR Mornmped: T08611.4; CE23958.
DR InterPro: IPR000051; SAM_bind.
DR InterPro: IPR003402; Unk_Met10.
DR Pfam: PF02475; Met_10; 1.
SQ SEQUENCE 566 AA; 65446 MW; E59BB1E0A5BC62A CRC64;

Query Match 100.0%; Score 34; DB 5; Length 566;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
DB 133 SYWLH 137

RESULT 13
O8TNP4 PRELIMINARY; PRT; 675 AA.
AC O8TNP4;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Hypothetical protein MA2239.
GN MA2239.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., MacDonald P.,
RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., Deatellano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuetner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
and physiological diversity."
RL Genome Res. 12:532-542(2002).
DR EMBL: AE010910; AAM05634.1; -.
DR InterPro: IPR001237; Postsynaptic.
DR InterPro: IPR001440; TPR.
DR Pfam: PF00515; TPR; 8.
DR ProDom: PD012428; Postsynaptic; 1.
DR SMART: SM00028; TPR; 8.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 675 AA; 77117 MW; 551931ADC3EC8680 CRC64;

Query Match 100.0%; Score 34; DB 17; Length 675;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
DB 230 SYWLH 234

RESULT 14
O9P7T1 PRELIMINARY; PRT; 4924 AA.
AC O9P7T1;

DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Putative peptide synthetase, with 3 Phosphopantetheine attachment
sites.
GN SPAC2363.02C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972h-;
RA Badcock K., Churcher C.M., Wood V., Barrell B.G., Rajandream M.A.;
RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AL138854; CAB72227.1; -.
DR HSSP: P14687; 1AMU.
DR GeneDB_Spombe: SPAC2363.02c; -.
DR InterPro: IPR002086; Aldehyde_dehydr.
DR InterPro: IPR000873; AMP_bind.
DR InterPro: IPR001242; Condensatn.
DR InterPro: IPR006162; pentne_attach.
DR InterPro: IPR006163; PP_bind.
DR Pfam: PF00501; AMP-binding; 4.
DR Pfam: PF00668; Condensation; 4.
DR Pfam: PF00550; pp-binding; 4.
DR PROSITE: PS0075; ACP DOMAIN; 6.
DR PROSITE: PS00070; ALDEHYDE_DEHYDR_CYS; 1.
DR PROSITE: PS00455; AMP_BINDING; 2.
DR PROSITE: PS00012; PHOSPHOPANTHETHEINE; 3.
SQ SEQUENCE 4924 AA; 559835 MW; 985D30FED3406E2C CRC64;

Query Match 100.0%; Score 34; DB 3; Length 4924;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYWLH 5
DB 1794 SYWLH 1798

RESULT 15
Q9JL81 PRELIMINARY; PRT; 114 AA.
AC Q9JL81;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Anti-myosin Immunoglobulin heavy chain variable region
(Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/C;
RX MEDLINE=20448942; PubMed=10992488;
RA Maiktel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-cell-dependent antibody response to the dominant epitope of
streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
with cardiac myosin."
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL: AF206025; AAF6323.1; -.
DR HSSP: P01810; 2FBD.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG-LIKE; 1.
FT NON_TER 1

FT NON_TER 114 114
SQ SEQUENCE 114 AA: 12829 MM: 40485FDE6BA56F8 CRC64;
Query Match 94.1%; Score 32; DB 11; Length 114;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYWLH 5
111:1
DB 23 SYWMH 27

Search completed: October 7, 2003, 19:20:01
Job time : 5.98276 secs


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XX 12-AUG-1994; 94US-0289576.
XX (IMMU-) IMMUNOMEDICS INC.
XX Hansen H, Leung S;
XX WPI; 1996-139454/14.
XX N-PSDB; AAT15802.
XX
XX Chimeric and humanised LL2 antibodies - used to produce conjugates
XX for the therapy and diagnosis of B-cell lymphoma(s) and
XX Leukaemia(s).
XX
XX Claim 5; Page 36-37; 70pp; English.
XX
XX The complementarity determining regions (CDRs) of mouse monoclonal
XX antibody (Mab) LL2 VK (AAR92215) and VH (AAR92216) regions were
XX recombinantly linked to the framework sequences of human VK and VH
XX regions, respectively, to give humanised LL2 VK (AAR92217) and VH
XX (AAR92218). These were subsequently linked, respectively, to human
XX kappa and IgG1 constant regions. A humanised Mab was obtd. that
XX retained the B-lymphoma and leukaemia cell targeting and
XX internalisation characteristics of the parental LL2 Mab, and which
XX exhibited a lowered HAMA reaction. It can be linked to e.g. a
XX cytostatic agent for therapeutic appln.
XX
XX Sequence 116 AA;
XX
XX Query Match 100.0%; Score 99; DB 17; Length 116;
XX Best Local Similarity 100.0%; Pred. No. 6e-08;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 YINPRNDYTEYXNONFKD 17
XX |||||||||||||||
DB 50 YINPRNDYTEYXNONFKD 66
XX
XX RESULT 2
XX AAR92218 standard; Protein; 116 AA.
XX
XX AAR92218;
XX
XX 28-MAY-1996 (first entry)
XX
XX Humanised LL2 Mab VH region.
XX
XX Humanised antibody; monoclonal antibody; Mab; LL2; B-cell lymphoma;
XX leukaemia; therapy; diagnosis; complementarity determining region;
XX CDR; antibody engineering.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Region 31..35
XX /label= CDR1
XX Region 50..66
XX /label= CDR2
XX Region 99..105
XX /label= CDR3
XX
XX WO9604925-A1.
XX
XX 22-FEB-1996.
XX
XX 11-AUG-1995; 95WO-US09641.
XX
XX 12-AUG-1994; 94US-0289576.
XX
XX (IMMU-) IMMUNOMEDICS INC.
XX
XX Hansen H, Leung S;
XX

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XX WPI; 1996-139454/14.
XX N-PSDB; AAT15804.
XX
XX Chimeric and humanised LL2 antibodies - used to produce conjugates
XX for the therapy and diagnosis of B-cell lymphoma(s) and
XX Leukaemia(s).
XX
XX Claim 5; Page 39; 70pp; English.
XX
XX The complementarity determining regions (CDRs) of mouse monoclonal
XX antibody (Mab) LL2 VK (AAR92215) and VH (AAR92216) regions were
XX recombinantly linked to the framework sequences of human VK and VH
XX regions, respectively, to give humanised LL2 VK (AAR92217) and VH
XX (AAR92218). These were subsequently linked, respectively, to human
XX kappa and IgG1 constant regions. A humanised Mab was obtd. that
XX retained the B-lymphoma and leukaemia cell targeting and
XX internalisation characteristics of the parental LL2 Mab, and which
XX exhibited a lowered HAMA reaction. It can be linked to e.g. a
XX cytostatic agent for therapeutic appln.
XX
XX Sequence 116 AA;
XX
XX Query Match 100.0%; Score 99; DB 17; Length 116;
XX Best Local Similarity 100.0%; Pred. No. 6e-08;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 YINPRNDYTEYXNONFKD 17
XX |||||||||||||||
DB 50 YINPRNDYTEYXNONFKD 66
XX
XX RESULT 3
XX AAR92219 standard; Protein; 116 AA.
XX
XX AAR92219;
XX
XX 28-MAY-1996 (first entry)
XX
XX Humanised LL2 Mab VH region (version hLL2-1).
XX
XX Humanised antibody; monoclonal antibody; Mab; LL2; B-cell lymphoma;
XX leukaemia; therapy; diagnosis; complementarity determining region;
XX CDR; antibody engineering.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Region 31..35
XX /label= CDR1
XX Region 50..66
XX /label= CDR2
XX Region 99..105
XX /label= CDR3
XX
XX WO9604925-A1.
XX
XX 22-FEB-1996.
XX
XX 11-AUG-1995; 95WO-US09641.
XX
XX 12-AUG-1994; 94US-0289576.
XX
XX (IMMU-) IMMUNOMEDICS INC.
XX
XX Hansen H, Leung S;
XX
XX WPI; 1996-139454/14.
XX
XX Chimeric and humanised LL2 antibodies - used to produce conjugates
XX for the therapy and diagnosis of B-cell lymphoma(s) and
XX Leukaemia(s).
XX

```

XX Example 1: Page 40; 70pp; English.
 PS
 CC The complementarity determining regions (CDRs) of mouse monoclonal
 CC antibody (Mab) LL2 VK (AAR92215) and VH (AAR92216) regions were
 CC recombinantly linked to the framework sequences of human VK and VH
 CC regions, respectively, to give humanised LL2 VK (AAR92217) and VH
 CC (AAR92218). In an alternative version, a glutamine was introduced
 CC at position 5 of the humanised VH (AAR92219) to include a PstI site
 CC useful for subcloning. The humanised VK and VH were subsequently
 CC linked, respectively, to human kappa and IgG1 constant regions. A
 CC humanised Mab was obtd. that retained the B-lymphoma and leukaemia
 CC cell targeting and internalisation characteristics of the parental
 CC LL2 Mab, and which exhibited a lowered HAMA reaction. It can be
 CC linked to a cytostatic agent for therapeutic appln.
 CC
 CC
 SQ Sequence 116 AA:
 Query Match 100.0%; Score 99; DB 17; Length 116;
 Best Local Similarity 100.0%; Pred. No. 6e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YINPRNDYTEYNQNFKD 17
 ||||||||||||||||
 DB 50 YINPRNDYTEYNQNFKD 66
 RESULT 4
 AAW27696
 ID AAW27696 standard; Protein: 116 AA.
 AC
 XX AAW27696;
 DT 14-APR-1998 (first entry)
 DE Variable heavy chain of Mab LL2.
 XX
 KW Variable heavy chain; B cell; monoclonal antibody; Mab; LL2;
 KW B cell lymphoma; lymphocytic leukaemia cell; murine;
 KW diagnosis; treatment; B cell malignancy; non-Hodgkins lymphoma;
 KW chronic lymphocytic leukaemia.
 XX
 OS Mus sp.
 OS Synthetic.
 OS
 XX
 FH Key Location/Qualifiers
 FH Region 31..35
 FT /note= "complementarity determining region 1"
 FT 50..66
 FT /note= "complementarity determining region 2"
 FT 99..105
 FT Region /note= "complementarity determining region 3"
 FT
 FT
 XX
 PN WO9734632-A1.
 XX
 PD 25-SEP-1997.
 XX
 PR 19-MAR-1997; 97WO-US04196.
 XX
 PR 20-MAR-1996; 96US-0013709.
 XX
 XX (IMMU-) IMMUNOMEDICS INC.
 PA
 XX Hansen H, Leung S, Qu Z;
 PI
 XX WPI: 1997-479995/44.
 DR N-PSDB; AAT88129.
 DR
 XX
 XX Monoclonal antibody engineered to contain glycosylation site - in
 PT non-Fc constant heavy or light chain region, useful to diagnose or
 PT treat B cell malignancies, e.g. non-Hodgkins lymphoma
 XX
 PS Example 3; Fig 4B; 88pp; English.

XX
 CC The present sequence is the variable heavy chain of the
 CC B cell specific monoclonal antibody (Mab) LL2, which contains an
 CC engineered tri-peptide N-glycan acceptor sequence. LL2 is a highly
 CC specific anti-B cell lymphoma and anti-lymphocytic leukaemia cell
 CC murine Mab. The Mab can be used to diagnose or treat B
 CC cell malignancies, e.g. non-Hodgkins lymphoma or chronic
 CC lymphocytic leukaemia. The glycosylation site allows a label or
 CC therapeutic agent of increased size to be conjugated to the
 CC carbohydrate moiety, without affecting the Mab's binding affinity
 CC or specificity.
 CC
 CC
 SQ Sequence 116 AA:
 Query Match 100.0%; Score 99; DB 18; Length 116;
 Best Local Similarity 100.0%; Pred. No. 6e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YINPRNDYTEYNQNFKD 17
 ||||||||||||||||
 DB 50 YINPRNDYTEYNQNFKD 66
 RESULT 5
 AAW27698
 ID AAW27698 standard; Protein: 116 AA.
 AC
 XX AAW27698;
 DT 14-APR-1998 (first entry)
 DE Variable heavy chain of Mab hLL2.
 XX
 KW Variable heavy chain; B cell; monoclonal antibody; Mab; hLL2;
 KW B cell lymphoma; lymphocytic leukaemia cell; murine; humanised;
 KW diagnosis; treatment; B cell malignancy; non-Hodgkins lymphoma;
 KW chronic lymphocytic leukaemia.
 XX
 OS Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FH Region 31..35
 FT /note= "complementarity determining region 1"
 FT 50..66
 FT /note= "complementarity determining region 2"
 FT 99..105
 FT Region /note= "complementarity determining region 3"
 FT
 FT
 XX
 PN WO9734632-A1.
 XX
 PD 25-SEP-1997.
 XX
 PR 19-MAR-1997; 97WO-US04196.
 XX
 PR 20-MAR-1996; 96US-0013709.
 XX
 XX (IMMU-) IMMUNOMEDICS INC.
 PA
 XX Hansen H, Leung S, Qu Z;
 PI
 XX WPI: 1997-479995/44.
 DR N-PSDB; AAT88131.
 DR
 XX
 XX Monoclonal antibody engineered to contain glycosylation site - in
 PT non-Fc constant heavy or light chain region, useful to diagnose or
 PT treat B cell malignancies, e.g. non-Hodgkins lymphoma
 XX
 PS Example 3; Fig 5B; 88pp; English.
 CC The present sequence is the variable heavy chain of the
 CC B cell specific monoclonal antibody (Mab) hLL2. hLL2 is a highly
 CC specific anti-B cell lymphoma and anti-lymphocytic leukaemia cell

```

CC humanised murine Mab. The Mab can be used to diagnose or treat B
CC cell malignancies, e.g. non-Hodgkins lymphoma or chronic
CC lymphocytic leukaemia.
CC
SQ Sequence 116 AA;
Query Match 100.0%; Score 99; DB 18; Length 116;
Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YINPRNDYTEYNQNFKD 17
   |||||
DQ 50 YINPRNDYTEYNQNFKD 66
   |||||

RESULT 6
AAP93079
ID AAP93079 standard; peptide; 159 AA.
XX
AC AAP93079;
XX
DT 25-MAR-2003 (updated)
DT 31-OCT-2002 (updated)
DT 15-MAR-1990 (first entry)
XX
DE Heavy chain of monoclonal antibody 6A4.
XX
KM Monoclonal antibody 6A4; heavy chain; Pseudomonas aeruginosa; OMP-1.
XX
OS Unidentified.
XX
PN EP338395-A.
XX
PD 25-OCT-1989.
XX
PF 12-APR-1989; 89EP-0106463.
XX
PR 19-APR-1988; 88DE-3613023.
XX
PA (BEHW ) BEHRINGWERKE AG.
XX
PI Domdey H, Marget M, Vonspecht B;
XX
DR WPI: 1989-310861/43.
XX
DR N-PSDB; AAN91645.
XX
PT Monoclonal antibody to Pseudomonas aeruginosa - and DNA coding for
XX
PS variable antibody regions.
XX
PS Claim 1; page 6; 7pp; german.
XX
CC The peptide is encoded by the heavy chain of monoclonal antibody 6A4.
CC 6A4 reacts with the OMP-1 protein of all 19 known serotypes of
CC P.aeruginosa. It is used for therapy and diagnosis of infection, and as
CC a carrier for drugs. The antibody is IgG2a subclass.
CC (Updated on 31-OCT-2002 to add missing OS field.)
CC (Updated on 25-MAR-2003 to correct PA field.)
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 159 AA;
Query Match 81.8%; Score 81; DB 10; Length 159;
Best Local Similarity 82.4%; Pred. No. 5.9e-05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 YINPRNDYTEYNQNFKD 17
   |||||
DQ 69 YINPRNDYTEYNQNFKD 85
   |||||

RESULT 7
AAR21278
ID AAR21278 standard; Protein; 114 AA.

```

```

XX AAR21278;
AC
XX 21-MAY-1992 (first entry)
DT
XX
DE Murine VH group 1 chain O specific for phox.
XX
KM Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
KM plus; g3p; binding; adsorption; gene VIII; diverse repertoire;
KM specific binding pairs; replicable genetic display package.
XX
OS Synthetic.
XX
FH Key
FH Binding-site 31..35
FH /label= CDR1
FH Binding-site 50..66
FH /label= CDR2
FH Binding-site 99..103
FH /label= CDR3
FH /note=" D/N-X-G-X-X motif "
XX
PD WO9201047-A.
XX
PD 23-JAN-1992.
XX
PF 10-JUL-1991; 91WO-GB01134.
XX
PR 15-MAY-1991; 91GB-0010549.
PR 10-JUL-1990; 90GB-0015198.
PR 19-OCT-1990; 90GB-0022885.
PR 12-NOV-1990; 90GB-0024503.
PR 06-MAR-1991; 91GB-0004744.
XX
PA (CAMP-) CAMBRIDGE ANTIBODY.
PA (MEDI-) MED RES COUNCIL.
XX
PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
PI Winter GP, Bonnett TP;
XX
DR WPI: 1992-056862/07.
XX
PT Producing members of specific binding pairs - by expression in
PT recombinant host cells with a secreting replicable genetic
PT display package.
XX
PS Example 22; Fig 24; 209pp; English.
XX
CC The VH sequence is one of 22 (AAR21264-85) expressed from a single
CC chain Fv library. The library produces a diverse repertoire of
CC antibody fragments specific for 2-phenyl-5-oxazolone (phox). It was
CC prep'd. using cDNA generated from mRNA from mice immunised with phox
CC coupled to chicked serum albumin. The VH and VL kappa sequences
CC were separately amplified by PCR (AMQ23474-84) and ligated into
CC fcdm2 (AMQ23463) for expression on the phage surface as fusions with
CC gene III. The resulting library of clones was diverse; 23 hapten
CC binding clones were sequenced revealing 8 VH genes (A-H; AAR21264-71)
CC in a variety of pairings with 7 VK genes (A-G; AAR21286-92). Most
CC clones were VK-d combinations so a further hierarchical library was
CC prep'd. by "crossing" VK-d with the VH repertoire. The resulting
CC library was screened for hapten binding and 24 clones sequenced. 13
CC new partners (AAR21272-85) for VK-d were identified. Nearly all the
CC VH genes belonged to gp 1, with only one, "E", being of gp 2 (VHox1).
CC Of the 24 hierarchical clones, only one was of type "O". The Kd of
CC VH-B/VK-d for phox-GABA was 10 nM, one of the highest values found.
CC This suggests that phage bearing scfv fragments having weak affinity-
CC es can be selected with antigen, probably due to the avidity of the
CC multiple antibody heads on the phage. The different combinations
CC could also be isolated on a basis of antigen affinity.
CC See also AAR21260-307, 309-311; AAR22450, 565-581.
XX
SQ Sequence 114 AA;

```

Query Match 80.8%; Score 80; DB 13; Length 114;
 Best Local Similarity 82.4%; Pred. No. 5.9e-05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YINPRNDYTEYNQRFKD 17
 ||||| ||||| |||
 DB 50 YINPRTGTEYNQRFKD 66

RESULT 8

AAW76127
 ID AAW76127 standard; Protein; 138 AA.

AC AAW76127;
 XX
 DT 20-NOV-1998 (first entry)
 XX

DE Murine ICR-1.1 V-H region PCR product protein.

XX Interleukin adhesion molecule; ICAM-R; modulator; 14.3.3 family;
 KW HSI-beta; tubulin; inhibitor; stimulator; effector; immune response;
 KW inflammation; disorder; T cell activation; macrophage; Crohn's disease;
 KW adult respiratory distress syndrome; stroke; multiple sclerosis; asthma;
 KW rheumatoid arthritis; tumour growth; human immune deficiency virus;
 KW infection; diabetes; graft vs. host disease; passive immunisation.

OS Mus sp.

XX Key Location/Qualifiers
 FH Misc-difference 2 /Label= unknown
 FT Misc-difference 6 /Label= unknown
 FT Misc-difference 7 /Label= unknown
 FT Misc-difference 7 /Label= unknown
 FT Misc-difference 8 /Label= unknown
 FT Misc-difference 8 /Label= unknown

PN US5773218-A.

XX 30-JUN-1998.

PD 07-JUN-1995; 95US-0482882.

XX 05-AUG-1994; 94US-0286754.
 PR 27-JAN-1992; 92US-0827689.
 PR 26-MAY-1992; 92US-0889724.
 PR 05-JUN-1992; 92US-0894061.
 PR 22-JAN-1993; 93US-0009266.
 PR 26-JAN-1993; 93WO-US00787.
 PR 05-AUG-1993; 93US-0102852.
 PR 07-JUN-1995; 95US-0482882.

XX (ICOS-) ICOS CORP.

XX Gallatin WM, Vazeux R;

XX WPI; 1998-386989/33.

DR N-PSDB; AAV56413.

XX Identifying compounds that modulate interaction of intercellular
 PT adhesion molecule R - with ligands HSI-beta and tubulin using
 PT two-hybrid assay, useful for treating inflammation, T cell
 PT activation etc.

XX Example 13; Column 125-128; 108bp; English.

XX This sequence represents a murine ICR-1.1 V-H region amplified PCR
 CC product. This sequence is used in the isolation of a novel human
 CC intercellular adhesion molecule, ICAM-R. This sequence is used in a
 CC method which investigates modulators of the interaction between ICAM-R
 CC and the 14.3.3 family member HSI-beta and tubulin. An anti-ICAM-R

CC antibody optionally coupled to toxin or radionuclide, or an ICAM-R
 CC peptide, can block, inhibit or stimulate ligand/receptor interactions
 CC involving ICAM-R, particularly its effector functions involved in
 CC (non)specific immune responses. ICAM-R related agents may be used to
 CC treat or monitor inflammation, disorders involving T cell activation or
 CC macrophages, e.g. adult respiratory distress syndrome, stroke, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis, asthma, tumour growth,
 CC human immune deficiency virus infection, diabetes, graft vs. host disease
 CC and many others. Antibodies may also be used for passive immunisation,
 CC for purifying, detecting or quantifying ICAM-R and for identifying
 CC ICAM-R expressing cells.

SQ Sequence 138 AA;

Query Match 78.8%; Score 78; DB 19; Length 138;
 Best Local Similarity 76.5%; Pred. No. 0.00015;
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YINPRNDYTEYNQRFKD 17
 ||||| ||||| |||
 DB 69 YINPNTDYTEYNQRFKD 85

RESULT 9
 AAW71257
 ID AAW71257 standard; Protein; 138 AA.

XX AAW71257;

AC 25-MAR-2003 (updated)
 DT 18-NOV-1998 (first entry)
 XX

DE Murine antibody ICR-1.1 heavy chain amino acid sequence.

XX Human; ICAM-R; intercellular adhesion molecule; adhesion; treatment;
 KW inflammatory condition; asthma; tumour growth; metastasis;
 KW viral infection; antibody ICR-1.1.

OS Mus sp.

XX Key Location/Qualifiers
 FH Misc-difference 2 /note= "encoded by GRA"
 FT Misc-difference 6 /note= "encoded by RYC"
 FT Misc-difference 7 /note= "encoded by RYC"
 FT Misc-difference 7 /note= "encoded by WTB"
 FT Misc-difference 8 /note= "encoded by HRC"
 FT Misc-difference 8 /note= "encoded by HRC"

PN US5811517-A.

XX 22-SEP-1998.

PD 07-JUN-1995; 95US-0483389.

XX 05-AUG-1994; 94US-0286754.
 PR 26-JAN-1993; 93WO-US00787.
 PR 27-JAN-1992; 92US-0827689.
 PR 05-JUN-1992; 92US-0889724.
 PR 26-MAY-1992; 92US-0894061.
 PR 05-JUN-1992; 92US-0894061.
 PR 22-JAN-1993; 93US-0009266.
 PR 05-AUG-1993; 93US-0102852.

XX (ICOS-) ICOS CORP.

XX Gallatin WM, Vazeux R;

XX WPI; 1998-530940/45.

DR N-PSDB; AAV54863.

XX DNA encoding mutant ICAM-R poly:peptide(s) - useful for diagnosis
 PT and treatment of cell adhesion based disease conditions e.g.

PT Inflammation or asthma
 XX
 PS Example 13; Columns 125-126; 11pp; English.
 XX
 CC The present sequence represents the heavy chain of murine antibody
 CC ICR-1.1. This antibody is specific for ICAM-R (intercellular adhesion
 CC molecule-R). ICAMs are polypeptides that are expressed on blood vessel
 CC endothelial cell surfaces and are involved in the adhesion events in
 CC various conditions. ICAM-R variants (see AAW71264-69) can be used to
 CC treat or monitor inflammatory conditions involving specific or
 CC non-specific immune responses, asthma, tumour growth and/or metastasis
 CC and viral infections. The ICAM variants are produced recombinantly, from
 CC expression libraries of mutated sequences, and the ones that are
 CC claimed are the ones that have been found to be especially involved in
 CC adhesion events. They can also be used to raise antibodies, also for
 CC use as therapeutic or diagnostic agents.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC
 SQ Sequence 138 AA;
 Query Match 78.88; Score 78; DB 19; Length 138;
 Best Local Similarity 76.58; Pred. No. 0.00015;
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 OY 1 YINPRNDYTEXNQFKD 17
 |||| ||||| |:
 Db 69 YINPNTDYTEXNQRFQD 85
 RESULT 10
 AAW00783
 ID AAW00783 standard; Protein: 138 AA.
 XX
 AC AAW00783;
 XX
 DT 14-MAY-1999 (first entry)
 XX
 DE Antibody against ICAM-R.
 XX
 KW ICAM; immunoglobulin-like loop; intercellular adhesion molecule receptor;
 KW alpha d/CD18; antibody; immunisation; inflammatory response; asthma;
 KW tumour growth; viral infection; therapy.
 XX
 OS Mus sp.
 FH Key Location/Qualifiers
 FT Misc-difference 1..138
 FT /note= "Xaa- unspecified amino acid"
 XX
 PN US5880268-A.
 XX
 PD 09-MAR-1999.
 XX
 PF 07-JUN-1995; 95US-0483932.
 XX
 PR 05-AUG-1994; 94US-0286754.
 PR 27-JAN-1992; 92US-0827689.
 PR 26-MAY-1992; 92US-0889724.
 PR 05-JUN-1992; 92US-0894061.
 PR 22-JAN-1993; 93US-0009266.
 PR 26-JAN-1993; 93WO-US00787.
 PR 05-AUG-1993; 93US-0102852.
 PR 07-JUN-1995; 95US-0483932.
 XX
 PA (ICOS-) ICOS CORP.
 XX
 PI Gallatin WM, Vazeux R;
 XX
 DR WPI; 1999-204041/17.
 DR N-PSDB; AAX21879.
 XX
 PT New intercellular adhesion molecule receptor (ICAM-R) specific
 PT antibodies - useful for modulating ligand/receptor binding and

PT biological activities involving ICAM-R, especially those of the
 PT specific and non-specific immune systems
 XX
 PS Example 13; Column 125-126; 108pp; English.
 XX
 CC This sequence represents an antibody specific for ICAM-R.
 CC The invention relates to antibodies (Ab) which bind specifically
 CC to the intercellular adhesion molecule receptor (ICAM-R), inhibiting the
 CC interaction between ICAM-R and alpha d/CD18. Abs with specific ICAM-R
 CC binding are useful in compositions for immunisation, and for purifying
 CC ICAM-R polypeptides and identifying cells expressing ICAM-R on their cell
 CC surface, modulating ligand/receptor binding and biological activities
 CC involving ICAM-R, especially inflammatory responses of the specific
 CC immune system, the non-specific immune system, monitoring and treating
 CC asthma, tumour growth, and/or metastasis, and viral infection (e.g. HIV
 CC infection). In particular diseases involving an essential T cell
 CC activation (e.g. asthma, psoriasis, diabetes, graft vs. host disease,
 CC tissue transplant rejection, and multiple sclerosis) may be treated with
 CC anti-ICAM-R antibodies. The Abs specifically bind to and identify ICAM-R
 CC and disrupt ICAM-R to cell adhesion molecule, especially alpha d/CD18
 CC binding.
 CC
 SQ Sequence 138 AA;
 Query Match 78.88; Score 78; DB 20; Length 138;
 Best Local Similarity 76.58; Pred. No. 0.00015;
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 OY 1 YINPRNDYTEXNQFKD 17
 |||| ||||| |:
 Db 69 YINPNTDYTEXNQRFQD 85
 RESULT 11
 AAW81451
 ID AAW81451 standard; Protein: 138 AA.
 XX
 AC AAW81451;
 XX
 DT 17-FEB-1999 (first entry)
 XX
 DE Murine antibody ICR-1.1 Vh region.
 XX
 KW Intercellular adhesion molecule polypeptide; ICAM-R; humanised; ICR-1.1;
 KW ICR-8.1; monoclonal antibody; therapeutic; inflammatory; asthma; tumour;
 KW graft-versus-host disease; viral infection; toxin; radionuclide;
 KW neovascularisation site; murine.
 XX
 OS Mus sp.
 FH Key Location/Qualifiers
 FT Misc-difference 2
 FT /label= unknown
 FT /note= "encoded by GRA"
 FT
 FT Misc-difference 6
 FT /label= unknown
 FT /note= "encoded by RTC"
 FT
 FT Misc-difference 7
 FT /label= unknown
 FT /note= "encoded by WTB"
 FT
 FT Misc-difference 8
 FT /label= unknown
 FT /note= "encoded by HTC"
 FT
 FT Misc-difference 32
 FT /note= "encoded by AAA"
 XX
 PN US5837822-A.
 XX
 PD 17-NOV-1998.
 XX
 PF 07-JUN-1995; 95US-0487113.
 PF 07-JUN-1995; 95US-0487113.
 PR 07-JUN-1995; 95US-0487113.


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PR 27-JAN-1992; 92US-0827689.
PR 26-MAY-1992; 92US-0889724.
PR 05-JUN-1992; 92US-0894061.
PR 22-JAN-1993; 93US-0009266.
PR 26-JAN-1993; 93MO-US00787.
PR 05-AUG-1993; 93US-0102852.
XX
XX (ICOS-) ICOS CORP.
XX
XX Gallatin WM, Vazeux R;
XX
XX MPI: 1999-023535/02.
XX N-PSDB; AAV69185.
XX
XX Humanised antibodies specific for intercellular adhesion molecule
XX polypeptide - useful for therapeutic or diagnostic purposes
XX
XX Example 13; Columns 137-138; 116pp; English.
XX
XX The invention relates to humanised ICR-1.1 and ICR-8.1 antibodies
XX targeted to the human intercellular adhesion molecule polypeptide
XX (ICAM-R) polypeptide. Antibodies specific for ICAM-R's are potentially
XX useful as therapeutic compounds, for treating e.g. immune-mediated
XX inflammatory conditions (e.g. graft-versus-host disease) asthma,
XX tumours or viral infections. Monoclonal antibodies specific for ICAM-R,
XX or their conjugates formed with e.g. toxins or radionuclides are useful
XX for therapeutically targeting or detecting neovascularisation sites.
XX The present sequence represents the amino acid sequence of the Vh region
XX of the murine antibody ICR-1.1.
XX
XX Sequence 138 AA:
SQ
Query Match 78.8%; Score 78; DB 20; Length 138;
Best Local Similarity 76.5%; Pred. No. 0.00015;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 1 YINPRNDYTEYNQNFKD 17
Db 69 YINPNTDYTEYNQRFOD 85
RESULF 12
AAB13047
ID AAB13047 standard; Protein; 138 AA.
XX
XX AAB13047;
AC
XX
XX 19-DEC-2000 (first entry)
DT
XX
XX Murine ICR-1.1 Vh protein sequence.
DE
XX
XX Anti-human immunodeficiency virus; HIV; cytostatic; ICAM-R; ARDS; stroke;
KW intercellular adhesion molecule; immunoglobulin heavy chain; septicemia;
KW inflammatory conditions; glomerulonephritis; arthritis; dermatosis;
KW haemodialysis; leukapheresis; ulcerative colitis; Crohn's disease;
KW necrotising enterocolitis; atherosclerosis; psoriasis; asthma;
KW transplant rejection; diabetes; tumour.
XX
XX Mus sp.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 2
FT Misc-difference /Label- Unknown
FT Misc-difference 6
FT Misc-difference /Label- Unknown
FT Misc-difference 7
FT Misc-difference /Label- Unknown
FT Misc-difference 8
FT Misc-difference /Label- Unknown
XX
XX US6100383-A.
XX
XX 08-AUG-2000.

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XX
XX 07-JUN-1995; 95US-0475680.
XX
XX 05-AUG-1994; 94US-0286754.
XX 26-JAN-1993; 93MO-US00787.
XX 27-JAN-1993; 92US-0827689.
XX 26-MAY-1992; 92US-0889724.
XX 05-JUN-1992; 92US-0894061.
XX 22-JAN-1993; 93US-0009266.
XX 05-AUG-1993; 93US-0102852.
XX
XX (ICOS-) ICOS CORP.
XX
XX Gallatin WM, Vazeux R;
XX
XX MPI: 2000-542449/49.
XX N-PSDB; AAA97155.
XX
XX Hybrid fusion proteins comprising intercellular adhesion molecule or
XX its variants useful, for treating inflammatory conditions, Crohn's
XX disease, atherosclerosis and diabetes
XX
XX Example 13; Column 127-128; 109pp; English.
XX
XX This invention relates to a hybrid fusion protein comprising an
XX intercellular adhesion molecule (ICAM-R) amino acid fragment at its
XX amino terminus and a constant domain of an immunoglobulin heavy chain at
XX its carboxy terminus. ICAM-R polypeptides are useful for treating and
XX monitoring inflammatory conditions such as adult respiratory distress
XX syndrome, multiple organ injury syndrome secondary to septicemia or
XX trauma, reperfusion injury of tissue, acute glomerulonephritis, reactive
XX arthritis, dermatosis, stroke, thermal injury, haemodialysis,
XX leukapheresis, ulcerative colitis, Crohn's disease, necrotising
XX enterocolitis, granulocyte transfusion associated syndrome,
XX atherosclerosis and cytokine induced toxicity. ICAM-R polypeptides are
XX also useful for treating conditions resulting from a response of the
XX specific immune system in a mammal e.g. psoriasis, organ/tissue
XX transplant rejection and autoimmune diseases including Raynaud's
XX syndrome, autoimmune thyroiditis, multiple sclerosis, rheumatoid
XX arthritis, diabetes and lupus erythematosus. ICAM-R products and ICAM-R
XX related products are also useful in monitoring and treating asthma,
XX tumour growth and/or metastasis, and viral infection (e.g. HIV
XX infection). Sequences AAA97090 and AAB13036 represent the human ICAM-R
XX DNA and protein sequences. Sequences AAA97091-A97112 represent ICAM-R
XX DNA fragments, PCR primers and probes, all used in the identification of
XX the ICAM-R DNA sequence. AAA97113-A97123 and AAA97129-A97152 represent
XX primers used in the production of humanised anti-ICAM-R antibody ICR-8.1,
XX and fragments of the humanised antibody. Sequences AAA97124-A97128,
XX AAA97132, AAA97144 represent ICR-8.1 sequences. Sequences AAA97153-A97176
XX excluding AAA97155-A97156 represent primers used in the production of
XX humanised anti-ICAM-R antibody ICR-1.1, and fragments of the humanised
XX antibody. Sequences AAA97155-A97156 and AAB13047-B13048 represent murine
XX ICR-1.1 sequences. DNA and peptide sequences used in the production of
XX the chimeric protein of the invention include AAA97177-A97188 and
XX AAB13050-B13051.
XX
XX Sequence 138 AA:
SQ
Query Match 78.8%; Score 78; DB 21; Length 138;
Best Local Similarity 76.5%; Pred. No. 0.00015;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 1 YINPRNDYTEYNQNFKD 17
Db 69 YINPNTDYTEYNQRFOD 85
RESULF 13
AAV82446
ID AAV82446 standard; Protein; 138 AA.
XX
XX AAV82446;
AC
XX
XX

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DT 28-JUN-2000 (first entry)
 XX Murine ICR-1.1 antibody VH protein sequence SEQ ID NO:78.
 XX
 KM Human; ICAM-R; chromosome 19; intracellular adhesion molecule receptor;
 KM CAM; ICAM-1; ICAM-2; humanised; antibody; mutagenic; chimeric; vulnarary;
 KM nephropathic; antirheumatic; cerebroprotective; antileuc; cytosolic;
 KM antileucocytotoxic; immunosuppressive; antidiabetic; neuroprotective;
 KM antileucoid; dermatological; antileuc; antileuc; antileuc; antileuc;
 KM anti-HIV; vasotropic; antileuc; immunomodulator; antileuc; antileuc;
 KM cell adhesion mediator; inflammatory condition; immunisation;
 KM immune response.
 XX
 OS Mus sp.
 XX
 PN US6040176-A.
 XX
 PD 21-MAR-2000.
 XX
 PE 12-SEP-1996; 96US-0714017.
 XX
 PR 05-AUG-1994; 94US-0286754.
 PR 27-JAN-1992; 92US-0827689.
 PR 26-MAY-1992; 92US-0889724.
 PR 05-JUN-1992; 92US-0894061.
 PR 22-JAN-1993; 93US-0009266.
 PR 26-JAN-1993; 93WO-0500787.
 PR 05-AUG-1993; 93US-0102852.
 XX
 PA (ICOS-) ICOS CORP.
 XX
 PI Gallatin WM, Vazeux R;
 XX
 DR WPI; 2000-270138/23.
 XX
 PT Novel monoclonal antibody directed against ICAM-R proteins useful for
 PT treating acute glomerulonephritis, ulcerative colitis, psoriasis
 PT rheumatoid arthritis, diabetes, multiple sclerosis, asthma and viral
 PT infection -
 PT
 PS Example 13; Column 139; 117pp; English.
 XX
 CC The present invention describes a monoclonal antibody (Mab) (I),
 CC produced by the hybridoma cell line 81K2F (ATCC HB 11692). Also described
 CC are: (1) a hybridoma cell line 81K2F; and (2) a Mab (II), that competes
 CC with (I) for binding to ICAM-R (intracellular adhesion molecule
 CC receptor) (III). (II) mimics the activity of natural binding proteins
 CC through which intercellular and intracellular activities of (III) are
 CC modulated. (II) is also used for modulating the immune responses. (I) is
 CC used for immunisation as well as for purifying (III). They are also
 CC useful in modulating the ligand/receptor binding biological activity
 CC involving (III) especially those effector functions of (III) involved in
 CC specific and non-specific immune system responses. Inflammatory
 CC conditions which may be treated or monitored with related products of
 CC (III) include conditions resulting from a response of the non-specific
 CC immune system in a mammal e.g. adult respiratory distress syndrome,
 CC multiple organ injury syndrome secondary to septicemia or trauma,
 CC reperfusion injury of tissue, acute glomerulonephritis, reactive
 CC arthritis, stroke, ulcerative colitis and atherosclerosis, and conditions
 CC resulting from a response of the specific immune system in a mammal, e.g.
 CC psoriasis, organ/tissue transplantation rejection, autoimmune diseases
 CC such as autoimmune thyroiditis, multiple sclerosis, rheumatoid arthritis,
 CC diabetes and lupus erythematosus. AA08236 to AA08334, and AA08243 to
 CC AA08251 represent sequences used in the exemplification of the present
 CC invention.
 CC
 XX
 SO Sequence 138 AA:
 Query Match 78.88; Score 78; DB 21; Length 138;
 Best Local Similarity 76.5%; Pred. No. 0.00015;
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 1 YINPRNDYTEYNQNFKD 17

DB 69 YINPNTDYTEYNQNFOD 85
 ||||| ||||| ||:|
 RESULT 14
 AA050754
 ID AA050754 standard; Protein: 138 AA.
 XX
 AC AA050754;
 XX
 DT 16-FEB-2000 (first entry)
 XX
 DE Murine antibody ICR-1.1 VH region protein.
 XX
 KM ICAM-R; murine; intercellular adhesion molecule; phosphorylation;
 KM protein kinase C; modulator; ICR-1.1; antibody.
 XX
 OS Mus sp.
 XX
 PN US5989843-A.
 XX
 PD 23-NOV-1999.
 XX
 PE 27-SEP-1996; 96US-0720420.
 XX
 PR 27-JAN-1992; 92US-0827689.
 PR 26-MAY-1992; 92US-0889724.
 PR 05-JUN-1992; 92US-0894061.
 PR 22-JAN-1993; 93US-0009266.
 PR 26-JAN-1993; 93WO-0500787.
 PR 05-AUG-1993; 93US-0102852.
 PR 07-JUN-1993; 93US-0487113.
 XX
 PA (ICOS-) ICOS CORP.
 XX
 PI Gallatin WM, Vazeux R;
 XX
 DR WPI; 2000-022778/02.
 DR N-PSDB; AA224327.
 XX
 PT Identifying modulators of protein kinase C phosphorylation of human
 PT intercellular adhesion molecule polypeptide -
 PT
 PS Example 14; Column 143-144; 122pp; English.
 XX
 CC This invention describes a novel method for identifying a compound that
 CC modulates phosphorylation of human intercellular adhesion molecule
 CC polypeptide (ICAM-R) by protein kinase C isoform. The method comprises:
 CC (a) exposing a purified peptide consisting of the cytoplasmic domain of
 CC ICAM-R to protein kinase C isoform and labeled adenosine triphosphate in
 CC the presence and absence of a test compound; (b) measuring labeled
 CC phosphate transferred to the peptide; and (c) identifying a test compound
 CC that affects transfer of the labeled phosphate as a modulator compound.
 CC The method is useful for identifying compounds that modulate the
 CC phosphorylation of human intercellular adhesion molecule polypeptide
 CC which might form the basis for the development of therapeutic and
 CC diagnostic agents. This sequence represents the murine ICR-1.1 antibody
 CC VH region which is used in the method of the invention.
 CC
 XX
 SO Sequence 138 AA:
 Query Match 78.88; Score 78; DB 21; Length 138;
 Best Local Similarity 76.5%; Pred. No. 0.00015;
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 1 YINPRNDYTEYNQNFOD 17
 ||||| ||||| ||:|
 RESULT 15
 AA070939
 ID AA070939 standard; Protein: 138 AA.

XX AAU70939;
 AC
 XX 26-FEB-2002 (first entry)
 DT
 XX
 DE Murine monoclonal antibody ICR-1.1 VH region.
 XX
 KW Human; intercellular adhesion molecule; ICAM; antiinflammatory; stroke;
 KW antibacterial; vulnery; vasotropic; nephrotropic; antiarthritic;
 KW cerebroprotective; dermatological; antilicer; immunosuppressive; tumour;
 KW antiporiatic; antiatherosclerotic; neuroprotective; antithyroid;
 KW vitruclide; antirheumatic; antidiabetic; antiastrmatic; cytosatic; asthma;
 KW hybridoma cell line; ATCC HB 12190; inflammation; septicemia; trauma;
 KW adult respiratory distress syndrome; multiple organ injury syndrome;
 KW tissue reperfusion injury; acute glomerulonephritis; arthritis; vaccine;
 KW dermatosis; thermal injury; haemodialysis; leukopheresis; psoriasis;
 KW Crohn's disease; ulcerative colitis; multiple sclerosis; infection.
 XX
 OS Mus sp.
 XX
 XX US2001029293-A1.
 XX
 XX 11-OCT-2001.
 XX
 PD 03-JAN-2001; 2001US-0753436.
 XX
 PF 24-AUG-1999; 99US-0382289.
 XX PR 27-JAN-1992; 92US-0827689.
 PR 26-MAY-1992; 92US-0889724.
 PR 05-JUN-1992; 92US-0894061.
 PR 22-JAN-1993; 93US-0009266.
 PR 26-JAN-1993; 93WO-0500787.
 PR 05-AUG-1993; 93US-0102852.
 PR 07-JUN-1995; 95US-0487113.
 XX
 XX (ICOS-) ICOS CORP.
 XX
 PA Gallatin WM, Vazeux R;
 XX
 P1
 XX
 DR WPI; 2002-009992/01.
 DR P-PSDB; AAU70939.
 XX
 PT Novel hybridoma cell line useful for producing monoclonal antibody for
 PT treating inflammatory conditions, immune system disorders and
 PT infectious diseases, is deposited under specified ATCC accession number
 PT
 XX
 PS Page 78; Example 14; 126pp; English.
 XX
 CC The invention relates to a novel hybridoma cell line (I) ATCC HB 12190.
 CC (I) is useful for producing an intercellular adhesion molecule (ICAM)
 CC monoclonal antibody (II). (II) is useful for treating inflammatory
 CC conditions including adult respiratory distress syndrome, multiple organ
 CC injury syndrome secondary to septicemia or trauma, tissue reperfusion
 CC injury, acute glomerulonephritis, reactive arthritis, dermatosis with
 CC acute inflammatory components, stroke, thermal injury, haemodialysis,
 CC leukopheresis, ulcerative colitis, Crohn's disease, necrotising
 CC enterocolitis, granulocyte transfusion associated syndrome, diabetes,
 CC atherosclerosis, cytokine-induced toxicity, psoriasis, organ/tissue
 CC transplant rejection, autoimmune diseases including Raynaud's syndrome,
 CC autoimmune thyroiditis, multiple sclerosis, rheumatoid arthritis,
 CC lupus erythematosus, asthma, tumour growth and/or metastasis, viral
 CC infection, tissue transplant rejection, graft versus host disease and
 CC multiple sclerosis. (II) is also useful for immunisation, for purifying
 CC ICAM-R polypeptides and for identifying cells that display the
 CC polypeptides on their surfaces. AAU70928-AAU70946 represent ICAM
 CC amino acid sequences of the invention.
 CC
 XX
 SQ Sequence 138 AA;

OY 1 YINPRNDYEXNONFKD 17
 |||| ||||| :|
 DB 69 YINPNTDYEXNQRFQD 85

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Query Match 78.8%; Score 78; DB 23; Length 138;
 Best Local Similarity 76.5%; Pred. No. 0.00015;
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: October 7, 2003, 19:07:41 ; Search time 8.7931 Seconds

(without alignments)
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Total number of hits satisfying chosen parameters: 587654

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	99	100.0	116	11	US-09-894-839-4
5	99	100.0	116	11	US-09-894-839-8
6	99	100.0	116	11	US-09-894-839-21
7	99	100.0	116	11	US-09-898-013A-4
8	99	100.0	116	11	US-09-898-013A-8
9	99	100.0	116	11	US-09-898-013A-9
10	99	100.0	116	11	US-09-898-013A-9
11	99	100.0	116	12	US-10-127-890-167
12	99	100.0	116	12	US-10-127-890-167
13	99	100.0	116	12	US-10-127-890-169
14	99	100.0	116	12	US-10-244-821-91
15	99	100.0	116	12	US-10-244-821-91

16	70	70.7	256	15	US-10-247-488-2	Sequence 2, Appl1
17	70	70.7	258	15	US-10-247-488-4	Sequence 4, Appl1
18	69	69.7	119	11	US-09-795-515-11	Sequence 11, Appl1
19	69	69.7	119	11	US-09-795-515-30	Sequence 30, Appl1
20	69	69.7	119	15	US-10-267-286A-10	Sequence 10, Appl1
21	69	69.7	119	15	US-10-267-286A-12	Sequence 12, Appl1
22	69	69.7	119	15	US-10-267-286A-13	Sequence 13, Appl1
23	69	69.7	119	15	US-10-267-286A-14	Sequence 14, Appl1
24	69	69.7	468	11	US-09-795-515-7	Sequence 7, Appl1
25	69	69.7	468	11	US-10-168-809-22	Sequence 22, Appl1
26	68	68.7	116	12	US-10-127-890-168	Sequence 168, App
27	65	65.7	17	14	US-10-032-482-9	Sequence 9, Appl1
28	65	65.7	104	14	US-10-032-482-1	Sequence 1, Appl1
29	65	65.7	127	12	US-09-998-831-7	Sequence 7, Appl1
30	64	64.6	195	12	US-10-360-053-6	Sequence 6, Appl1
31	64	64.6	195	12	US-10-360-053-8	Sequence 8, Appl1
32	64	64.6	195	12	US-10-283-349-41	Sequence 41, Appl1
33	63	63.6	17	15	US-10-283-349-27	Sequence 27, Appl1
34	63	63.6	140	15	US-10-283-349-63	Sequence 63, Appl1
35	63	63.6	140	15	US-10-283-349-74	Sequence 74, Appl1
36	63	63.6	140	15	US-10-283-349-78	Sequence 78, Appl1
37	63	63.6	140	15	US-10-283-349-83	Sequence 83, Appl1
38	63	63.6	242	16	US-10-259-087A-20	Sequence 20, Appl1
39	63	63.6	119	11	US-09-795-515-12	Sequence 12, Appl1
40	62	62.6	119	11	US-09-795-515-13	Sequence 13, Appl1
41	62	62.6	119	11	US-09-795-515-14	Sequence 14, Appl1
42	62	62.6	119	11	US-09-795-515-15	Sequence 15, Appl1
43	62	62.6	119	11	US-09-795-515-16	Sequence 16, Appl1
44	62	62.6	119	11	US-09-795-515-17	Sequence 17, Appl1
45	62	62.6	119	11	US-09-795-515-17	Sequence 17, Appl1

ALIGNMENTS

RESULT 1

US-09-741-843-4

; Sequence 4, Application US/09741843

; Patent No. US20020102254A1

; GENERAL INFORMATION:

; APPLICANT: LEUNG, Shui-on

; APPLICANT: HANSEN, Hens

; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL

; FILE REFERENCE: 018733/0996

; CURRENT APPLICATION NUMBER: US/09/741.843

; CURRENT FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: US 09/127,902

; PRIOR FILING DATE: 1998-08-03

; PRIOR APPLICATION NUMBER: US 08/690,102

; PRIOR FILING DATE: 1996-07-06

; PRIOR APPLICATION NUMBER: US 08/289,576

; PRIOR FILING DATE: 1994-08-12

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 116

; TYPE: PRT

; ORGANISM: Murinae gen. sp.

US-09-741-843-4

Query Match 100.0%; Score 99; DB 10; Length 116;

Best Local Similarity 100.0%; Pred. No. 9.8e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YINPRNDYTEYNONFKD 17

DB 50 YINPRNDYTEYNONFKD 66

RESULT 2

US-09-741-843-8

; Sequence 8, Application US/09741843

```
; Patent No. US20020102254A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL LYM
; FILE REFERENCE: 018733/0996
; CURRENT APPLICATION NUMBER: US/09/741,843
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/127,902
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/690,102
; PRIOR FILING DATE: 1996-07-06
; PRIOR APPLICATION NUMBER: US 08/289,576
; PRIOR FILING DATE: 1994-08-12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-741-843-8
```

```
Query Match          100.0%; Score 99; DB 10; Length 116;
Best Local Similarity 100.0%; Pred. No. 9,8e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 YINPRNDYTEYNONFMD 17
        |||
Db      50 YINPRNDYTEYNONFMD 66
```

```
RESULT 3
US-09-741-843-9
; Sequence 9, Application US/09741843
; Patent No. US20020102254A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL LYM
; FILE REFERENCE: 018733/0996
; CURRENT APPLICATION NUMBER: US/09/741,843
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/127,902
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/690,102
; PRIOR FILING DATE: 1996-07-06
; PRIOR APPLICATION NUMBER: US 08/289,576
; PRIOR FILING DATE: 1994-08-12
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-741-843-9
```

```
Query Match          100.0%; Score 99; DB 10; Length 116;
Best Local Similarity 100.0%; Pred. No. 9,8e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 YINPRNDYTEYNONFMD 17
        |||
Db      50 YINPRNDYTEYNONFMD 66
```

```
RESULT 4
US-09-894-839-4
; Sequence 4, Application US/09894839
; Publication No. US20030035800A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
```

```
; APPLICANT: HANSEN, Hans
; APPLICANT: QU, Zhengxing
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/1049
; CURRENT APPLICATION NUMBER: US/09/894,839
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/155,107
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 60/013,709
; PRIOR FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-894-839-4
```

```
Query Match          100.0%; Score 99; DB 11; Length 116;
Best Local Similarity 100.0%; Pred. No. 9,8e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 YINPRNDYTEYNONFMD 17
        |||
Db      50 YINPRNDYTEYNONFMD 66
```

```
RESULT 5
US-09-894-839-8
; Sequence 8, Application US/09894839
; Publication No. US20030035800A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/1049
; CURRENT APPLICATION NUMBER: US/09/894,839
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/155,107
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 60/013,709
; PRIOR FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-894-839-8
```

```
Query Match          100.0%; Score 99; DB 11; Length 116;
Best Local Similarity 100.0%; Pred. No. 9,8e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 YINPRNDYTEYNONFMD 17
        |||
Db      50 YINPRNDYTEYNONFMD 66
```

```
RESULT 6
US-09-894-839-21
; Sequence 21, Application US/09894839
; Publication No. US20030035800A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; APPLICANT: QU, Zhengxing
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/1049
; CURRENT APPLICATION NUMBER: US/09/894,839
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/155,107
```

;; PRIOR FILING DATE: 1998-11-17
;; PRIOR APPLICATION NUMBER: US 60/013,709
;; PRIOR FILING DATE: 1996-03-20
;; NUMBER OF SEQ ID NOS: 47
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 21
;; LENGTH: 116
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-894-839-21

Query Match 100.0%; Score 99; DB 11; Length 116;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YINPRNDYTEYNONFKD 17
|||||
DB 50 YINPRNDYTEYNONFKD 66

RESULT 7
US-09-988-013A-4
;; Sequence 4, Application US/09988013A
;; Publication No. US20030103979A1
;; GENERAL INFORMATION:
;; APPLICANT: LEUNG, Shui-on
;; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-
;; FILE REFERENCE: 18733/1082
;; CURRENT FILING DATE: 2002-10-29
;; PRIOR APPLICATION NUMBER: US 09/741,843
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: US 09/127,902
;; PRIOR FILING DATE: 1998-08-03
;; PRIOR APPLICATION NUMBER: US 08/690,102
;; PRIOR FILING DATE: 1996-07-06
;; PRIOR APPLICATION NUMBER: US 08/289,576
;; PRIOR FILING DATE: 1994-08-12
;; NUMBER OF SEQ ID NOS: 25
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 4
;; LENGTH: 116
;; TYPE: PRT
;; ORGANISM: Murinae gen. sp.
US-09-988-013A-4

Query Match 100.0%; Score 99; DB 11; Length 116;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YINPRNDYTEYNONFKD 17
|||||
DB 50 YINPRNDYTEYNONFKD 66

RESULT 8
US-09-988-013A-8
;; Sequence 8, Application US/09988013A
;; Publication No. US20030103979A1
;; GENERAL INFORMATION:
;; APPLICANT: LEUNG, Shui-on
;; APPLICANT: HANSEN, Hans
;; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-
;; FILE REFERENCE: 18733/1082
;; CURRENT FILING DATE: 2002-10-29
;; PRIOR APPLICATION NUMBER: US 09/741,843
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: US 09/127,902
;; PRIOR FILING DATE: 1998-08-03

;; PRIOR APPLICATION NUMBER: US 08/690,102
;; PRIOR FILING DATE: 1996-07-06
;; PRIOR APPLICATION NUMBER: US 08/289,576
;; PRIOR FILING DATE: 1994-08-12
;; NUMBER OF SEQ ID NOS: 25
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 8
;; LENGTH: 116
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-988-013A-8

Query Match 100.0%; Score 99; DB 11; Length 116;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YINPRNDYTEYNONFKD 17
|||||
DB 50 YINPRNDYTEYNONFKD 66

RESULT 9
US-09-988-013A-9
;; Sequence 9, Application US/09988013A
;; Publication No. US20030103979A1
;; GENERAL INFORMATION:
;; APPLICANT: LEUNG, Shui-on
;; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-
;; FILE REFERENCE: 18733/1082
;; CURRENT FILING DATE: 2002-10-29
;; PRIOR APPLICATION NUMBER: US 09/741,843
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: US 09/127,902
;; PRIOR FILING DATE: 1998-08-03
;; PRIOR APPLICATION NUMBER: US 08/690,102
;; PRIOR FILING DATE: 1996-07-06
;; PRIOR APPLICATION NUMBER: US 08/289,576
;; PRIOR FILING DATE: 1994-08-12
;; NUMBER OF SEQ ID NOS: 25
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 9
;; LENGTH: 116
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-988-013A-9

Query Match 100.0%; Score 99; DB 11; Length 116;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YINPRNDYTEYNONFKD 17
|||||
DB 50 YINPRNDYTEYNONFKD 66

RESULT 10
US-09-753-436-78
;; Sequence 78, Application US/09753436
;; Patent No. US20010029293A1
;; GENERAL INFORMATION:
;; APPLICANT: Gallatin, W. Michael
;; TITLE OF INVENTION: ICAM-Related Materials and Methods
;; NUMBER OF SEQUENCES: 120
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;; STREET: 6300 Sears Tower, 233 South Wacker Drive
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: United States of America

ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/753,436
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/382,289
FILING DATE:
APPLICATION NUMBER: US 08/487,113
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,754
FILING DATE: 05-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Joseph A., Jr.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 33282
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6500
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-753-436-78

Query Match 78.88; Score 78; DB 9; Length 138;
Best Local Similarity 76.58; Pred. No. 0.00018;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 YINPRNDYTEYNOKFD 17
||||| ||||| 1:1
Db 69 YINPRNDYTEYNOKFD 85

RESULT 11
US-10-127-890-167
Sequence 167, Application US/10127890
Publication No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago

STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 167:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 167:
US-10-127-890-167

Query Match 74.78; Score 74; DB 12; Length 116;
Best Local Similarity 76.58; Pred. No. 0.00059;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 YINPRNDYTEYNOKFD 17
||||| ||||| 1:1
Db 50 YINPRNDYTEYNOKFD 66

RESULT 12
US-10-127-890-169
Sequence 169, Application US/10127890
Publication No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible


```
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 169:
US-10-127-890-169

Query Match      74.7%; Score 74; DB 12; Length 116;
Best Local Similarity 76.5%; Pred. No. 0.00059;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY      1 YINPRNDYTEYNQKFD 17
      |||| ||||| |||
Db      50 YINPSTGYTEYNQKFD 66

RESULT 13
US-10-244-821-91
; Sequence 91, Application US/10244821
; Publication No. US20030143233A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen Charles
; APPLICANT: Graves, Scott Stoll
; APPLICANT: Schultz, Joanne Elaine
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James Allen
; APPLICANT: Reno, John M.
; APPLICANT: Dearstyn, Erica A.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; FILE REFERENCE: 690022.547C3
; CURRENT APPLICATION NUMBER: US/10/244,821
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-244-821-91

Query Match      74.7%; Score 74; DB 12; Length 135;
Best Local Similarity 76.5%; Pred. No. 0.0007;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      1 YINPRNDYTEYNQKFD 17
      |||| ||||| |||
Db      69 YINPSTGYTEYNQKFD 85

RESULT 14
US-10-244-821-88
; Sequence 88, Application US/10244821
; Publication No. US20030143233A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen Charles
; APPLICANT: Graves, Scott Stoll
; APPLICANT: Schultz, Joanne Elaine
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James Allen
; APPLICANT: Reno, John M.
; APPLICANT: Dearstyn, Erica A.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; FILE REFERENCE: 690022.547C3
; CURRENT APPLICATION NUMBER: US/10/244,821
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-244-821-88

Query Match      74.7%; Score 74; DB 12; Length 438;
Best Local Similarity 76.5%; Pred. No. 0.0025;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY      1 YINPRNDYTEYNQKFD 17
      |||| ||||| |||
Db      72 YINPSTGYTEYNQKFD 88

RESULT 15
US-09-753-436-86
; Sequence 86, Application US/09753436
; Patent No. US20010029293A1
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICAM-Related Materials and Methods
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/753,436
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/382,289
; FILING DATE:
; APPLICATION NUMBER: US 08/487,113
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,754
; FILING DATE: 05-AUG-1994
```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Joseph A., Jr.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 33282
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3836
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-753-436-86

Query Match 72.78; Score 72; DB 9; Length 123;
Best Local Similarity 75.08; Pred. No. 0.0013;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 1 YINPRNDYTEYNQNF 16
||| ||||| |:
Db 54 YINPNTDYTEYNQRFQ 69

Search completed: October 7, 2003, 19:24:27
Job time: 8.7931 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 19:07:11 ; Search time 6.33103 Seconds

(without alignments)
258.231 Million cell updates/sec

Title: US-09-988-013a-4_COPY_50_66

Perfect score: 99

Sequence: 1 YINPRNDYTEYNQNFKD 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR.76:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	81.8	139	2 PS0024	Ig heavy chain pre
2	80	80.8	96	2 SI7615	Ig heavy chain v r
3	75	75.8	102	2 S26471	Ig heavy chain v r
4	75	75.8	106	2 PH1005	Ig heavy chain v r
5	75	75.8	139	2 A27609	Ig heavy chain pre
6	74	74.7	96	2 SI7612	Ig heavy chain v r
7	74	74.7	96	2 SI7621	Ig heavy chain v r
8	74	74.7	96	2 SI7606	Ig heavy chain v r
9	74	74.7	96	2 SI7616	Ig heavy chain v r
10	74	74.7	96	2 SI7602	Ig heavy chain v r
11	74	74.7	96	2 SI7611	Ig heavy chain v r
12	74	74.7	96	2 SI7619	Ig heavy chain v r
13	74	74.7	96	2 SI7607	Ig heavy chain v r
14	74	74.7	96	2 SI7613	Ig heavy chain v r
15	74	74.7	96	2 SI7617	Ig heavy chain v r
16	72	72.7	84	2 PH1487	Ig heavy chain v r
17	70	70.7	96	2 SI7230	Ig heavy chain v r
18	70	70.7	96	2 SI7618	Ig heavy chain v r
19	70	70.7	96	2 SI7620	Ig heavy chain v r
20	70	70.7	96	2 SI7614	Ig heavy chain v r
21	70	70.7	96	2 SI7610	Ig heavy chain v r
22	70	70.7	121	2 A21854	Ig heavy chain v r
23	69	69.7	98	2 B24754	Ig heavy chain v r
24	67	67.7	114	2 PL0247	Ig heavy chain v r
25	67	67.7	117	2 JC2269	PL7-6 antibody hea
26	67	67.7	123	2 G48677	Ig heavy chain v-D
27	66	66.7	98	2 A28572	Ig heavy chain v r
28	66	66.7	114	2 PH1522	Ig heavy chain v r
29	66	66.7	114	2 PH1523	Ig heavy chain v r

30	66	66.7	118	2 S38565	Ig heavy chain v r
31	66	66.7	119	2 PH1517	Ig heavy chain v r
32	66	66.7	119	2 PH1521	Ig heavy chain v r
33	66	66.7	119	2 PH1504	Ig heavy chain v r
34	66	66.7	119	2 PH1500	Ig heavy chain v r
35	66	66.7	119	2 PH1502	Ig heavy chain v r
36	66	66.7	119	2 PH1505	Ig heavy chain v r
37	66	66.7	119	2 PH1512	Ig heavy chain v r
38	66	66.7	119	2 PH1520	Ig heavy chain v r
39	66	66.7	121	2 A26405	Ig heavy chain v r
40	66	66.7	140	2 PH1482	Ig heavy chain v r
41	66	66.7	140	2 PH1484	Ig heavy chain v r
42	64	64.6	107	2 S26320	Ig heavy chain v r
43	63	63.6	94	2 PH0996	Ig heavy chain v r
44	63	63.6	97	2 SI7603	Ig heavy chain v r
45	63	63.6	98	2 S26313	Ig heavy chain v r

ALIGNMENTS

RESULT 1

PS0024

Ig heavy chain precursor V region (6A4) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 22-Nov-1996

C:Accession: PS0024

R:Margel, M.; Eckhardt, A.; Ehret, W.; von Specht, B.U.; Duchene, M.; Domdey, H.

Gene 74, 335-345, 1988

A:Title: Cloning and characterization of cDNAs coding for the heavy and light chains

A:Reference number: PS0023; MUID:85232725; PMID:314944

A:Accession: PS0024

A:Molecule type: mRNA

A:Residues: 1-139 <MAR>

A:Experimental source: strain BALB/c

C:Comment: This chain is obtained from an IgG2a monoclonal antibody against Pseudomon

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin; pyroglyutamic acid

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-139/Domain: Ig heavy chain V region #status predicted <IGV>

F:34-117/Domain: immunoglobulin homology <IMM>

F:20/Modified site: pyrrolidone carboxylic acid (Gln) (1n mature form) #status predic

Query Match

Best Local Similarity 81.8%; Score 81; DB 2; Length 139;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YINPRNDYTEYNQNFKD 17

DB 69 YINPNTGYTEYNQNFKD 85

RESULT 2

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997

C:Accession: SI7615

R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.

Nature 352, 624-628, 1991

A:Title: Making antibody fragments using phage display libraries.

A:Reference number: SI7230; MUID:91326098; PMID:1907718

A:Accession: SI7615

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-96 <CIA>

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F:8-91/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 80.8%; Score 80; DB 2; Length 96;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YINPRNDYTEYNONFKD 17
||||| ||||| |||
Db 43 YINPRTGYTEYNOKFKD 59

RESULT 3

S26471
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_rev1sion 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S26471
R:Kavaler, J.
submitted to the EMBL Data Library, April 1991
A:Reference number: S26459
A:Accession: S26471
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-102 <RAY>
A:Cross-references: EMBL:X59110; NID:951951; PIDN:CAA41836.1; PID:951952
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; Immunoglobulin
F:15-98/Domain: Immunoglobulin homology <IMM>

Query Match 75.8%; Score 75; DB 2; Length 102;
Best Local Similarity 76.5%; Pred. No. 0.00015;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YINPRNDYTEYNONFKD 17
||||| ||||| |||
Db 50 YINPSSGYTEYNOKFKD 66

RESULT 4

PH1005
Ig heavy chain V region (clone 202.54) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1993 #sequence_rev1sion 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH1005
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cells
A:Reference number: PH0971; MVID:92381444; PMID:1512540
A:Accession: PH1005
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1106 <RIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; Immunoglobulin
F:15-98/Domain: Immunoglobulin homology <IMM>

Query Match 75.8%; Score 75; DB 2; Length 106;
Best Local Similarity 76.5%; Pred. No. 0.00015;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YINPRNDYTEYNONFKD 17
||||| ||||| |||
Db 50 YINPSSGYTEYNOKFKD 66

RESULT 5

A27609
Ig heavy chain precursor V region (129) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 15-Dec-1988 #sequence_rev1sion 30-Jun-1991 #text_change 23-Jul-1999
C:Accession: A27609
R:Klein, D.; Nieuwkoop, J.; Sirin, S.; Stavnezer, J.
J. Immunol. 140, 1676-1684, 1988
A:Title: L.29 lymphoma cells express a nonmutated V-H gene before and after H chain switch
A:Reference number: A27609; MVID:88154467; PMID:3126234
A:Accession: A27609
A:Molecule type: DNA

A:Residues: 1-139 <KLE>
A:Cross-references: EMBL:M19401; NID:9195441; PIDN:AAA38303.1; PID:9553992
C:Genetics: 16/1
A:Insertions: 16/1
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; Immunoglobulin
F:1-19/Domain: signal sequence #status predicted <Sig>
F:20-139/Product: Ig heavy chain V region 129 #status predicted <VAR>
F:34-117/Domain: Immunoglobulin homology <IMM>

Query Match 75.8%; Score 75; DB 2; Length 139;
Best Local Similarity 81.2%; Pred. No. 0.00021;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YINPRNDYTEYNONFK 16
||||| ||||| |||
Db 69 YINPRNDYTEYNOKFK 84

RESULT 6

S17612
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 22-Nov-1993 #sequence_rev1sion 10-Nov-1995 #text_change 06-Jun-1997
C:Accession: S17612
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: S17230; MVID:91326098; PMID:1907718
A:Accession: S17612
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-96 <CLA>
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; Immunoglobulin
F:8-91/Domain: Immunoglobulin homology <IMM>

Query Match 74.7%; Score 74; DB 2; Length 96;
Best Local Similarity 76.5%; Pred. No. 0.0002;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 YINPRNDYTEYNONFKD 17
||||| ||||| |||
Db 43 YINPRTGYTEYNOKFKD 59

RESULT 7

S17621
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 22-Nov-1993 #sequence_rev1sion 10-Nov-1995 #text_change 06-Jun-1997
C:Accession: S17621
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: S17230; MVID:91326098; PMID:1907718
A:Accession: S17621
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-96 <CLA>
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; Immunoglobulin
F:8-91/Domain: Immunoglobulin homology <IMM>

Query Match 74.7%; Score 74; DB 2; Length 96;
Best Local Similarity 76.5%; Pred. No. 0.0002;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 YINPRNDYTEYNONFKD 17
||||| ||||| |||
Db 43 YINPRTGYTEYNOKFKD 59

```
RESULT 8
S17606
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C:Accession: S17606
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: S17230; MUID:91326098; PMID:1907718
A:Accession: S17606
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-96 <C1A>
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-91/Domain: immunoglobulin homology <IMM>

Query Match          74.7%; Score 74; DB 2; Length 96;
Best Local Similarity 76.5%; Pred. No. 0.0002;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 YINPRNDYTEYNQNFKD 17
    |||| ||||| |||
Db 43 YINPSTGYTEYNQNFKD 59

RESULT 9
S17616
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C:Accession: S17616
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: S17230; MUID:91326098; PMID:1907718
A:Accession: S17616
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-96 <C1A>
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-91/Domain: immunoglobulin homology <IMM>

Query Match          74.7%; Score 74; DB 2; Length 96;
Best Local Similarity 76.5%; Pred. No. 0.0002;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 YINPRNDYTEYNQNFKD 17
    |||| ||||| |||
Db 43 YINPSTGYTEYNQNFKD 59

RESULT 10
S17602
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C:Accession: S17602
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: S17230; MUID:91326098; PMID:1907718
A:Accession: S17602
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-96 <C1A>
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-91/Domain: immunoglobulin homology <IMM>

Query Match          74.7%; Score 74; DB 2; Length 96;
Best Local Similarity 76.5%; Pred. No. 0.0002;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 YINPRNDYTEYNQNFKD 17
    |||| ||||| |||
Db 43 YINPSTGYTEYNQNFKD 59
```

```
Best Local Similarity 76.5%; Pred. No. 0.0002;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 YINPRNDYTEYNQNFKD 17
    |||| ||||| |||
Db 43 YINPSTGYTEYNQNFKD 59

RESULT 11
S17611
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C:Accession: S17611
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: S17230; MUID:91326098; PMID:1907718
A:Accession: S17611
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-96 <C1A>
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-91/Domain: immunoglobulin homology <IMM>

Query Match          74.7%; Score 74; DB 2; Length 96;
Best Local Similarity 76.5%; Pred. No. 0.0002;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 YINPRNDYTEYNQNFKD 17
    |||| ||||| |||
Db 43 YINPSTGYTEYNQNFKD 59

RESULT 12
S17619
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C:Accession: S17619
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: S17230; MUID:91326098; PMID:1907718
A:Accession: S17619
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-96 <C1A>
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-91/Domain: immunoglobulin homology <IMM>

Query Match          74.7%; Score 74; DB 2; Length 96;
Best Local Similarity 76.5%; Pred. No. 0.0002;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 YINPRNDYTEYNQNFKD 17
    |||| ||||| |||
Db 43 YINPSTGYTEYNQNFKD 59

RESULT 13
S17607
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C:Accession: S17607
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: S17230; MUID:91326098; PMID:1907718
A:Accession: S17607
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A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-96 <CLIA>
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotetramer; Immunoglobulin
 F:8-91/Domain: Immunoglobulin homology <IMM>

Query Match 74.7%; Score 74; DB 2; Length 96;
 Best Local Similarity 76.5%; Pred. No. 0.0002;
 Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 YINPRNDYTEYNQNFKD 17
 |||| ||||| |||
 DB 43 YINPSTGYTEYNQNFKD 59

RESULT 14

S17613
 Ig heavy chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
 C:Accession: S17613
 R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
 Nature 352, 624-628, 1991
 A>Title: Making antibody fragments using phage display libraries.
 A:Reference number: S17230; MOID:91326098; PMID:1907718
 A:Accession: S17613
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-96 <CLIA>
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotetramer; Immunoglobulin
 F:8-91/Domain: Immunoglobulin homology <IMM>

Query Match 74.7%; Score 74; DB 2; Length 96;
 Best Local Similarity 76.5%; Pred. No. 0.0002;
 Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 YINPRNDYTEYNQNFKD 17
 |||| ||||| |||
 DB 43 YINPSTGYTEYNQNFKD 59

RESULT 15

S17617
 Ig heavy chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
 C:Accession: S17617
 R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
 Nature 352, 624-628, 1991
 A>Title: Making antibody fragments using phage display libraries.
 A:Reference number: S17230; MOID:91326098; PMID:1907718
 A:Accession: S17617
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-96 <CLIA>
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotetramer; Immunoglobulin
 F:8-91/Domain: Immunoglobulin homology <IMM>

Query Match 74.7%; Score 74; DB 2; Length 96;
 Best Local Similarity 76.5%; Pred. No. 0.0002;
 Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 YINPRNDYTEYNQNFKD 17
 |||| ||||| |||
 DB 43 YINPSTGYTEYNQNFKD 59

Search completed: October 7, 2003, 19:21:50
 Job time : 6.33103 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 19:03:46 ; Search time 3.45862 Seconds
(without alignments)
231.148 Million cell updates/sec

Title: US-09-988-013A-4_COPY_50_66
Perfect score: 99
Sequence: 1 YINPRNDYTEYNONFKD 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Swissprot_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66.7	120	1	HY03_MOUSE	P01747 mus musculu
2	59.6	140	1	HY02_MOUSE	P01746 mus musculu
3	53.5	117	1	HY12_MOUSE	P01756 mus musculu
4	53.5	117	1	HY13_MOUSE	P01757 mus musculu
5	53.5	118	1	HY51_MOUSE	P06330 mus musculu
6	49.5	120	1	HY50_MOUSE	P06329 mus musculu
7	48.5	117	1	HY04_MOUSE	P01748 mus musculu
8	48.5	117	1	HY14_MOUSE	P01758 mus musculu
9	48.5	982	1	MSHM_SARGL	O63852 sarcophyton
10	47.5	48.0	284	HPRT_SCHMA	P03383 schistosoma
11	47.5	117	1	HY05_MOUSE	P01749 mus musculu
12	44.4	117	1	VN01_VACCV	P17361 vaccinia vi
13	44.4	532	1	YHB7_YEAST	P38745 saccharomyc
14	44.4	1783	1	V468_MYCCE	O49460 mycoplasma
15	43.9	43.4	821	VOIG_ECOLI	P76655 escherichia
16	43.4	117	1	HY06_MOUSE	P01750 mus musculu
17	43.4	138	1	HY48_MOUSE	P03980 mus musculu
18	43.4	512	1	YE94_SCHPO	O13766 schizosacch
19	43.4	623	1	VGLE_VZVD	P09259 varicella-z
20	43.4	640	1	EX5A_HAETN	P45158 haemophilus
21	43.4	1168	1	MYSC_ACACA	P10569 acanthamoeb
22	42.5	398	1	TXB1_HUMAN	O43435 homo sapien
23	42.5	881	1	YFCU_ECOLI	P77196 escherichia
24	42.4	193	1	SODF_COXBU	P19685 coxiella bu
25	42.4	393	1	ILIS_CERAE	O28612 cercopithec
26	42.4	398	1	ILIS_HUMAN	P27930 homo sapien
27	42.4	430	1	PURA_LISTIN	O92195 listeria in
28	42.4	2515	1	TUD_DROME	P25823 drosophila
29	41.5	174	1	Y281_PYRHO	O58010 pyrococcus
30	41.5	41.9	1	TX37_CAEBL	O942c9 caenorhabdi
31	41.5	704	1	MSG2_YEAST	P33748 saccharomyc
32	41.4	117	1	HY09_MOUSE	P01753 mus musculu
33	41.4	117	1	HY10_MOUSE	P01754 mus musculu

34	41	41.4	117	1	HY49_MOUSE	P06328 mus musculu
35	41	41.4	139	1	HY07_MOUSE	P01751 mus musculu
36	41	41.4	232	1	RFAY_ECOLI	P27240 escherichia
37	41	41.4	271	1	PYR6_FREDI	P14880 fremyella d
38	41	41.4	325	1	HRCA_STAM	P45556 straphylococ
39	41	41.4	325	1	HRCA_STAM	O8hw8 straphylococ
40	41	41.4	331	1	SR49_CAEBL	O09212 caenorhabdi
41	41	41.4	650	1	PEX8_PICAN	O09225 pichia angu
42	41	41.4	704	1	Y590_METVA	O58010 methanococc
43	41	41.4	804	1	FPS_DROME	P18100 drosophila
44	41	41.4	826	1	CRAA_BACUH	O94597 bacillus th
45	41	41.4	2547	1	PAFX_HUMAN	O93008 h probable

ALIGNMENTS

```
RESULT 1
HY03_MOUSE STANDARD; PRT; 120 AA.
ID HY03_MOUSE
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 1g heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Siekevitz M., Gelfer M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT *The genetic basis of antibody production: the dominant anti-arsenate
RT idotype response of the strain A mouse.*;
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC HSSP; P01789; IMCP.
DR InterPro: IPR007110; Ig-1-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig-V.
DR Pfam: PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 111 IG-LIKE.
FT NON_TER 120 120
SQ SEQUENCE 120 AA: 13307 MW: FF04E9A167B654AF CRC64:
Query Match 66.7%; Score 66; DB 1; Length 120;
Best Local Similarity 68.8%; Pred. No. 0.0035;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 YINPRNDYTEYNONFK 16
DB 49 YINPENGTYKYNKFK 64
RESULT 2
HY02_MOUSE STANDARD; PRT; 140 AA.
ID HY02_MOUSE
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 1g heavy chain V region 9367 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbits T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RL Science 216:309-311(1982).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J00493; AAA8128.1; -.
DR PIR: A94264; HVMSC7.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR007110; Ig_1like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG-LIKE; 1.
DR Immunoglobulin V region; HydrIdoma; Signal.
KM DOMAIN 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 9367.
FT NON_TER 20 139 IG-LIKE.
FT SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;
SQ
Query Match 59.6%; Score 59; DB 1; Length 140;
Best Local Similarity 62.5%; Pred. No. 0.045;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 YINPRNDYTEYNQNFK 16
DB 69 YINPGNGTSTYNQFK 84
RESULT 3
HV12_MOUSE
ID HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RX MEDLINE=83075344; PubMed=6816276;
RA Khury M.R., Fuhman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RL Biochemistry 21:5415-5424(1982).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC PIR: A02039; MHMS4E.
DR HSSP: P01789; IMCP.
DR InterPro: IPR007110; Ig-1like.

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DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG-LIKE; 1.
KM Immunoglobulin V region; Glycoprotein.
FT DOMAIN 1 16
FT DISULFID 22 96 IG-LIKE.
FT CARBOHYD 55 55 BY SIMILARITY.
FT NON_TER 117 117 N-LINKED (GLCNAC. . .) (COMPLEX).
FT SEQUENCE 117 AA; 12983 MW; 3CF8ACF8BE447E41 CRC64;
SQ
Query Match 53.5%; Score 53; DB 1; Length 117;
Best Local Similarity 66.7%; Pred. No. 0.29;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 INPRNDYTEYNQNFK 16
DB 51 INPNGGTSTYNQFK 65
RESULT 4
HV13_MOUSE
ID HV13_MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RL Nature 283:35-40(1980).
CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC PIR: A26242; MHMSJ5.
DR HSSP: P01789; IMCP.
DR InterPro: IPR007110; Ig_1like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG-LIKE; 1.
KM Immunoglobulin V region.
FT DOMAIN 1 16 IG-LIKE.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 117 117
FT SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;
SQ
Query Match 53.5%; Score 53; DB 1; Length 117;
Best Local Similarity 66.7%; Pred. No. 0.29;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 INPRNDYTEYNQNFK 16
DB 51 INPNGGTSTYNQFK 65
RESULT 5
HV51_MOUSE
ID HV51_MOUSE STANDARD; PRT; 118 AA.
AC P06350;
DT 01-JAN-1988 (Rel. 06, Created)

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DT	01-JAN-1988 (Rel. 06, last sequence update)
DT	15-JUL-1999 (Rel. 38, last annotation update)
DE	Ig heavy chain V region AC38 205.12.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxId=10090;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=84182519; PubMed=6201362;
RA	Dillard R., Boyens J., Stekevitz M., Beyreuther K., Rajewsky K.;
RT	"A V region determinant (idiotope) expressed at high frequency in B
RT	lymphocytes is encoded by a large set of antibody structural genes."
RL	EMBO J. 3:517-523(1984).
DR	PIR: A02040; MHMS38.
DR	HSSP: P01789; IMCP.
DR	InterPro: IPR007110; Ig_1like.
DR	InterPro: IPR003006; Ig_MHC.
DR	InterPro: IPR003596; Ig_V.
DR	Pfam: PF00047; Ig; 1.
DR	SMART: SM00406; Igv; 1.
DR	PROSITE: PS50835; IG_LIKE; 1.
KW	immunoglobulin V region.
FT	DOMAIN 1 98 V SEGMENT.
FT	DOMAIN 99 104 D SEGMENT.
FT	DOMAIN 105 118 J SEGMENT.
FT	DISULFID 22 96 BY SIMILARITY.
FT	NON_TER 118 118
SQ	SEQUENCE 118 AA; 12934 MW; 94FTBEEAC76ZAO18 CRC64;
OY	2 IMPRDYTEYNQNRK 16
DB	51 INPNNGSTYNQNRK 65
RESULT 6	
HVS0_MOUSE	
ID	HVS0_MOUSE STANDARD; PRG; 120 AA.
AC	P06329;
DT	01-JAN-1988 (Rel. 06, Created)
DT	01-JAN-1988 (Rel. 06, last sequence update)
DT	15-JUL-1999 (Rel. 38, last annotation update)
DE	Ig heavy chain V region AC38 15.3.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxId=10090;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=84182519; PubMed=6201362;
RA	Dillard R., Boyens J., Stekevitz M., Beyreuther K., Rajewsky K.;
RT	"A V region determinant (idiotope) expressed at high frequency in B
RT	lymphocytes is encoded by a large set of antibody structural genes."
RL	EMBO J. 3:517-523(1984).
DR	PIR: A02037; MHMS15.
DR	HSSP: P01810; ZEBJ.
DR	InterPro: IPR007110; Ig_1like.
DR	InterPro: IPR003006; Ig_MHC.
DR	InterPro: IPR003596; Ig_V.
DR	Pfam: PF00047; Ig; 1.
DR	SMART: SM00406; Igv; 1.
DR	PROSITE: PS50835; IG_LIKE; 1.
KW	immunoglobulin V region.
FT	DOMAIN 1 98 V SEGMENT.
FT	DOMAIN 99 105 D SEGMENT.
FT	DOMAIN 106 120 J SEGMENT.
FT	DISULFID 22 96 BY SIMILARITY.
FT	NON_TER 120 120
SQ	SEQUENCE 120 AA; 13311 MW; 914453FA26F09834 CRC64;

QY	2	INPRNDYTEYNOMRK	16
			:
Db	51	INPNSGCTNYNEKPK	65
RESULT 7			
ID	HV04_MOUSE	STANDARD;	PRT; 117 AA.
AC	P01748;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	Ig heavy chain V region 23 precursor.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6;		
RX	MEDLINE=81234548; PubMed=6788376;		
RA	Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K., Baltimore D.;		
RT	"Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region.";		
RL	Cell 24:625-637(1981).		
CC	-1 MISCELLANEOUS: THIS GERM LINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.		
DR	PIR: A02030; HWSZ23.		
DR	HSSP; P01810; ZFBJ.		
DR	InterPro: IPR007110; Ig_Like.		
DR	InterPro: IPR003006; Ig_MHC.		
DR	InterPro: IPR003596; Ig_V.		
DR	Pfam: PF00047; Ig_1.		
DR	SMART: SM00406; IgV_1.		
KW	PROSITE; PS50835; IG_LIKE; 1.		
FT	Immunoglobulin V region; Signal.		
FT	SIGNAL	1	19
FT	CHAIN	20	117
FT	DOMAIN	20	49
FT	DOMAIN	50	54
FT	DOMAIN	55	68
FT	DOMAIN	69	85
FT	DOMAIN	86	117
FT	DISULFID	41	115
FT	NON TER	117	117
SO	SEQUENCE	117 AA; 12772 MW; C530F829C906F69B CRC64;	
Query Match 48.5%; Score 48; DB 1; Length 117;			
Best Local Similarity 60.0%; Pred. No. 1.6;			
Matches	9; Conservative	1; Mismatches	5; Indels 0; Gaps 0;
QY	2	INPRNDYTEYNOMRK	16
			:
Db	70	INPGNGCTNYNEKPK	84
RESULT 8			
ID	HV14_MOUSE	STANDARD;	PRT; 117 AA.
AC	P01758;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DT	15-SEP-2003 (Rel. 42, Last annotation update)		
DE	Ig heavy chain V region 108a precursor.		
GN	IGH-VJ558.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		

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CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81245215; PubMed=6789211;
RA Glyvol D., Zakut R., Effron K., Rechavi G., Ram D., Cohen J.B.;
RT "Diversity of germ-line immunoglobulin VH genes.*";
RL Nature 292:426-430(1981).
CC -----
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
DR EMBL: J00488; AAA38519.1; -
DR PIR: A02041; HVMS8A.
DR HSSP: P01810; ZFBJ.
DR MGD: MGI:96486; Igh-VJ558.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
DR PROSITE: PS00835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 108A.
FT DOMAIN 20 >117 IG-LIKE.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;

Query Match 48.5%; Score 48; DB 1; Length 117;
Best Local Similarity 62.5%; Pred. No. 1.6;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 YINPRNDYTEYNQNFK 16
   ||| | | | | | | |
DB 69 YIYPYNGTGYNQFK 84

RESULT 9
MSHM_SARGL STANDARD; PRT; 982 AA.
AC 063852;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 15-DEC-1998 (Rel. 37, Last annotation update)
DE Mitochondrial Muts protein homolog.
OS Sarcophyton glaucum.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Anthozoa; Alcyonaria; Alcyonacea;
OC Alcyonidae; Sarcophyton.
OX NCBI_TaxID=70919;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98210322; PubMed=9541536;
RA Pont-Kingdon G., Okada N.A., Macfarlane J.L., Beagley C.T.,
RA Watkins-Sims C.D., Cavalier-Smith T., Clark-Walker G.D.,
RA Wolstenholme D.R.;
RT "Mitochondrial DNA of the coral sarcophyton glaucum contains a gene
RT from the nucleus of bacterial muts: a possible case of gene transfer
RT J. Mol. Evol. 46:419-431(1998).
CC -----
CC -1- FUNCTION: NOT KNOWN.
CC -1- SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTS FAMILY.
CC -----
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CC -----
DR EMBL: AF063191; AAC16386.1; -
DR InterPro: IPR002711; HNH.
DR InterPro: IPR003615; HNH_nuc.
DR InterPro: IPR000432; Muts_C.
DR InterPro: IPR002863; Muts_N.
DR Pfam: PF01644; HNH_1.
DR Pfam: PF01624; Muts_I_1.
DR Pfam: PF05192; Muts_IIT_1.
DR Pfam: PF00488; Muts_V_1.
DR ProDom: PD001263; Muts_C_1.
DR SMART: SM00507; HNH_C_1.
DR SMART: SM00534; MutsSac_1.
DR SMART: SM00533; MutsSq_1.
DR PROSITE: PS00486; DNA_MISMATCH_REPAIR_2; 1.
DR ATP-Binding; DNA-binding; Mitochondrion.
FT NP_BIND 698 705 ATP (POTENTIAL).
SQ SEQUENCE 982 AA; 111912 MW; A3F107319BC0E023 CRC64;

Query Match 48.5%; Score 48; DB 1; Length 982;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 IMPRNDYTEYNQNFK 17
   || | | | | | | | |
DB 377 LNPIDYSELNRYKD 392

RESULT 10
HPRT_SCHMA STANDARD; PRT; 284 AA.
AC P03383;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8) (HGPR)
DE (HGPRase).
GN HGPR.
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoidae;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6183;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Puerto Rican;
RX MEDLINE=8830331; PubMed=3136439;
RA Craig S.P., McKerrow J.H., Newport G.N., Wang C.C.;
RT "Analysis of cDNA encoding the hypoxanthine-guanine
RT phosphoribosyltransferase (HGPRase) of Schistosoma mansoni; a
RT putative target for chemotherapy."
RL Nucleic Acids Res. 16:7087-7101(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=Puerto Rican;
RX MEDLINE=89160320; PubMed=2701934;
RA Craig S.P., Muralidhar M.G., McKerrow J.H., Wang C.C.;
RT "Evidence for a class of very small introns in the gene for
RT hypoxanthine-guanine phosphoribosyltransferase in Schistosoma
RT mansoni."
RL Nucleic Acids Res. 17:1635-1647(1989).
CC -----
CC -1- CATALYTIC ACTIVITY: IMP + diphosphate = hypoxanthine + 5-phospho-
CC alpha-D-ribose 1-diphosphate.
CC -1- CATALYTIC ACTIVITY: GMP + diphosphate = guanine + 5-phospho-
CC alpha-D-ribose 1-diphosphate.
CC -1- PATHWAY: Purine salvage.
CC -1- SUBUNIT: Homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.

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-----
DR EMBL; X07883; CAA30730.1; ALT-SEQ.
DR EMBL; X13531; CAA31885.1; -.
DR EMBL; X13532; CAA31885.1; JOINED.
DR EMBL; X13533; CAA31885.1; JOINED.
DR EMBL; X13534; CAA31885.1; JOINED.
DR PIR; S04278; S04278.
DR HSSP; P00492; IHP.
DR InterPro; IPR005904; Hxn.phospho.trans.
DR InterPro; IPR002375; Pr/PY JP.transf.
DR InterPro; IPR000836; PRTtransferase.
DR Pfam; PF00156; Pribosyltran; 1.
DR TIGRFAMs; TIGR01203; HGPRTase; 1.
DR PROSITE; PS00103; PUR_PYR_TRANSF; 1.
KW Transferase; Glycosyltransferase; Purine salvage; Magnesium.
FT METAL 194 194 MAGNESIUM (BY SIMILARITY).
FT METAL 195 195 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 284 AA; 31853 MW; 5C2492D6ADF6654 CRC64;

Query Match 48.0%; Score 47.5; DB 1; Length 284;
Best Local Similarity 31.2%; Pred. No. 4.7;
Matches 10; Conservative 3; Mismatches 2; Indels 17; Gaps 1;

OY 3 NPNRDY-----TEYNONEKD 17
Db 229 SPRNDYRDVGFVEVNPREFVGYALDYNDFRD 260

RESULT 11
HV05_MOUSE STANDARD; PRT; 117 AA.
ID HV05_MOUSE
AC P01749;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 19 heavy chain V region 3 precursor.
GN IGH-VJ558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Borhwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1 MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
-----
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-----
DR EMBL; J00536; AAA38605.1; -.
DR PIR; A02031; HVMS3.
DR HSSP; P01810; 2PBJ.
DR MGD; MGI:96486; Igh-VJ558.

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DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 3.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13016 MW; 427C861C53975EDC CRC64;

Query Match 47.5%; Score 47; DB 1; Length 117;
Best Local Similarity 56.2%; Pred. No. 2.2;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 2 INPRDYTEYNONEKD 17
Db 70 IYPSDSETHYNONEKD 85

RESULT 12
VN01_VACCV STANDARD; PRT; 117 AA.
ID VN01_VACCV
AC P17361;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Protein NL.
GN NL.
OS Vaccinia virus (strain WR).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxId=10254;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89073756; PubMed=2849238;
RA Kotwal G.J., Moss B.;
RT "Analysis of a large cluster of nonessential genes deleted from a
RT vaccinia virus terminal transposition mutant.";
RL Virology 167:524-537(1988).
CC -----
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-----
DR EMBL; M22812; AAA69608.1; -.
DR PIR; H33348; WZVZB8.
RW Early protein.
SQ SEQUENCE 117 AA; 13961 MW; 9E5E2110CE51B3A1 CRC64;

Query Match 44.4%; Score 44; DB 1; Length 117;
Best Local Similarity 72.7%; Pred. No. 6.3;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 6 NDYTEYNONEK 16
Db 15 NDQTYINDFK 25

RESULT 13
YHB7_YEAST STANDARD; PRT; 532 AA.
ID YHB7_YEAST

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AC p38745;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hypothetical 61.2 kDa protein in APM2-DUR3 intergenic region
DE precursor.
GN YHL017W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SOURCE FROM N.A.
RC STRAIN=8286C / AB972;
RX MEDLINE=94378003; PubMed=8091229;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
RA Du Z., Faveille A., Fulton L., Gattung S., Gelsel C., Kirsten J.,
RA Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
RA Latreille P., Louis E.J., Macri C., Mardis E., Meneses S., Mouser L.,
RA Nhan M., Rifkin L., Riles L., St Peter H., Trevaekis E., Vaughan K.,
RA Vignelli D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
RA Vaudin M.;
RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
RT VIII."
RL Science 265:2077-2082(1994).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: Strong, to yeast PTM1 and some, to S.pombe
CC SPAC6B5.07c.
CC -----
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CC -----
DR EMBL: U11583; AAB65070.1; -
DR PIR: S46831; S46831.
DR SGD: S0001009; YHL017W.
KW Hypothetical protein; Transmembrane; Signal.
FT FT SIGNAL 1 20
FT CHAIN 21 532
FT FT POTENTIAL.
FT FT HYPOTHEICAL 61.2 kDa protein in
FT FT OP11-DUR3 INTERGENIC REGION.
FT TRANSMEM 194 214 POTENTIAL.
FT TRANSMEM 226 247 POTENTIAL.
FT TRANSMEM 263 283 POTENTIAL.
FT TRANSMEM 302 322 POTENTIAL.
FT TRANSMEM 331 351 POTENTIAL.
FT TRANSMEM 376 396 POTENTIAL.
FT TRANSMEM 416 436 POTENTIAL.
SQ SEQUENCE 532 AA; 61205 MW; EF2CB7CB74006503 CRC64;

Query Match 44.4%; Score 44; DB 1; Length 532;
Best Local Similarity 63.6%; Pred. No. 30;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 PRNDYTEYKON 14
DB 480 PRNDYQEDHN 490

RESULT 14
Y468_MYCGE STANDARD; PRT; 1783 AA.
AC Q49460;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MG468.
GN MG468.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.

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OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann J.L., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhmann J.L.,
RA Nguyen D.T., Uterback T.R., Sauder D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.-F., Dougherty B.A., Bort K.F., Hu P.-C., Lucier T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT "The minimal gene complement of Mycoplasma genitalium."
RL Science 270:397-403(1995).
RN [2]
RP REVISIONS.
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann J.L., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhmann J.L.,
RA Nguyen D.T., Uterback T.R., Sauder D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.-F., Dougherty B.A., Bort K.F., Hu P.-C., Lucier T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 879-985 FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=94075230; PubMed=8253680;
RA Peterson S.N., Hu P.-C., Bort K.F., Hutchison C.A. III;
RT "A survey of the Mycoplasma genitalium genome by using random
RT sequencing."
RL J. Bacteriol. 175:7918-7930(1993).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: SOME, TO MG064.
CC -----
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CC -----
DR EMBL: U39728; AAC72488.1; -
DR EMBL: U01808; AAD12339.1; -
DR TTGR: MG468; -
DR InterPro: IPR003838; DUF214.
DR Pfam: PF02687; FtsX; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT FT SIGNAL 16 36
FT TRANSMEM 917 937 POTENTIAL.
FT TRANSMEM 967 987 POTENTIAL.
FT TRANSMEM 1010 1030 POTENTIAL.
FT TRANSMEM 1084 1104 POTENTIAL.
FT TRANSMEM 1660 1680 POTENTIAL.
FT TRANSMEM 1709 1729 POTENTIAL.
FT TRANSMEM 1730 1750 POTENTIAL.
FT TRANSMEM 1752 1772 POTENTIAL.
SQ SEQUENCE 1783 AA; 200168 MW; 87BD575AEC2E374B CRC64;

Query Match 44.4%; Score 44; DB 1; Length 1783;
Best Local Similarity 46.7%; Pred. No. 1e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 YINPRNDYTEYKONF 15
DB 1425 YIKPKWATRYSEKF 1439

RESULT 15
YQIG_ECOLI STANDARD; PRT; 821 AA.
AC P76655; P77034; P77035;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)

```

Search completed: October 7, 2003, 19:15:03
 Job time : 5.45862 secs

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DT 28-FEB-2003 (Rel. 41, last annotation update)
DE Hypothetical outer membrane usher protein yqig precursor.
GN YQIG OR B3046.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
CC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID:562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE-97426617; PubMed-9278503;
RA Blatter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Coliado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE-97349980; PubMed-9205837;
RA Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K.,
RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
RA Oshima T., Oyama S., Saito N., Sempel G., Satoh Y., Sivasubaram S.,
RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
RA Yamagata S., Horuchi T.;
RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
RT - K12 genome corresponding to 50.0-68.8 min on the linkage map and
RT analysis of its sequence features.";
RL DNA Res. 4:91-113(1997).
CC -1- FUNCTION: INVOLVED IN THE EXPORT AND ASSEMBLY OF A FIMBRIAL
CC SUBUNIT ACROSS THE OUTER MEMBRANE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane
CC (By similarity).
CC -1- SIMILARITY: BELONGS TO THE FIMBRIAL EXPORT USHER FAMILY.
CC -1- CAUTION: Ref.2 sequence differs from that shown due to a
CC frameshift in position 302.
CC -----
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CC -----
DR EMBL: AE000386; AAC76082.1; -
DR EMBL: D90897; BAA16574.1; ALT_FRAME.
DR EMBL: D90897; BAA16575.1; ALT_FRAME.
DR PIR: D65092; D65092.
DR EcoGene: EG14228; yqig.
DR InterPro: IPR000015; Fimb_usher.
DR Pfam: PF00577; Usher. 1.
DR PROSITE: PS01151; FIMBRIAL_USHER. 1.
KW Hypothetical protein; Outer membrane; Transmembrane; Fimbria;
KW Transport; Signal; Complete proteome.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 821 HYPOTHETICAL OUTER MEMBRANE USHER PROTEIN
FT FT YQIG.
FT DISULFID 798 817 POTENTIAL.
FT CONFLICT 121 121 F -> L (IN REF. 2).
FT CONFLICT 131 131 F -> S (IN REF. 2).
FT CONFLICT 728 730 AIG -> CYW (IN REF. 2).
SO SEQUENCE 821 AA; 91886 MW; CAC9BCC9DA210286 CRC64;

Query Match 43.9%; Score 43.5; DB 1; Length 821;
Best Local Similarity 58.8%; Pred. No. 55;
Matches 10; Conservative 1; Mismatches 5; Indels 1; Gaps 1;
OY 1 YINPRNDYTEXNONFKD 17
DB 464 YINDTNYHTNY-ONEKE 479

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 19:04:06 ; Search time 16.9414 Seconds
(without alignments)
258.946 Million cell updates/sec

Title: US-09-988-013a-4_COPY_50_66

Perfect score: 99

Sequence: 1 YINPRNDYTEYNQNFKD 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69.7	119	5	09GYZ2	09GYZ2 schistosoma
2	63.6	109	11	09JL75	09JL75 mus musculus
3	53.5	117	11	09QXK9	09QXK9 mus musculus
4	53.5	117	11	09QXK9	09QXK9 mus musculus
5	53.5	143	11	091V67	091V67 mus musculus
6	53.5	143	11	0924P9	0924P9 mus musculus
7	52.5	1824	5	0815A3	0815A3 plasmidium
8	52.5	142	11	0924Q2	0924Q2 mus musculus
9	51.5	138	16	08Y729	08Y729 listeria mo
10	51.5	473	11	09JL75	09JL75 mus musculus
11	51.5	481	11	091WR3	091WR3 mus musculus
12	51.5	488	11	091WR1	091WR1 mus musculus
13	50.5	823	2	050330	050330 escherichia
14	50.5	1170	5	022624	022624 caenorhabdi
15	49.5	140	11	0924P8	0924P8 mus musculus
16	49.5	142	11	0924Q1	0924Q1 mus musculus

17	49	49.5	481	11	08VCV5	08VCV5 mus musculus
18	47	47.5	374	5	081J26	081J26 plasmidium
19	47	47.5	829	2	091U08	091U08 rhizobium m
20	47	47.5	831	2	09KIS9	09KIS9 bruceella ab
21	47	47.5	831	16	08YDZ4	08YDZ4 bruceella me
22	47	47.5	831	16	08FXK3	08FXK3 bruceella su
23	47	47.5	836	2	09RPY1	09RPY1 bruceella su
24	47	47.5	836	5	077347	077347 plasmidium
25	46	46.5	278	11	0921K1	0921K1 mus musculus
26	46	46.5	378	5	0814R1	0814R1 plasmidium
27	46	46.5	826	2	091UX4	091UX4 escherichia
28	46	46.5	2226	5	097225	097225 plasmidium
29	45.5	46.0	840	16	08CV9	08CV9 escherichia
30	45	45.5	110	11	09JL77	09JL77 mus musculus
31	45	45.5	279	16	08DDW9	08DDW9 vibrio vuln
32	45	45.5	442	5	096138	096138 plasmidium
33	45	45.5	506	17	097VP1	097VP1 sulfolobus
34	45	45.5	635	5	081JY1	081JY1 plasmidium
35	45	45.5	2631	2	09RNB5	09RNB5 microcystis
36	45	45.5	2632	2	09PDT8	09PDT8 microcystis
37	44	44.4	123	11	08VJ31	08VJ31 mus musculus
38	44	44.4	293	5	0815P6	0815P6 plasmidium
39	44	44.4	312	5	018369	018369 caenorhabdi
40	44	44.4	474	5	096837	096837 drosophila
41	44	44.4	491	17	029081	029081 archaeglob
42	44	44.4	500	17	08Q096	08Q096 methanosarc
43	44	44.4	513	2	024719	024719 comamonas t
44	44	44.4	513	2	046334	046334 comamonas t
45	44	44.4	550	16	09C1L3	09C1L3 lactococcus

ALIGNMENTS

RESULT 1	ID	Q9GYZ2	PRELIMINARY:	PRT:	119 AA.
AC	01-MAR-2001 (TREMBLrel. 16, Created)				
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)				
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)				
DE	Monoclonal anti-Idiotypic antibody NP30 heavy chain variable region				
DE	(Fragment)				
OS	Schistosoma japonicum (Blood fluke).				
OC	Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoidae;				
OC	Schistosomatidae; Schistosomatidae; Schistosoma.				
OX	NCBI_TaxID=6182;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Song X.T., Feng Z.Q., Guan X.H.;				
RT	*Amplification, cloning and sequence analysis of the heavy chain				
RT	variable region gene of monoclonal anti-Idiotypic antibody NP30 of				
RT	Schistosoma japonicum."				
RL	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AF282622; AAG01452.1; -				
DR	HSSP; P01772; 2F84.				
DR	InterPro: IPR007110; Ig-1like.				
DR	InterPro: IPR003006; Ig_MHC.				
DR	InterPro: IPR003596; Ig_v.				
DR	Pfam: PF00047; Ig_1.				
DR	SMART; SM00406; IGV; 1.				
DR	PROSITE; PS50835; IG_LIKE; 1.				
FT	NON_TER	1			
FT	NON_TER	119	119		
SO	SEQUENCE	119 AA;	13567 MW;	BA893873P05FA6AB	CRC64;
QY	Query Match	69.7%;	Score 69;	DB 5;	Length 119;
QY	Best Local Similarity	70.6%;	Pred. No. 0.0046;		
QY	Matches	12;	Conservative	0;	Mismatches 5;
QY					Indels 0;
QY					Gaps 0;
DB	1 YINPRNDYTEYNQNFKD 17				
DB	50 YINPRGRYTNVQNFKD 66				

RESULT 2

09JUL75 PRELIMINARY; PRT; 109 AA.
AC 09JUL75;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Anti-myosin immunoglobulin heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.
RT "T-cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin."
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL: AF206031; AAF69329.1; -.
DR HSSP: P01810; 2FBJ
DR InterPro: IPR007110; Ig_1like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PSS0835; IG_LIKE; 1.
FT NON_TER 1 109 1
FT NON_TER 1 109 1
SQ SEQUENCE 109 AA; 12118 MW; FF65E441BFF936A6 CRC64;

Query Match

Best Local Similarity 63.6%; Score 63; DB 11; Length 109;

Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 YINPRNDYTEYQNFK 16

Db 41 YINPYNDGTFYKNEFK 56

RESULT 3

09QXEX PRELIMINARY; PRT; 117 AA.
AC 09QXEX;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Immunoglobulin heavy chain V-D-J region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Rademakers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ225174; CAB65237.1; -.
DR HSSP: P01810; 2FBJ
DR InterPro: IPR007110; Ig_1like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PSS0835; IG_LIKE; 1.
FT NON_TER 1 117 1
FT NON_TER 1 117 1
SQ SEQUENCE 117 AA; 13000 MW; CDD82AF84D49734 CRC64;

Query Match 53.5%; Score 53; DB 11; Length 117;
Best Local Similarity 66.7%; Pred. NO. 1.3;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 INPRNDYTEYQNFK 16

Db 51 INPNGGTSTYQKFK 65

RESULT 4

09QXFO PRELIMINARY; PRT; 117 AA.
AC 09QXFO;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Immunoglobulin heavy chain V-D-J region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Rademakers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ225171; CAB65236.1; -.
DR HSSP: P01789; IMCP.
DR InterPro: IPR007110; Ig_1like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PSS0835; IG_LIKE; 1.
FT NON_TER 1 117 1
FT NON_TER 1 117 1
SQ SEQUENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;

Query Match

Best Local Similarity 53.5%; Score 53; DB 11; Length 117;

Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 INPRNDYTEYQNFK 16

Db 51 INPNGGTSTYQKFK 65

RESULT 5

091V67 PRELIMINARY; PRT; 143 AA.
AC 091V67;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE V304-D-J-C mu protein (V304-D-J-C mu protein) (Fragment).
GN V304-D-J-C MU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Kozono Y., Kozono H., Azuma T.;
RL Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)acetyl (NP).
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB069912; BAB63928.1; -.
DR EMBL: AB069914; BAB63930.1; -.
DR InterPro: IPR007110; Ig_1like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.


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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 143 AA; 15775 MW; 91BC6012B44EFEBF CRC64;

Query Match
Best Local Similarity 53.5%; Score 53; DB 11; Length 143;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 INPRNDYTEXNONFK 16
DB 51 IDPSDIYTYNOKFK 65

RESULT 6
O924P9 PRELIMINARY; PRT; 143 AA.
AC O924P9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE V303-D-J-C mu protein (Fragment).
GN V303-D-J-C MU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069916; BAB63932.1; -.
DR InterPro; IPR007110; I9-1like.
DR InterPro; IPR003006; I9_MHC.
DR Pfam; PF00047; I9_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 143
SQ SEQUENCE 143 AA; 15704 MW; 43CD8C72D52134F6 CRC64;

Query Match
Best Local Similarity 53.5%; Score 53; DB 11; Length 143;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 INPRNDYTEXNONFK 16
DB 51 IDPSDIYTYNOKFK 65

RESULT 7
O815A3 PRELIMINARY; PRT; 1824 AA.
AC O815A3;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DE Asparagine-rich protein, putative.
GN PFL1530W.
OS Plasmodium falciparum (Isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxId=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=2255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,

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RA Carlton J.M., Palm A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Valdes A.B.,
RA Martin D.M.A., Fairclimb L.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Nature 419:498-511(2002).
DR EMBL; AE014849; AAN36392.1; -.
SQ SEQUENCE 1824 AA; 212658 MW; 6ECED0EA6960084E CRC64;

Query Match
Best Local Similarity 40.0%; Score 52.5; DB 5; Length 1824;
Matches 10; Conservative 4; Mismatches 2; Indels 9; Gaps 1;

OY 2 INPR-----NDYTEXNONFKD 17
DB 1751 LNDKFNLDUTLNNTYNTDNDKFD 1775

RESULT 8
O924Q2 PRELIMINARY; PRT; 142 AA.
AC O924Q2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE V303-D-J-C mu protein (Fragment).
GN V303-D-J-C MU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069910; BAB63926.1; -.
DR InterPro; IPR007110; I9-1like.
DR InterPro; IPR003006; I9_MHC.
DR InterPro; IPR003596; I9_V.
DR Pfam; PF00047; I9_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 142
SQ SEQUENCE 142 AA; 15684 MW; 048809F90C0FBD7B CRC64;

Query Match
Best Local Similarity 52.5%; Score 52; DB 11; Length 142;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 INPRNDYTEXNONFK 16
DB 51 IDPSDIYTYNOKFK 65

RESULT 9
O8Y7Z9 PRELIMINARY; PRT; 138 AA.
AC O8Y7Z9;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE Hypothetical protein lmo1120.
GN LMO1120.

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OS Listeria monocytogenes.
OC Bacteria: Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-EGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Franjeul L., Buchrieser C., Rusnock C., Amend A.,
RA Baquero F., Berche P., Bloecher H., Brandt P., Chakraborty T.,
RA Chardot A., Chetoui F., Couve E., de Darivar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurgeat O.,
RA Entian K.-D., Fajhl H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hahn T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitounan A., Mata Vicente J., Ng E., Medjert H.,
RA Nodtlex G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehlund J., Cossart P.;
RT *Comparative genomics of Listeria species.*;
RL Science 294:849-852(2001);
DR EMBL: AL591977; CAC99198.1; -
DR Listlist: LMO01120; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 138 AA; 15807 MW; 0C1AC34EE7A7AC2 CRC64;

Query Match 51.5%; Score 51; DB 16; Length 138;
Best Local Similarity 52.9%; Pred. No. 3.1;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 YINPRNDYTEYNONFKD 17
   |||: | | | | |
DB 66 YINPKOFWEFENOPFLD 82

RESULT 10
Q99L25 PRELIMINARY; PRT; 473 AA.
ID 099L25;
AC 099L25;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Similar to RIKEN cDNA 181006009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC003888; AAH03888.1; -
DR HSP; P01842; FAB.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 3.
DR SMART: SM00406; Igv; 1.
DR PROSITE: PS50835; Ig_LIKE; 4.
DR PROSITE: PS00290; Ig_MHC; 1.
DR PROSITE: PS00290; Ig_MHC; 1.
SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match 51.5%; Score 51; DB 11; Length 473;
Best Local Similarity 56.2%; Pred. No. 11;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 YINPRNDYTEYNONFK 16
   || | | | | | | |
DB 69 YIYPRDSTKYNEKFK 84

RESULT 11
Q91WT3 PRELIMINARY; PRT; 481 AA.
ID Q91WT3
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AC Q91WT3;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical 52.0 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strauberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC013488; AAH13488.1; -
DR MGD: MGI:96486; Igh-VJ558.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 4.
DR SMART: SM00406; Igv; 1.
DR PROSITE: PS50835; Ig_LIKE; 4.
DR PROSITE: PS00290; Ig_MHC; 2.
DR PROSITE: PS00290; Ig_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52022 MW; 4EEB5C253038B718 CRC64;

Query Match 51.5%; Score 51; DB 11; Length 481;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 INPRNDYTEYNONFK 16
   | | | | | | | |
DB 70 IDPFDSYSYNOKFK 84

RESULT 12
Q91WR1 PRELIMINARY; PRT; 488 AA.
ID Q91WR1;
AC Q91WR1;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical 53.0 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC013539; AAH13539.1; -
DR MGD: MGI:96486; Igh-VJ558.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 4.
DR SMART: SM00406; Igv; 1.
DR PROSITE: PS50835; Ig_LIKE; 4.
DR PROSITE: PS00290; Ig_MHC; 2.
DR PROSITE: PS00290; Ig_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 488 AA; 52964 MW; F12068460B400B9D CRC64;

Query Match 51.5%; Score 51; DB 11; Length 488;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 INPRNDYTEYNONFK 16
   || | | | | | | |
DB 70 INPYNGSTSYNOKFK 84
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RESULT 13
ID 050330 PRELIMINARY; PRT; 823 AA.
AC 050330: 093732;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Trk protein.
GN Trk.
OS Escherichia coli.
OC plasmid R388.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_Taxid=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K-12; PLASMD-R388;
RX MEDLINE=97467347; PubMed=9325277;
RA Bolland S., Lloza M., de la Cruz F.;
RT "Genetic organization of the region involved in conjugative pilus
synthesis, export and assembly of the Incw plasmid R388.";
RL J Biol. Chem. 272:25583-25590(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K-12; PLASMD=R388;
RA de la Cruz F.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC PLASMD-R388;
RA Rabel C., Lanka E.;
RT "Direct Submision.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; X81123; CA57024.2; -
DR EMBL; AJ316617; CAC78962.1; -
DR InterPro; IPR004346; CAGE_Tpde_Vlrb.
DR Pfam; PF03135; CAGE_Tpde_Vlrb. 1.
DR TIGRfams; TIGR00929; Vlrb4_Cage; 1.
KW Plasmid.
SQ SEQUENCE 823 AA; 93660 MW; 5AE3115FECFA8208 CRC64;

Query Match 50.5%; Score 50; DB 2; Length 823;
Best Local Similarity 57.1%; Pred. No. 29;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 INPRNDYTEYNONFK 16
DB 714 NPKADYEDYTGFK 727

RESULT 14
ID 022624 PRELIMINARY; PRT; 1170 AA.
AC 022624;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE T21B10.3 protein.
GN T21B10.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Baynes C.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
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RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z68318; CA92693.2; -
DR WormPep; T21B10.3; CE23993
SQ SEQUENCE 1170 AA; 135533 MW; 461F6BA1A2B6BF04 CRC64;

Query Match 50.5%; Score 50; DB 5; Length 1170;
Best Local Similarity 80.0%; Pred. No. 42;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 PRNDYTEYNQ 13
DB 984 PRNDYSEYDQ 993

RESULT 15
ID 0924P8 PRELIMINARY; PRT; 140 AA.
AC 0924P8;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE V23-D-J-C mu protein (Fragment).
GN V23-D-J-C MU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069917; BAB63933.1; -
DR InterPro; IPR007110; IG-1-like.
DR InterPro; IPR003006; IG-MHC.
DR InterPro; IPR003596; IG-V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 140 AA; 15392 MW; 904C80C82548C936 CRC64;

Query Match 49.5%; Score 49; DB 11; Length 140;
Best Local Similarity 60.0%; Pred. No. 6.4;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 INPRNDYTEYNONFK 16
DB 51 INPSNGTNYMEKFK 65
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Search completed: October 7, 2003, 19:20:03
Job time : 18.9414 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 19:03:26 ; Search time 8.81034 Seconds

(without alignments)
126.112 Million cell updates/sec

Title: US-09-988-013A-4_COPY_99_105

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Scoring table: BL0SUM62

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Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	38	100.0	116 17 AAR92216	IL2 Mab VH region.
2	38	100.0	116 17 AAR92218	Humanised IL2 Mab
3	38	100.0	116 17 AAR92219	Humanised IL2 Mab
4	38	100.0	116 18 AAW27696	Variable heavy cha
5	38	100.0	116 18 AAW27698	Variable heavy cha
6	33	86.8	146 22 AAU30864	Novel human secret
7	33	86.8	203 22 AAB94060	Human protein sequ
8	33	86.8	277 21 AAG07543	Arabidopsis thalia
9	33	86.8	277 21 AAG53675	Arabidopsis thalia

10	33	86.8	333 21 AAG07542	Arabidopsis thalia
11	33	86.8	337 21 AAG53674	Arabidopsis thalia
12	33	86.8	337 22 AAG93332	Maize patatin homo
13	33	86.8	343 21 AAB93724	Human protein sequ
14	33	86.8	361 21 AAG53673	Arabidopsis thalia
15	33	86.8	362 21 AAG07541	Arabidopsis thalia
16	33	86.8	406 22 AAB28193	Novel human secret
17	33	86.8	406 22 AAB93146	Human protein sequ
18	33	86.8	410 18 AAW01538	Maize insecticidal
19	33	86.8	410 22 AAG93327	Maize patatin homo
20	33	86.8	410 22 AAG93329	Maize patatin homo
21	33	86.8	410 22 AAG93330	Maize patatin homo
22	33	86.8	410 22 AAG93331	Maize patatin homo
23	33	86.8	410 22 AAE02393	Pentaclethra macro
24	33	86.8	508 22 AAG93328	Maize patatin homo
25	33	86.8	870 18 AAW19725	Truncated cell cyc
26	33	86.8	2410 18 AAW19723	Cell cycle checkpo
27	33	86.8	2480 18 AAW19724	Cell cycle checkpo
28	33	86.8	2644 18 AAW13152	Human ataxia and r
29	33	86.8	2644 20 AAW84271	A human ATR protei
30	32	84.2	44 22 AAG02608	Human haematologic
31	32	84.2	53 22 AAM81420	Novel human diagno
32	32	84.2	53 22 AAM82166	Human haematologic
33	32	84.2	54 22 ABG11381	Novel human diagno
34	32	84.2	63 22 ABG02611	Novel human diagno
35	32	84.2	77 22 AAG02612	Novel human diagno
36	32	84.2	120 22 AAV31565	Novel human secret
37	32	84.2	155 22 AAO01309	Human polypeptide
38	32	84.2	218 21 AAB43797	Human cancer assoc
39	32	84.2	225 22 ABG11378	Novel human diagno
40	32	84.2	377 11 AAR06922	Feline infectious
41	32	84.2	377 12 AAR10934	Feline infectious
42	32	84.2	377 16 AAR78144	FlPV N protein. F
43	32	84.2	377 22 AAE04306	Feline infectious
44	32	84.2	406 22 AAE10163	RNA helicase conse
45	32	84.2	407 20 AAY21683	Human eukaryotic I

ALIGNMENTS

RESULT 1				
ID	AAR92216	standard: Protein; 116 AA.		
XX	XX	XX		
AC	AAR92216;			
XX	XX	28-MAY-1996 (first entry)		
XX	XX	XX		
DE	XX	IL2 Mab VH region.		
XX	XX	Humanised antibody; monoclonal antibody; Mab; IL2; B-cell lymphoma;		
KW	XX	leukaemia; therapy; diagnosis; complementarity determining region;		
KM	XX	CDR; antibody engineering.		
OS	XX	Mus musculus.		
XX	XX	XX		
XX	XX	XX		
FT	FT	Key		
FT	FT	Region		
FT	FT	Location/Qualifiers		
FT	FT	/label= CDR1		
FT	FT	/note= "claim 9, page 44"		
FT	FT	50..66		
FT	FT	/label= CDR2		
FT	FT	/note= "claim 10, page 45"		
FT	FT	99..105		
FT	FT	/label= CDR3		
FT	FT	/note= "claim 11, page 45"		
PN	XX	WO9604925-A1.		
XX	XX	22-FEB-1996.		
PD	XX	11-AUG-1995;		
XX	XX	95WO-US09641.		

XX 12-AUG-1994; 94US-0289576.
PR (IMMU-) IMMUNOMEDICS INC.
XX Hansen H, Leung S;
PI WPI; 1996-139454/14.
XX N-PSDB; AAT15802.
DR
XX Chimeric and humanised LL2 antibodies - used to produce conjugates
PT for the therapy and diagnosis of B-cell lymphoma(s) and
PT Leukaemia(s).
PS Claim 5; Page 36-37; 70pp; English.
XX The complementarity determining regions (CDRs) of mouse monoclonal
CC antibody (Mab) LL2 VK (AAR92215) and VH (AAR92216) regions were
CC recombinantly linked to the framework sequences of human VK and VH
CC regions, respectively, to give humanised LL2 VK (AAR92217) and VH
CC (AAR92218). These were subsequently linked, respectively, to human
CC kappa and IgG1 constant regions. A humanised Mab was obtd. that
CC retained the B-lymphoma and leukaemia cell targeting and
CC internalisation characteristics of the parental LL2 Mab, and which
CC exhibited a lowered HAMA reaction. It can be linked to e.g. a
CC cytostatic agent for therapeutic appln.
XX
SQ Sequence 116 AA;
Query Match 100.0%; Score 38; DB 17; Length 116;
Best Local Similarity 100.0%; Pred. No. 2.3; Mismatches 0; Gaps 0;
Matches 7; Conservative 0; Indels 0; Gaps 0;
OY 1 RDITTFY 7
DB 99 RDITTFY 105
RESULT 2
AAR92218
ID AAR92218 standard; Protein; 116 AA.
XX
AC AAR92218;
XX
DT 28-MAY-1996 (first entry)
XX
XX Humanised LL2 Mab VH region.
DE
XX Humanised antibody; monoclonal antibody; Mab; LL2; B-cell lymphoma;
KW Leukaemia; therapy; diagnosis; complementarity determining region;
KW CDR; antibody engineering.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Region 31..35
FT /label= CDR1
FT 50..66
FT /label= CDR2
FT 99..105
FT Region /label= CDR3
FT
PN WO9604925-A1.
XX
PD 22-FEB-1996.
XX
PE 11-AUG-1995; 95WO-US09641.
XX
PR 12-AUG-1994; 94US-0289576.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX Hansen H, Leung S;
PI

XX WPI; 1996-139454/14.
DR N-PSDB; AAT15804.
XX
XX Chimeric and humanised LL2 antibodies - used to produce conjugates
PT for the therapy and diagnosis of B-cell lymphoma(s) and
PT Leukaemia(s).
PS Claim 5; Page 39; 70pp; English.
XX The complementarity determining regions (CDRs) of mouse monoclonal
CC antibody (Mab) LL2 VK (AAR92215) and VH (AAR92216) regions were
CC recombinantly linked to the framework sequences of human VK and VH
CC regions, respectively, to give humanised LL2 VK (AAR92217) and VH
CC (AAR92218). These were subsequently linked, respectively, to human
CC kappa and IgG1 constant regions. A humanised Mab was obtd. that
CC retained the B-lymphoma and leukaemia cell targeting and
CC internalisation characteristics of the parental LL2 Mab, and which
CC exhibited a lowered HAMA reaction. It can be linked to e.g. a
CC cytostatic agent for therapeutic appln.
XX
SQ Sequence 116 AA;
Query Match 100.0%; Score 38; DB 17; Length 116;
Best Local Similarity 100.0%; Pred. No. 2.3; Mismatches 0; Gaps 0;
Matches 7; Conservative 0; Indels 0; Gaps 0;
OY 1 RDITTFY 7
DB 99 RDITTFY 105
RESULT 3
AAR92219
ID AAR92219 standard; Protein; 116 AA.
XX
AC AAR92219;
XX
DT 28-MAY-1996 (first entry)
XX
XX Humanised LL2 Mab VH region (version hLL2-1).
DE
XX Humanised antibody; monoclonal antibody; Mab; LL2; B-cell lymphoma;
KW Leukaemia; therapy; diagnosis; complementarity determining region;
KW CDR; antibody engineering.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Region 31..35
FT /label= CDR1
FT 50..66
FT /label= CDR2
FT 99..105
FT Region /label= CDR3
FT
PN WO9604925-A1.
XX
PD 22-FEB-1996.
XX
PE 11-AUG-1995; 95WO-US09641.
XX
PR 12-AUG-1994; 94US-0289576.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX Hansen H, Leung S;
PI WPI; 1996-139454/14.
XX Chimeric and humanised LL2 antibodies - used to produce conjugates
PT for the therapy and diagnosis of B-cell lymphoma(s) and
PT Leukaemia(s).
PT

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XX Example 1: Page 40; 70pp: English.
PS
XX The complementarily determining regions (CDRs) of mouse monoclonal
CC antibody (Mab) LL2 VK (AAR92215) and VH (AAR92216) regions were
CC recombinantly linked to the framework sequences of human VK and VH
CC regions, respectively, to give humanised LL2 VK (AAR92217) and VH
CC (AAR92218). In an alternative version, a glutamine was introduced
CC at position 5 of the humanised VH (AAR92219) to include a PstI site
CC useful for subcloning. The humanised VK and VH were subsequently
CC linked, respectively, to human kappa and IgG1 constant regions. A
CC humanised Mab was obtd. that retained the B-lymphoma and leukaemia
CC cell targeting and internalisation characteristics of the parental
CC LL2 Mab, and which exhibited a lowered HAMA reaction. It can be
CC linked to a cytostatic agent for therapeutic appln.
XX
SQ Sequence 116 AA;

Query Match 100.0%; Score 38; DB 17; Length 116;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDIITFFY 7
Db 99 RDIITFFY 105

RESULT 4
AAM27696
ID AAM27696 standard; Protein; 116 AA.
AC
XX AAM27696;
XX
DT 14-APR-1998 (first entry)
XX
DE Variable heavy chain of Mab LL2.
XX
KW Variable heavy chain; B cell; monoclonal antibody; Mab; LL2;
KW B cell lymphoma; lymphocytic leukaemia cell; murine;
KW diagnosis; treatment; B cell malignancy; non-Hodgkins lymphoma;
KW chronic lymphocytic leukaemia.
XX
XX Mus sp.
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX FH Region 31..35
XX FT /note= "complementarity determining region 1"
XX FT Region 50..66
XX FT /note= "complementarity determining region 2"
XX FT Region 99..105
XX FT /note= "complementarity determining region 3"
XX
XX W09734632-A1.
XX
XX 25-SEP-1997.
XX
XX 19-MAR-1997; 97WO-US04196.
XX
XX 20-MAR-1996; 96US-0013709.
XX
XX (IMMU-) IMMUNOMEDICS INC.
XX
XX Hansen H, Leung S, Qu Z;
XX
XX WPI: 1997-479995/44.
XX DR N-PSDB: AAT88129.
XX
XX Monoclonal antibody engineered to contain glycosylation site - in
XX non-Fc constant heavy or light chain region, useful to diagnose or
XX treat B cell malignancies, e.g. non-Hodgkins lymphoma
XX
XX Example 3; Fig 4B; 86pp: English.

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XX The present sequence is the variable heavy chain of the
CC B cell specific monoclonal antibody (Mab) LL2, which contains an
CC engineered tri-peptide N-glycan acceptor sequence. LL2 is a highly
CC specific anti-B cell lymphoma and anti-lymphocytic leukaemia cell
CC murine Mab. The Mab can be used to diagnose or treat B
CC cell malignancies, e.g. non-Hodgkins lymphoma or chronic
CC lymphocytic leukaemia. The glycosylation site allows a label or
CC therapeutic agent of increased size to be conjugated to the
CC carbohydrate moiety, without affecting the Mab's binding affinity
CC or specificity.
XX
SQ Sequence 116 AA;

Query Match 100.0%; Score 38; DB 18; Length 116;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDIITFFY 7
Db 99 RDIITFFY 105

RESULT 5
AAM27698
ID AAM27698 standard; Protein; 116 AA.
AC
XX AAM27698;
XX
DT 14-APR-1998 (first entry)
XX
DE Variable heavy chain of Mab hLL2.
XX
KW Variable heavy chain; B cell; monoclonal antibody; Mab; hLL2;
KW B cell lymphoma; lymphocytic leukaemia cell; murine; humanised;
KW diagnosis; treatment; B cell malignancy; non-Hodgkins lymphoma;
KW chronic lymphocytic leukaemia.
XX
XX Chimeric - Mus sp.
XX OS Chimeric - Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH Region 31..35
XX FT /note= "complementarity determining region 1"
XX FT Region 50..66
XX FT /note= "complementarity determining region 2"
XX FT Region 99..105
XX FT /note= "complementarity determining region 3"
XX
XX W09734632-A1.
XX
XX 25-SEP-1997.
XX
XX 19-MAR-1997; 97WO-US04196.
XX
XX 20-MAR-1996; 96US-0013709.
XX
XX (IMMU-) IMMUNOMEDICS INC.
XX
XX Hansen H, Leung S, Qu Z;
XX
XX WPI: 1997-479995/44.
XX DR N-PSDB: AAT88131.
XX
XX Monoclonal antibody engineered to contain glycosylation site - in
XX non-Fc constant heavy or light chain region, useful to diagnose or
XX treat B cell malignancies, e.g. non-Hodgkins lymphoma
XX
XX Example 3; Fig 5B; 86pp: English.
XX
XX The present sequence is the variable heavy chain of the
XX B cell specific monoclonal antibody (Mab) hLL2. hLL2 is a highly
XX specific anti-B cell lymphoma and anti-lymphocytic leukaemia cell

```

CC humanised murine Mab. The Mab can be used to diagnose or treat B
CC cell malignancies, e.g. non-Hodgkins lymphoma or chronic
CC lymphocytic leukaemia.

XX
SQ Sequence 116 AA;

Query Match 100.0%; Score 38; DB 18; Length 116;
Best Local Similarity 100.0%; Pred. No. 2.3;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDITTFY 7
|:|:|:|:

Db 99 RDITTFY 105

RESULT 6
AAU30864
ID AAU30864 standard; Protein; 146 AA.

AC AAU30864;

DT 18-DEC-2001 (first entry)

DE Novel human secreted protein #1355.

KM Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW Immune suppression; Immune stimulation; anti-inflammatory; leukaemia.

OS Homo sapiens.

PN MO200179449-A2.

PD 25-OCT-2001.

PF 16-APR-2001; 2001MO-US08656.

PR 18-APR-2000; 2000US-0552929.

PR 26-JAN-2001; 2001US-0770160.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-611725/70.

PT Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy -

PS Claim 20; Page 363; 765pp; English.

XX The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising
CC the nucleic acids encoding the polypeptides and cells genetically
CC engineered to express them are also useful for producing the proteins.
CC The proteins are useful in genetic vaccination, testing and
CC therapy, and can be used as nutritional supplements. They may be used to
CC increase stem cell proliferation; to regulate haematopoiesis; and in
CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
CC immune suppression and/or stimulation; as anti-inflammatory agents; and
CC in treatment of leukemias. AAU29510-AAU33304 represent the amino acid
CC sequences of novel human secreted proteins of the invention.

XX Sequence 146 AA;

Query Match 86.8%; Score 33; DB 22; Length 146;
Best Local Similarity 71.4%; Pred. No. 34;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDITTFY 7
|:|:|:|:

Db 28 RDITTFY 34

RESULT 7
AAB94060
ID AAB94060 standard; Protein; 203 AA.

AC AAB94060;

DT 26-JUN-2001 (first entry)

DE Human protein sequence SEQ ID NO:14236.

KM Human; primer; detection; diagnosis; antisense therapy; gene therapy.

OS Homo sapiens.

PN EP1074617-A2.

PD 07-FEB-2001.

PF 28-JUL-2000; 2000EP-0116126.

PR 29-JUL-1999; 99JP-0248036.

PR 27-AUG-1999; 99JP-0300253.

PR 11-JAN-2000; 2000JP-0118776.

PR 02-MAY-2000; 2000JP-0183767.

PR 09-JUN-2000; 2000JP-0241899.

PA (HELI-) HELIX RES INST.

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

DR WPI; 2001-318749/34.

PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -

PS Claim 8; SEQ ID 14236; 2537pp + CD ROM; English.

XX The present invention describes primer sets for synthesizing 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.

XX Sequence 203 AA;

Query Match 86.8%; Score 33; DB 22; Length 203;

Best Local Similarity 71.4%; Pred. No. 48;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDITTFY 7
||:||||:
Db 85 RDVTTF 91

RESULT 8
AAG07543
ID AAG07543 standard; Protein: 277 AA.

AC AAG07543;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4737.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hydridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-0301439.
XX
PF 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.

PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144684.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0145386.
PR 02-AUG-1999; 99US-0145388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.

PR 12-AUG-1999; 990S-0148341.
PR 13-AUG-1999; 990S-0148565.
PR 13-AUG-1999; 990S-0148684.
PR 16-AUG-1999; 990S-0149368.
PR 17-AUG-1999; 990S-0149175.
PR 18-AUG-1999; 990S-0149426.
PR 20-AUG-1999; 990S-0149722.
PR 20-AUG-1999; 990S-0149723.
PR 20-AUG-1999; 990S-0149929.
PR 23-AUG-1999; 990S-0149902.
PR 23-AUG-1999; 990S-0149930.
PR 25-AUG-1999; 990S-0150566.
PR 26-AUG-1999; 990S-0150884.
PR 27-AUG-1999; 990S-0151065.
PR 27-AUG-1999; 990S-0151066.
PR 27-AUG-1999; 990S-0151080.
PR 30-AUG-1999; 990S-0151303.
PR 31-AUG-1999; 990S-0151438.
PR 01-SEP-1999; 990S-0151930.
PR 07-SEP-1999; 990S-0152363.
PR 10-SEP-1999; 990S-0153070.
PR 13-SEP-1999; 990S-0153758.
PR 15-SEP-1999; 990S-0154018.
PR 16-SEP-1999; 990S-0154039.
PR 20-SEP-1999; 990S-0154779.
PR 22-SEP-1999; 990S-0155139.
PR 23-SEP-1999; 990S-0155486.
PR 24-SEP-1999; 990S-0155659.
PR 28-SEP-1999; 990S-0156458.
PR 29-SEP-1999; 990S-0156596.
PR 04-OCT-1999; 990S-0157117.
PR 05-OCT-1999; 990S-0157753.
PR 06-OCT-1999; 990S-0157865.
PR 07-OCT-1999; 990S-0158029.
PR 08-OCT-1999; 990S-0158232.
PR 12-OCT-1999; 990S-0158369.
PR 13-OCT-1999; 990S-0159293.
PR 13-OCT-1999; 990S-0159294.
PR 13-OCT-1999; 990S-0159295.
PR 14-OCT-1999; 990S-0159329.
PR 14-OCT-1999; 990S-0159330.
PR 14-OCT-1999; 990S-0159331.
PR 14-OCT-1999; 990S-0159637.
PR 14-OCT-1999; 990S-0159638.
PR 18-OCT-1999; 990S-0159584.
PR 21-OCT-1999; 990S-0160741.
PR 21-OCT-1999; 990S-0160767.
PR 21-OCT-1999; 990S-0160768.
PR 21-OCT-1999; 990S-0160770.
PR 21-OCT-1999; 990S-0160814.
PR 21-OCT-1999; 990S-0160815.
PR 22-OCT-1999; 990S-0160880.
PR 22-OCT-1999; 990S-0160981.
PR 22-OCT-1999; 990S-0160989.
PR 25-OCT-1999; 990S-0161404.
PR 25-OCT-1999; 990S-0161405.
PR 25-OCT-1999; 990S-0161406.
PR 26-OCT-1999; 990S-0161359.
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PR 28-OCT-1999; 990S-0161993.
PR 29-OCT-1999; 990S-0162142.

Query Match Best Local Similarity 86.8%; Score 33; DB 21; Length 277;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db 142 REVTFY 148

RESULT 9
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ID AAG53675 standard; Protein; 277 AA.
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XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68358.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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PR 29-OCT-1999; 99US-0162142.

Query Match 86.8%; Score 33; DB 21; Length 277;
Best Local Similarity 71.4%; Pred. No. 68;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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Db 142 REVITFY 148

RESULT 10
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ID AAG07542 standard; Protein; 333 AA.
XX
AC AAG07542;
XX

DT 17-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 4736.
DE
XX Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
XX Arabidopsis thaliana.
OS
XX EP1033405-A2.
PN
XX 06-SEP-2000.
PD
XX
PF 25-FEB-2000; 2000EP-0301439.
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XX 25-FEB-1999; 99US-0121825.
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Query Match 86.8%; Score 33; DB 21; Length 333;
Best Local Similarity 71.4%; Pred. No. 83;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db 198 REVTFY 204

RESULT 11
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AC AAG53674;
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XX 18-OCT-2000 (first entry)
DT
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XX Arabidopsis thaliana protein fragment SEQ ID NO: 68357.
DE
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.
OS
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XX EPI033405-A2.
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XX 06-SEP-2000.
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XX 25-FEB-2000; 2000EP-0301439.
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DB 198 REVTFY 204

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AC AAG99332;
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DT 28-SEP-2001 (first entry)
XX

DE Maize patatin homolog corn5 pep.
XX

KW Insecticidal; immunosuppressive; potato; patatin; enzyme;
KW allergenicity; larva growth; lipid acyl hydrolase; insecticide.
XX

OS Zea mays.
XX

PN WO200149834-A2.
XX

PD 12-JUL-2001.
XX

PF 05-JAN-2001; 2001WO-US00342.

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XX 06-JAN-2000; 2000US-0174669.
PR (MONS ) MONSANTO CO.
PA
XX Alldhal MF, Astwood JD, McWherter CA, Sampson HA;
XX WPI; 2001-441874/47.
XX Modified potato patatin proteins with reduced antigenicity, useful as
XX insecticides for controlling e.g. round worm and root worm -
XX
XX Claim 55; Pages 222-223; 223pp; English.
XX
XX The present invention relates to modified potato patatins that maintain
XX enzymatic and insecticidal activity but which have reduced allergenicity.
XX Groups (especially Tyr) which bind to anti-patatin antibodies were
XX identified and glycosylation sites involved in antibody binding were
XX removed via site directed mutagenesis. The patatins stunt the growth of
XX larvae so that maturation is prevented or delayed. The patatins also have
XX also useful for inhibiting the activity of corn round worms.
XX Deallergeised protein can be used as insecticides, as nutritional
XX supplements and as immunising agents. The present sequence was used to
XX illustrate the present invention.
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XX Sequence 337 AA;
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XX Best Local Similarity 71.4%; Pred. No. 84;
XX Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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Db 95 KDLTFY 101
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XX ID AAB93724 standard; Protein; 343 AA.
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XX AAB93724;
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XX 26-JUN-2001 (first entry)
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XX Human protein sequence SEQ ID NO:13343.
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XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX
XX Homo sapiens.
XX
XX EP1074617-A2.
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XX 07-FEB-2001.
XX
XX 28-JUL-2000; 2000EP-0116126.
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XX 29-JUL-1999; 99JP-0248036.
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XX 02-MAY-2000; 2000JP-0183767.
XX 09-JUN-2000; 2000JP-0241899.
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XX
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX WPI; 2001-318749/34.
XX
XX Primer sets for synthesizing polynucleotides, particularly the 5602
XX full-length cDNAs defined in the specification, and for the detection
XX and/or diagnosis of the abnormality of the proteins encoded by the
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```
PT full-length cDNAs -
XX
XX Claim 8; SEQ ID 13343; 2537pp + CD ROM; English.
XX
XX The present invention describes primer sets for synthesizing 5602
XX full-length cDNAs defined in the specification. Where a primer set
XX comprises: (a) an oligo-dT primer and an oligonucleotide complementary
XX to the complementary strand of a polynucleotide which comprises one of
XX the 5602 nucleotide sequences defined in the specification, where the
XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination
XX of an oligonucleotide comprising a sequence complementary to the
XX complementary strand of a polynucleotide which comprises a 5'-end
XX sequence and an oligonucleotide comprising a sequence complementary to a
XX polynucleotide which comprises a 3'-end sequence, where the
XX oligonucleotide comprises at least 15 nucleotides and the combination of
XX the 5'-end sequence/3'-end sequence is selected from those defined in
XX the specification. The primer sets can be used in antisense therapy and
XX in gene therapy. The primers are useful for synthesizing polynucleotides,
XX particularly full-length cDNAs. The primers are also useful for the
XX detection and/or diagnosis of the abnormality of the proteins encoded by
XX the full-length cDNAs. The primers allow obtaining of the full-length
XX cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
XX AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
XX AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
XX represent oligonucleotides, all of which are used in the exemplification
XX of the present invention.
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Db 225 RDTTFY 231
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XX AAG53673
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XX 18-OCT-2000 (first entry)
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XX Arabidopsis thaliana protein fragment SEQ ID NO: 68356.
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XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
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XX 06-SEP-2000.
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XX 25-FEB-2000; 2000EP-0301439.
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DB 226 REVTFY 232

RESULT 15
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AC AAC07541;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 4735.

KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.

OS Arabidopsis thaliana.

OS EPI033405-A2.

PD 06-SEP-2000.

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PR 30-AUG-1999; 99US-0151303.
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OM protein - protein search, using sw model

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Title: US-09-988-013a-4_COPY_99_105
Perfect score: 38
Sequence: 1 RDITTFY 7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	38	100.0	116	11	US-09-894-839-4
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6	38	100.0	116	11	US-09-894-839-21
7	38	100.0	116	11	US-09-888-013a-4
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17	32	84.2	406	15	US-10-228-897-12	Sequence 12, Appl
18	31	81.6	543	15	US-10-156-761-8387	Sequence 8387, Ap
19	31	81.6	565	12	US-10-132-134-26	Sequence 26, Appl
20	31	81.6	1395	10	US-09-808-602-67	Sequence 67, Appl
21	31	81.6	1395	11	US-09-800-198-56	Sequence 56, Appl
22	31	81.6	1395	12	US-10-289-776-15	Sequence 15, Appl
23	30	78.9	544	9	US-09-809-342a-2	Sequence 2, Appl
24	30	78.9	544	11	US-09-946-374-118	Sequence 118, Ap
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26	30	78.9	544	12	US-10-006-130a-118	Sequence 118, Ap
27	30	78.9	544	12	US-10-199-672-274	Sequence 274, Ap
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ALIGNMENTS

RESULT 1
US-09-741-843-4
; Sequence 4, Application US/09741843
; Patent No. US20020102254A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-con
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL
; FILE REFERENCE: 018733/0996
; CURRENT APPLICATION NUMBER: US/09/741,843
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/127,902
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/690,102
; PRIOR FILING DATE: 1996-07-06
; PRIOR APPLICATION NUMBER: US 08/289,576
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-741-843-4
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Db 99 RDITTFY 105
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US-09-741-843-8
; Sequence 8, Application US/09741843

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Patent No. US20020102254A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL LY
; FILE REFERENCE: 018733/0996
; CURRENT APPLICATION NUMBER: US/09/741,843
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/127,902
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/690,102
; PRIOR FILING DATE: 1996-07-06
; PRIOR APPLICATION NUMBER: US 08/289,576
; PRIOR FILING DATE: 1994-08-12
; NUMBER OF SEQ ID NOS: 21
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US-09-741-843-8
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; Patent No. US20020102254A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL LY
; FILE REFERENCE: 018733/0996
; CURRENT APPLICATION NUMBER: US/09/741,843
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/127,902
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/690,102
; PRIOR FILING DATE: 1996-07-06
; PRIOR APPLICATION NUMBER: US 08/289,576
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US-09-741-843-9
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; Publication No. US20030035800A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
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; APPLICANT: HANSEN, Hans
; APPLICANT: OU, Zhengxing
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/1049
; CURRENT APPLICATION NUMBER: US/09/894,839
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/155,107
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 60/013,709
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US-09-894-839-4
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; Publication No. US20030035800A1
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; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/1049
; CURRENT APPLICATION NUMBER: US/09/894,839
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/155,107
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 60/013,709
; PRIOR FILING DATE: 1996-03-20
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US-09-894-839-8
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; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/1049
; CURRENT APPLICATION NUMBER: US/09/894,839
; CURRENT FILING DATE: 2001-06-29
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; PRIOR FILING DATE: 1998-11-17
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; APPLICANT: LEUNG, Shui-on
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-
; FILE REFERENCE: 18733/1082
; CURRENT APPLICATION NUMBER: US/09/988,013A
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 09/741,843
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/127,902
; PRIOR FILING DATE: 1998-08-03
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US-09-988-013a-4

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; FILE REFERENCE: 18733/1082
; CURRENT APPLICATION NUMBER: US/09/988,013A
; PRIOR FILING DATE: 2002-10-29
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US-09-988-013a-8

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; Publication No. US20030103979A1
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; APPLICANT: LEUNG, Shui-on
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-
; FILE REFERENCE: 18733/1082
; CURRENT APPLICATION NUMBER: US/09/988,013A
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 09/741,843
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/127,902
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/690,102
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; PRIOR APPLICATION NUMBER: US 08/289,576
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; APPLICANT: ELEDGE, STEPHEN J.
; APPLICANT: CORREZ, DAVID K.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN CHECKPOINT SIGNALING
; FILE REFERENCE: P02339US
; CURRENT APPLICATION NUMBER: US/10/300,453A
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: 60/331,821
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 47
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US-10-300-453a-39

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; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
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; PRIOR APPLICATION NUMBER: 60/200,545
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; PRIOR APPLICATION NUMBER: 60/200,999
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; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1784
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-692-1784

Query Match
Best Local Similarity 84.2%; Score 32; DB 10; Length 53;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RDITTFY 7
Db 32 RDITTFY 38

RESULT 12
US-09-796-692-2530
; Sequence 2530, Application US/09796692
```

```
;; Publication No. US20020198362A1
;; GENERAL INFORMATION:
;; APPLICANT: Gaiger, Alexander
;; APPLICANT: Algate, Paul A.
;; APPLICANT: Mannion, Jane
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
;; FILE REFERENCE: 2077.001200
;; CURRENT APPLICATION NUMBER: US/09/796,692
;; PRIOR FILING DATE: 2001-03-01
;; PRIOR APPLICATION NUMBER: 60/186,126
;; PRIOR FILING DATE: 2000-03-01
;; PRIOR APPLICATION NUMBER: 60/190,479
;; PRIOR FILING DATE: 2000-03-17
;; PRIOR APPLICATION NUMBER: 60/200,545
;; PRIOR FILING DATE: 2000-04-27
;; PRIOR APPLICATION NUMBER: 60/200,303
;; PRIOR FILING DATE: 2000-04-28
;; PRIOR APPLICATION NUMBER: 60/200,779
;; PRIOR FILING DATE: 2000-04-28
;; PRIOR APPLICATION NUMBER: 60/200,999
;; PRIOR FILING DATE: 2000-05-01
;; PRIOR APPLICATION NUMBER: 60/202,084
;; PRIOR FILING DATE: 2000-05-04
;; PRIOR APPLICATION NUMBER: 60/206,201
;; PRIOR FILING DATE: 2000-05-22
;; PRIOR APPLICATION NUMBER: 60/218,950
;; PRIOR FILING DATE: 2000-07-14
;; PRIOR APPLICATION NUMBER: 60/222,903
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: 60/223,416
;; PRIOR FILING DATE: 2000-08-04
;; PRIOR APPLICATION NUMBER: 60/223,378
;; PRIOR FILING DATE: 2000-08-07
;; NUMBER OF SEQ ID NOS: 9597
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 2530
;; LENGTH: 53
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-796-692-2530

Query Match
Best Local Similarity 84.2%; Score 32; DB 10; Length 53;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RDITTFY 7
Db 32 RDITTFY 38

RESULT 13
US-10-040-862-1784
; Sequence 1784, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Cortix Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Ther
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
```

```
;; PRIOR APPLICATION NUMBER: US 60/200,779
;; PRIOR FILING DATE: 2000-04-28
;; PRIOR APPLICATION NUMBER: US 60/200,999
;; PRIOR FILING DATE: 2000-05-01
;; PRIOR APPLICATION NUMBER: US 60/202,084
;; PRIOR FILING DATE: 2000-05-04
;; PRIOR APPLICATION NUMBER: US 60/206,201
;; PRIOR FILING DATE: 2000-05-22
;; PRIOR APPLICATION NUMBER: US 60/218,950
;; PRIOR FILING DATE: 2000-07-14
;; PRIOR APPLICATION NUMBER: US 60/222,903
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: US 09/796,692
;; PRIOR FILING DATE: 2001-03-01
;; NUMBER OF SEQ ID NOS: 10467
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 1784
;; LENGTH: 53
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-040-862-1784

Query Match      84.2%; Score 32; DB 15; Length 53;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 RDITFFY 7
        ||| |||
Db      32 RDITFFY 38

RESULT 14
US-10-040-862-2530
;; Sequence 2530, Application US/10040862
;; Publication No. US20030078396A1
;; GENERAL INFORMATION:
;; APPLICANT: Galger, Alexander
;; APPLICANT: Algate, Paul A.
;; APPLICANT: Mannion, Jane
;; APPLICANT: Retter, Marc
;; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
;; FILE REFERENCE: 014058-013520US
;; CURRENT APPLICATION NUMBER: US/10/040,862
;; PRIOR APPLICATION NUMBER: US 60/186,126
;; PRIOR FILING DATE: 2000-03-01
;; PRIOR APPLICATION NUMBER: US 60/190,479
;; PRIOR FILING DATE: 2000-03-17
;; PRIOR APPLICATION NUMBER: US 60/200,545
;; PRIOR FILING DATE: 2000-04-27
;; PRIOR APPLICATION NUMBER: US 60/200,303
;; PRIOR FILING DATE: 2000-04-28
;; PRIOR APPLICATION NUMBER: US 60/200,779
;; PRIOR FILING DATE: 2000-04-28
;; PRIOR APPLICATION NUMBER: US 60/200,999
;; PRIOR FILING DATE: 2000-05-01
;; PRIOR APPLICATION NUMBER: US 60/202,084
;; PRIOR FILING DATE: 2000-05-04
;; PRIOR APPLICATION NUMBER: US 60/206,201
;; PRIOR FILING DATE: 2000-05-22
;; PRIOR APPLICATION NUMBER: US 60/218,950
;; PRIOR FILING DATE: 2000-07-14
;; PRIOR APPLICATION NUMBER: US 60/222,903
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: US 60/223,416
;; PRIOR FILING DATE: 2000-08-04
```

```
;; PRIOR APPLICATION NUMBER: US 60/223,378
;; PRIOR FILING DATE: 2000-08-07
;; PRIOR APPLICATION NUMBER: US 09/796,692
;; PRIOR FILING DATE: 2001-03-01
;; NUMBER OF SEQ ID NOS: 10467
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 2530
;; LENGTH: 53
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-040-862-2530

Query Match      84.2%; Score 32; DB 15; Length 53;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 RDITFFY 7
        ||| |||
Db      32 RDITFFY 38

RESULT 15
US-09-925-301-1242
;; Sequence 1242, Application US/09925301
;; Patent No. US20020052308A1
;; GENERAL INFORMATION:
;; APPLICANT: Rosen et al.
;; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;; FILE REFERENCE: PA106
;; CURRENT APPLICATION NUMBER: US/09/925,301
;; PRIOR FILING DATE: 2001-08-10
;; PRIOR APPLICATION NUMBER: PCT/US00/05882
;; PRIOR FILING DATE: 2000-03-08
;; PRIOR APPLICATION NUMBER: 60/124,270
;; PRIOR FILING DATE: 1999-03-12
;; NUMBER OF SEQ ID NOS: 1694
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1242
;; LENGTH: 218
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (3)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: SITE
;; LOCATION: (7)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1242

Query Match      84.2%; Score 32; DB 9; Length 218;
Best Local Similarity 85.7%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 RDITFFY 7
        ||| |||
Db      197 RDITFFY 203

Search completed: October 7, 2003, 19:24:28
Job time : 4.62069 secs
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 19:07:11 ; Search time 2.6069 Seconds
(without alignments)
258.231 Million cell updates/sec

Title: US-09-988-013a-4_COPY_99_105

Perfect score: 38
Sequence: 1 RDITTFY 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 segs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR_76:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	89.5	98	D89856	hypothetical prote
2	33	86.8	168	T46298	hypothetical prote
3	33	86.8	333	D85068	D123-like protein
4	32	84.2	377	VHWH79	nucleocapsid prote
5	32	84.2	398	S13269	translation initia
6	32	84.2	406	F1MS4A	translation initia
7	32	84.2	406	S33681	translation initia
8	32	84.2	407	S00985	translation initia
9	31	81.6	35	H95100	hypothetical prote
10	31	81.6	166	T50172	hypothetical prote
11	31	81.6	278	A42400	probable transcrip
12	31	81.6	279	E69226	hypothetical prote
13	31	81.6	307	G69501	UDP-glucose 4-epim
14	31	81.6	447	S44133	histidine kinase -
15	31	81.6	695	E87397	transglycosylase,
16	31	81.6	830	T04848	protein kinase hom
17	31	81.6	6359	T31679	bactiracin synthe
18	30	78.9	107	B48677	Ig kappa chain V-J
19	30	78.9	166	S52308	pall protein - pse
20	30	78.9	167	S58217	outer membrane pro
21	30	78.9	168	G83525	outer membrane pro
22	30	78.9	1549	D86338	protein F5M15.18 l
23	29	76.3	203	A36365	transforming prote
24	29	76.3	276	D75015	hypothetical prote
25	29	76.3	285	T15252	hypothetical prote
26	29	76.3	299	T32094	hypothetical prote
27	29	76.3	302	B35271	protocaulate 4,
28	29	76.3	341	C86246	hypothetical prote
29	29	76.3	357	ATQO	actin - Oxytricha

30	29	76.3	375	2	A31134	actin, macronuclea
31	29	76.3	399	2	T01387	oxidoreductase hom
32	29	76.3	428	2	A89950	glutamate-1-semal
33	29	76.3	433	2	B90419	hypothetical prote
34	29	76.3	441	2	T50436	hypothetical prote
35	29	76.3	510	2	E71695	hypothetical prote
36	29	76.3	523	2	AD0506	probable secreted
37	29	76.3	588	2	D90750	hypothetical prote
38	29	76.3	588	2	AC0611	hypothetical prote
39	29	76.3	588	2	AC0611	transport ATP-bind
40	29	76.3	594	2	AC0167	ABC-type transport
41	29	76.3	594	2	AC0167	transport ATP-bind
42	29	76.3	642	2	T28866	hypothetical prote
43	29	76.3	716	2	C53292	penicillin-binding
44	29	76.3	880	2	D69427	conserved hypothet
45	29	76.3	971	2	S50912	probable membrane

ALIGNMENTS

RESULT 1

D89856
hypothetical protein SAS023 [Imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: D89856
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O
ma, A.; Mizutani-Tl, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramoto, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: D89856
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <KUR>
A:Cross-references: GB:BA000018; PID:913700710; PIDN:BA042007.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: SAS023

Query Match 89.5%; Score 34; DB 2; Length 98;
Best Local Similarity 71.4%; Pred. No. 3.2;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDITTFY 7
Db 8 KDVTTFY 14

RESULT 2

T46298
hypothetical protein DKFZp4341110.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C:Accession: T46298
R:Duisterhoef, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23035
A:Accession: T46298
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-168 <AAAX>
A:Cross-references: EMBL:AL137744
A:Experimental source: adult testis; clone DKFZp43411110
C:Genetics:
A:Note: DKFZp4341110.1

Query Match 86.8%; Score 33; DB 2; Length 168;
Best Local Similarity 71.4%; Pred. No. 9.1;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ROTTFY 7
DB 50 ROTTFY 56

RESULT 3
D85068
D123-like protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Mar-2001
C:Accession: D85068
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083468; PMID:10617198
A:Accession: D85068
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-333 <STO>
A:Cross-references: GB:NC_001268; NID:97267304; PIDN:CA81086.1; GSPDB:GN00140
C:Genetics:
A:Gene: AT4G05440
A:Map position: 4
C:Superfamily: Saccharomyces cerevisiae hypothetical protein YLR215c

Query Match 86.8%; Score 33; DB 2; Length 333;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ROTTFY 7
DB 198 ROTTFY 204

RESULT 4
VH179
nucleocapsid protein - feline infectious peritonitis virus (strain 79-1146)
C:Species: feline infectious peritonitis virus
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C:Accession: B38498
R:Venema, H.; De Groot, R.J.; Harbour, D.A.; Horzinek, M.C.; Spaan, W.J.M.
Virology 181, 327-335, 1991
A:title: Primary structure of the membrane and nucleocapsid protein genes of feline infe
A:Reference number: A38498; MUID:91134997; PMID:1847259
A:Accession: B38498
A:Molecule type: genomic RNA
A:Residues: 1-377 <VEN>
A:Cross-references: EMBL:X56496; NID:958918; PIDN:CAA39851.1; PID:958920
C:Superfamily: coronavirus nucleocapsid protein
C:Keywords: glycoprotein; nucleocapsid
F:334,154,158,172/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 84.2%; Score 32; DB 1; Length 377;
Best Local Similarity 83.3%; Pred. No. 34;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ROTTFY 7
DB 241 ROTTFY 246

RESULT 5
S13269
translation initiation factor eIF-4A.I - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 19-Mar-1997 #sequence_revision 17-Apr-1998 #text_change 02-Feb-2001
C:Accession: S13269; S78482
R:Conroy, S.C.; Dever, T.E.; Owens, C.L.; Merrick, W.C.
Arch. Biochem. Biophys. 282, 363-371, 1990
A:title: Characterization of the 46,000-dalton subunit of eIF-4F.
A:Reference number: S13269; MUID:91053155; PMID:2241157
A:Accession: S13269
A:Molecule type: mRNA

A:Residues: 5-394 <CON1>
A:Experimental source: reticulocyte
A:Accession: S78482
A:Molecule type: protein
A:Residues: 1-25;38-53;61-102;142-170;183-194;219-225;275-283;309-345;361-398 <CON2>
A:Experimental source: reticulocyte
C:Comment: This is one of the many factors involved in the complex assembly process o
a protein complex involved in "cap" recognition.
C:Genetics:
A:Gene: eIF-4A1
C:Function:
A:Description: translation initiation
C:Superfamily: translation initiation factor eIF-4A
C:Keywords: ATP; blocked amino end; nucleotide binding; P-loop; protein biosynthesis;
F:1-398/Product: translation initiation factor eIF-4A.I (fragment) #status experiment
F:68-75/Region: nucleotide-binding motif A (P-loop)
F:170-175/Region: nucleotide-binding motif B
F:174-177/Region: DEAD motif
F:74/Binding site: ATP (Lys) #status predicted

Query Match 84.2%; Score 32; DB 2; Length 398;
Best Local Similarity 85.7%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ROTTFY 7
DB 377 ROTTFY 383

RESULT 6
FIMS4A
translation initiation factor eIF-4A I - mouse
C:Species: Mus musculus (house mouse)
C>Date: 31-Mar-1988 #sequence_revision 09-Apr-1998 #text_change 19-Jan-2001
C:Accession: J50039; A24267; B24267; S00986; A58767
R:Reddy, N.S.; Roth, W.W.; Bragg, P.W.; Wabba, A.J.
Gene 70, 231-243, 1988
A:title: Isolation and mapping of a gene for protein synthesis initiation factor 4A a
A:Reference number: J50039; MUID:89108007; PMID:3215517
A:Accession: J50039
A:Molecule type: DNA
A:Residues: 1-299, 'C', 301-406 <RED>
A:Cross-references: GB:I36611; NID:9556306; PIDN:AAA50407.1; PID:9556308
A:Note: the authors translated the codon GAG for residue 143 as Gly
R:Nielsen, P.J.; McMaster, G.K.; Trachsel, H.
Nucleic Acids Res. 13, 6867-6880, 1985
A:title: Cloning of eukaryotic protein synthesis initiation factor genes: isolation a
A:Reference number: A24267; MUID:86041884; PMID:3840589
A:Accession: A24267
A:Molecule type: mRNA
A:Residues: 17-406 <NIE>
A:Cross-references: GB:X03039; NID:950812; PIDN:CAA26842.1; PID:950814; GB:X03040; NI
A:Accession: B24267
A:Molecule type: mRNA
A:Residues: 37-406 <NIE2>
A:Cross-references: GB:X03039; NID:950812; PIDN:CAA26843.1; PID:950815; GB:X03040; NI
R:Nielsen, P.J.; Trachsel, H.
EMBO J. 7, 2097-2105, 1988
A:title: The mouse protein synthesis initiation factor 4A gene family includes two re
A:Reference number: S00985; MUID:8838998; PMID:3046931
A:Accession: S00986
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 'W', 1-154, 'VI', 157-406 <NIE3>
A:Cross-references: EMBL:X14421; NID:950810
A:Accession: A58767
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-8 <NIE4>
A:Cross-references: EMBL:X14421; NID:950810; PIDN:CAA32584.1; PID:9581984
C:Comment: This is one of the many factors involved in the complex assembly process o
a protein complex involved in "cap" recognition.

C:Genetics:
A:Gene: MGI:Elf4a1
A:Cross-references: MGI:95303
A:Map position: 11:39.0
A:Introns: 8/2; 24/3; 68/3; 115/3; 172/1; 208/3; 256/3; 302/3; 332/3; 359/2
C:Superfamily: translation initiation factor eIF-4A
C:Keywords: ATP; nucleotide binding; P-loop; protein biosynthesis; RNA binding
F:76-83/Region: nucleotide-binding motif A (P-loop)
F:178-183/Region: nucleotide-binding motif B
F:182-185/Region: DEAD motif
F:82/Binding site: ATP (Lys) #status predicted

Query Match 84.2%; Score 32; DB 1; Length 406;
Best Local Similarity 85.7%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RDITTFY 7
DB 385 RDITTFY 391

RESULT 7
S33681
translation initiation factor eIF-4A.I - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 17-Nov-1995 #text_change 02-Feb-2001
C:Accession: S33681
R:Kim, N.S.; Kato, T.; Abe, N.; Kato, S.
Nucleic Acids Res. 21, 2012, 1993
A:Title: Nucleotide sequence of human cDNA encoding eukaryotic initiation factor 4A1.
A:Reference number: S33681; MUID:93261841; PMID:8493113
A:Accession: S33681
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-406 <KTM>
A:Cross-references: EMBL:DJ3748; MUD:9219402; PIDD:BA02897.1; PTD:9219403
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1992
C:Superfamily: translation initiation factor eIF-4A
C:Keywords: ATP; nucleotide binding; P-loop; protein biosynthesis; RNA binding
F:76-83/Region: nucleotide-binding motif A (P-loop)
F:178-183/Region: nucleotide-binding motif B
F:182-185/Region: DEAD motif

Query Match 84.2%; Score 32; DB 2; Length 406;
Best Local Similarity 85.7%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RDITTFY 7
DB 385 RDITTFY 391

RESULT 8
S00985
translation initiation factor eIF-4A II - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 02-Feb-2001
C:Accession: S00985; S12470
R:Nielsen, P.J.; Trachsel, H.
EMBO J. 7, 2097-2105, 1988
A:Title: The mouse protein synthesis initiation factor 4A gene family includes two related
A:Reference number: S00985; MUID:88328998; PMID:3046931
A:Accession: S00985
A:Molecule type: DNA
A:Residues: 1-407 <NTE>
A:Cross-references: EMBL:X12507
R:Nielsen, P.J.
Submitted to the EMBL Data Library, July 1989
A:Reference number: S12470
A:Accession: S12470
A:Molecule type: DNA
A:Residues: 1-199, 'RV', 202-293, 'Q', 295, 'IV', 298-386, 'H', 388-402, 'G', 404-407 <NIE2>
A:Cross-references: EMBL:X12507; MUD:950822; PIDD:CAA31025.1; PTD:950823

C:Superfamily: translation initiation factor eIF-4A
C:Keywords: ATP; nucleotide binding; P-loop; protein biosynthesis; RNA binding
F:77-84/Region: nucleotide-binding motif A (P-loop)
F:179-184/Region: nucleotide-binding motif B
F:183-186/Region: DEAD motif
F:83/Binding site: ATP (Lys) #status predicted

Query Match 84.2%; Score 32; DB 2; Length 407;
Best Local Similarity 85.7%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RDITTFY 7
DB 386 RDITTFY 392

RESULT 9
H95100
hypothetical protein SP0874 [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C:Accession: H95100
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; H
on, U.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapl
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: H95100
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-35 <KUR>
A:Cross-references: GB:AF005672; PIDD:AAK75001.1; PTD:914972347; GSPDB:GN00164; TIGR:
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP0874

Query Match 81.6%; Score 31; DB 2; Length 35;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 DITTFY 7
DB 21 DITTFY 26

RESULT 10
T50172
hypothetical protein SPAC227.16c [imported] - fission yeast (Schizosaccharomyces pombe
C:Species: Schizosaccharomyces pombe
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
C:Accession: T50172
R:Zimmermann, W.; Wandut, R.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, November 1999
A:Reference number: Z25036
A:Accession: T50172
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-166 <ZIM>
A:Cross-references: EMBL:ALJ33156; PIDD:CA861465.1; GSPDB:GN00066; SPDB:SPAC227.16c
A:Experimental source: strain 972h(-); cosmid c227
C:Genetics:
A:Gene: SPDB:SPAC227.16c
A:Map position: 1
A:Introns: 33/3; 53/2; 98/2; 147/1

Query Match 81.6%; Score 31; DB 2; Length 166;
Best Local Similarity 85.7%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RDITTFY 7
DB 21 DITTFY 26

Db 82 RDITTY 88

RESULT 11

A42400

probable transcription regulator msmr [similarity] - Streptococcus mutans

N.Alternate names: multiple sugar metabolism protein msmr

C.Species: Streptococcus mutans

C.Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000

C.Accession: A42400

R.Russell, R.R.; Aduse-Opoku, J.; Sutcliffe, I.C.; Tao, L.; Ferretti, J.J.

J. Biol. Chem. 267, 4631-4637, 1992

A.Title: A binding protein-dependent transport system in Streptococcus mutans responsible

A.Reference number: A42400; MUID:92165821; PMID:1537846

A.Accession: A42400

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-278 <RUS>

A.Note: sequence extracted from NCBI backbone (NCBI:83887, NCBI:83888)

Query Match

Best Local Similarity 81.6%; Score 31; DB 2; Length 278;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDITTY 7

Db 72 KDITTY 78

RESULT 12

E69226

hypothetical protein MTH944 - Methanobacterium thermoautotrophicum (strain Delta H)

C.Species: Methanobacterium thermoautotrophicum

C.Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999

C.Accession: E69226

R.Smith, D.R.; Doucette-Stamm, L.A.; Delonghery, C.; Lee, R.; Dubois, J.; Aldredge, T.;

Qiu, D.; Spadefors, R.; Vicaire, R.; Wang, Y.; Mierzbowski, J.; Gibson, R.; Jiwani, N.

Kl, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.M.

J. Bacteriol. 179, 7135-7155, 1997

A.Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct

A.Reference number: A69000; MUID:98037514; PMID:9371463

A.Accession: E69226

A.Status: preliminary; nucleic acid sequence not shown; translation not shown

A.Molecule type: DNA

A.Residues: 1-279 <KTH>

A.Cross-references: GB:AE000869; GB:AE000666; NID:g2622042; PIDN:AAB85442.1; PID:g262204

A.Experimental source: strain Delta H

C.Genetics:

A.Gene: MTH944

Query Match

Best Local Similarity 81.6%; Score 31; DB 2; Length 279;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RDITTY 7

Db 54 RDITTY 60

RESULT 13

G69501

UDP-glucose 4-epimerase (gale-2) homolog - Archaeoglobus fulgidus

C.Species: Archaeoglobus fulgidus

C.Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000

C.Accession: G69501

R.Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson

.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirschner, E.F.

Glodek, A.; Zhou, L.; Overbeck, R.; Cooney, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A.Authors: Ullrich, T.; Cotton, M.D.; Springs, T.; Artlich, P.; Kalne, B.P.; Sykes, S.

Smith, H.O.; Woese, C.R.; Venter, J.C.

A.Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo

A.Reference number: A69250; MUID:98049343; PMID:9389475

A.Accession: G69501

A.Status: preliminary; nucleic acid sequence not shown; translation not shown

A.Molecule type: DNA

A.Residues: 1-307 <KLE>

A.Cross-references: GB:AE000963; GB:AE000782; NID:g2689286; PIDN:AAB92234.1; PID:g264

C.Superfamily: Escherichia coli UDPglucose 4-epimerase; UDPglucose 4-epimerase homolo

Query Match

Best Local Similarity 81.6%; Score 31; DB 2; Length 307;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RDITTY 7

Db 122 KDITTY 128

RESULT 14

S44133

histidine kinase - Lactococcus lactis

C.Species: Lactococcus lactis

C.Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 15-Oct-1999

C.Accession: S44133

R.Engelke, G.; Glauski-Eckel, Z.; Klesau, P.; Slegers, K.; Hammelmann, M.; Enflen, K.

submitted to the EMBL Data Library, December 1993

A.Description: Regulation of nisin biosynthesis and immunity in L. lactis 6F3.

A.Reference number: S44130

A.Accession: S44133

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-447 <ENG>

A.Cross-references: EMBL:K76884; NID:g473019; PIDN:CA54212.1; PID:g473023

Query Match

Best Local Similarity 81.6%; Score 31; DB 2; Length 447;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DITTY 7

Db 332 DITTY 337

RESULT 15

E87397

transglycosylase, probable CCL194 [Imported] - Caulobacter crescentus

C.Species: Caulobacter crescentus

C.Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 17-Mar-2003

C.Accession: E87397

R.Nierman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,

B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwin, M.L.; Haft, D.H.; Ko

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A.Title: Complete genome sequence of Caulobacter crescentus.

A.Reference number: A87249; MUID:21173698; PMID:11259647

A.Accession: E87397

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-695 <STO>

A.Cross-references: GB:AE005673; NID:g13422517; PIDN:MAK23177.1; GSPDB:GN00148

C.Genetics:

A.Gene: CCL194

C.Superfamily: soluble lytic transglycosylase

Query Match

Best Local Similarity 81.6%; Score 31; DB 2; Length 695;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RDITTY 7

Db 401 RHITTY 407

Search completed: October 7, 2003, 19:21:52

Job time : 4.6069 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 19:03:46 ; Search time 1.42414 Seconds
(without alignments)
231.148 Million cell updates/sec

Title: US-09-988-013a-4_COPY_99_105
Perfect score: 38
Sequence: 1 RDITTFY 7

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	86.8	406	1	ARG1_HUMAN
2	33	86.8	414	1	ARG1_MOUSE
3	33	86.8	415	1	ARG1_RAT
4	32	84.2	377	1	NCAP_FITV
5	32	84.2	398	1	IF41_RABIT
6	32	84.2	406	1	IF41_HUMAN
7	32	84.2	407	1	IF42_MOUSE
8	32	84.2	407	1	IF42_MOUSE
9	31	81.6	278	1	MSMR_STRMU
10	31	81.6	447	1	NISK_LACIA
11	31	81.6	6359	1	BACC_BACCI
12	30	78.9	166	1	PAL_PSEPK
13	30	78.9	420	1	PUR2_STRSU
14	29	76.3	203	1	RASL_RHTRA
15	29	76.3	302	1	PCIB_PSEPA
16	29	76.3	357	1	ACT1_OXYFA
17	29	76.3	357	1	ACT1_OXYFA
18	29	76.3	375	1	ACT1_OXYNO
19	29	76.3	375	1	ACT1_OXYNO
20	29	76.3	375	1	ACT1_OXYTR
21	29	76.3	375	1	ACT2_OXYNO
22	29	76.3	428	1	GSA_STAMU
23	29	76.3	428	1	GSA_STAMU
24	29	76.3	473	1	HYA2_MOUSE
25	29	76.3	473	1	HYA2_MOUSE
26	29	76.3	510	1	Y382_RICPR
27	29	76.3	588	1	CYTD_ECOTI
28	29	76.3	716	1	PBPB_BACSU
29	29	76.3	880	1	YE21_ARCFU
30	29	76.3	951	1	SEF8_HUMAN
31	29	76.3	971	1	SEC5_YEAST
32	29	76.3	1061	1	DPOL_ADE12
33	29	76.3	1886	1	POL_COTMY

34	28	73.7	102	1	YD63_MYCPN
35	28	73.7	260	1	MCRG_METVA
36	28	73.7	265	1	YB46_MYCPN
37	28	73.7	308	1	Y178_TREPA
38	28	73.7	477	1	MRE2_ECOTI
39	28	73.7	499	1	CGAM_DROME
40	28	73.7	570	1	HEMA_NDVA
41	28	73.7	571	1	HEMA_NDVA
42	28	73.7	571	1	HEMA_NDVA3
43	28	73.7	571	1	HEMA_NDVA
44	28	73.7	571	1	HEMA_NDVA
45	28	73.7	571	1	HEMA_NDVA

ALIGNMENTS

RESULT 1

ARG1_HUMAN STANDARD; PRT; 406 AA.

AC 08N6T3; Q96KC4; Q96R02; Q9NSU3; Q9NVP6; Q9U1L0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE ADP-ribosylation factor GTPase activating protein 1 (ADP-ribosylation factor 1 GTPase activating protein) (ARF1 GAP) (ARF1-directed GTPase-activating protein) (GAP protein).
GN ARFGAP1 OR ARF1GAP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Kotsuka S., Yoshikawa Y., Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;
RT "NEDO human cDNA sequencing project."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R., Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggaley C.L., Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M., Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Kay M.P., Kimberley A.M., King A., Knights A., Laird G.R., Lawlor S., Leharashtio M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., Marsh V.L., Martin S.L., McConachie I.J., McKay K., McMurtry A., Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., Olliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Phillips M., Pritchard S., Prithalingam S.R., Plumb R.W., Ramsay H., Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Stewart C.A., Sulston J.E., Swann R.M., Symmore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A., Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20."
RL Nature 414:865-871(2001).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Fetal brain;

RA MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Pelngold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner C.M., Schuler G.D.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusla K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci T.L., Scheetz T.E.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Hellon E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smolius D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA *Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.*;
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RN SEQUENCE OF 240-406 FROM N.A. (ISOFORM 1).
 RP TISSUE=Testis;
 RA Duesterhoeft A., Lauber J., Mewes H.-W., Gassenhuber J., Wiemann S.;
 RA Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RN SEQUENCE OF 299-406 FROM N.A.
 RP TISSUE=Fetal brain;
 RA Deki N.;
 RT *HRI NTF human fetal brain cDNA project.*;
 RT Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: GTPase-activating protein (GAP) for the ADP ribosylation
 CC factor 1 (ARF1). Involved in membrane trafficking and /or vesicle
 CC transport. Promotes hydrolysis of the ARF1-bound GTP and thus, is
 CC required for the dissociation of coat proteins from Golgi-derived
 CC membranes and vesicles. Probably regulates ARF1-mediated transport via
 CC its interaction with the KDELR proteins and RNP24. Overexpression
 CC induces the redistribution of the entire Golgi complex to the
 CC endoplasmic reticulum, as when ARF1 is deactivated. Its activity
 CC is stimulated by phosphoinositides and inhibited by
 CC phosphatidylinositol (By similarity).
 CC -1- SUBUNIT: Interacts with ARF1. Interacts with the COPI coat
 CC proteins, KDELR1 and RNP24. The interaction with RNP24 inhibits
 CC the GAP activity (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic; associates with the Golgi
 CC complex (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q8N6T3-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q8N6T3-2; Sequence=VSP_000298; VSP_000299;
 CC Note=no experimental confirmation available;
 CC -1- DOMAIN: The region downstream of ARF-GAP domain is essential to
 CC GAP activity in vivo. This region may be required for its
 CC targeting to Golgi membranes (By similarity).
 CC -1- SIMILARITY: Contains 1 Arf-GAP domain.
 CC -1- CAUTION: Ref.4 sequence differs from that shown in that it seems
 CC to include intronic sequence.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AK021629; BAA91796.1; ALT. INT.
 CC EMBL: AK027268; BAB55009.1; ALT. INT.
 CC EMBL: AK027441; BAB55113.1; ALT. INT.

DR EMBL: AL121827; CAC36116.1; -;
 DR EMBL: BC028233; AAH28233.1; -;
 DR EMBL: AL137744; CAB70901.1; ALT-SEQ.
 DR EMBL: AB015340; BAB8117.1; -;
 DR Genew: HGNC:15852; ARFGAP1.
 DR InterPro: IPR001164; hRIP-like.
 DR Pfam: PF01412; ArfGAP.1.
 DR PRINTS: PR00405; REVINTACTNG.
 DR SMART: SM00105; ArfGAP.1.
 DR PROSITE: PS50115; ARFGAP.1.
 KM Transport: Protein transport; Golgi stack;
 KM Zinc-finger: Alternative splicing; Polymorphism.
 FT DOMAIN 7 124
 FT ZN-FING C4-TYPE.
 FT ZN-SPIC 239 239
 FT VARSPIC 279 280
 FT VARSPIC 279 280
 FT VARIANT 184 184
 FT V V->M (in dbSNP:2273499).
 FT FTId=VSP_000299.
 FT FTId=VAR_015187.
 FT CONFLICT 274 274
 FT Q -> R (in Ref. 1; BAB55009).
 SQ SEQUENCE 406 AA; 44668 MW; CAA1828DE660621 CRC64;
 Query Match 86.8%; Score 33; DB 1; Length 406;
 Best Local Similarity 71.4%; Pred. No. 8.3;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RIDITFEY 7
 Db 288 RDVTFYF 294
 RESULT 2
 ARG1_MOUSE STANDARD; PRT; 414 AA.
 ID 09EPY9;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ADP-ribosylation factor GTPase activating protein 1 (ADP-ribosylation
 DE factor 1 GTPase activating protein) (ARF1 GAP) (ARF1-directed GTPase-
 DE activating protein) (GAP protein).
 GN ARFGAP1 OR ARFGAP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Venkateswaru K.;
 RT Cloning and functional characterization of mouse ARFGAP.*;
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: GTPase-activating protein (GAP) for the ADP ribosylation
 CC factor 1 (ARF1). Involved in membrane trafficking and /or vesicle
 CC transport. Promotes hydrolysis of the ARF1-bound GTP and thus, is
 CC required for the dissociation of coat proteins from Golgi-derived
 CC membranes and vesicles. A prerequisite for vesicle's fusion with
 CC target compartment. Probably regulates ARF1-mediated transport via
 CC its interaction with the KDELR proteins and RNP24. Overexpression
 CC induces the redistribution of the entire Golgi complex to the
 CC endoplasmic reticulum, as when ARF1 is deactivated. Its activity
 CC is stimulated by phosphoinositides and inhibited by
 CC phosphatidylinositol (By similarity).
 CC -1- SUBUNIT: Interacts with ARF1. Interacts with the COPI coat
 CC proteins, KDELR1 and RNP24. It is probably a component of the COPI
 CC coat protein complex. The interaction with RNP24 inhibits the GAP
 CC activity (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic; associates with the Golgi
 CC complex (By similarity).
 CC -1- DOMAIN: The region downstream of ARF-GAP domain is essential to
 CC GAP activity in vivo. This region may be required for its
 CC targeting to Golgi membranes (By similarity).
 CC -1- SIMILARITY: Contains 1 Arf-GAP domain.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AJ401461; CAC18721.1; -
DR MGD: MGI:218359; ArfGAP1.
DR InterPro: IPR001164; hRIP-like.
DR Pfam: PF01412; ArfGAP.1.
DR PRINTS: PR00405; REVINTRACTING.
DR SMART: SM00105; ArfGAP.1.
DR PROSITE: PS50115; ARFGAP.1.
KW Transport; Protein transport; GTPase activation; Golgi stack;
KW Zinc-finger.
FT DOMAIN 7 124 ARF-GAP.
FT ZN_FING 22 45 C4-TYPE.
SQ SEQUENCE 414 AA; 45269 MW; 0A050D29DE90BC62 CRC64;
Query Match 86.8%; Score 33; DB 1; Length 414;
Best Local Similarity 71.4%; Pred. No. 8.7;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 RDITTFY 7
Db 288 RDVTTF 294

RESULT 3
ARG1_RAT
ID ARG1_RAT STANDARD; PRT; 415 AA.
AC Q62848;
DT 26-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ADP-ribosylation factor GTPase activating protein 1 (ADP-ribosylation
DE factor 1 GTPase activating protein) (ARF1 GAP) (ARF1-directed GTPase-
DE activating protein) (GAP protein).
GN ARFGAP1 OR ARF1GAP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, INTERACTION WITH ARF1, AND SEQUENCE OF
RP 82-95; 140-160; 183-191; 246-253; 264-278; 297-306 AND 361-375.
RC TISSUE=Liver;
RX MEDLINE=95197515; PubMed=7890632;
RA Maier V., Cukierman E., Rotman M., Admon A., Cassel D.;
RT "ADP-ribosylation factor-directed GTPase-activating protein.
RT Purification and partial characterization.",
RL J. Biol. Chem. 270:5232-5237(1995).
[2]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3), CHARACTERIZATION, AND
RP MUTAGENESIS OF CYS-22 AND CYS-25.
RC TISSUE=Liver;
RX MEDLINE=96123274; PubMed=8533093;
RA Cukierman E., Huber I., Rotman M., Cassel D.;
RT "The ARF1 GTPase-activating protein: zinc finger motif and Golgi
RT complex localization.",
RL Science 270:1999-2002(1995).
[3]
RN INTERACTION WITH KDELR1.
RP MEDLINE=98070308; PubMed=9405360;
RA Aoe T., Cukierman E., Lee A., Cassel D., Peters P.J., Hsu V.W.;
RT "The KDELR receptor, ERD2, regulates intracellular traffic by
RT recruiting a GTPase-activating protein for ARF1.",
RL EMBO J. 16:7305-7316(1997).
[4]
RN CHARACTERIZATION, AND MUTAGENESIS OF CYS-22.

RX MEDLINE=98406131; PubMed=9733781;
RA Huber I., Cukierman E., Aoe T., Hsu V.W., Cassel D.;
RT "Requirement for both the amino-terminal catalytic domain and a
RT noncatalytic domain for in vivo activity of ADP-ribosylation factor
RT GTPase-activating protein.",
RL J. Biol. Chem. 273:24786-24791(1998).
[5]
RN INTERACTION WITH RNP24.
RP MEDLINE=21629435; PubMed=11748249;
RA Lanoix J., Ouwendijk J., Stark A., Szafer E., Cassel D., Dejgaard K.,
RA Weiss M., Nilsson T.; Stark A., Szafer E., Cassel D., Dejgaard K.,
RT "Sorting of Golgi resident proteins into different subpopulations of
RT COP1 vesicles: a role for ArfGAP1.",
RL J. Cell Biol. 155:1199-1212(2001).
[6]
RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS) OF CATALYTIC DOMAIN IN COMPLEX
RP WITH HUMAN ARF1.
RX MEDLINE=99200399; PubMed=10102276;
RA Goldberg J.;
RT "Structural and functional analysis of the ARF1-ARFGAP complex reveals
RL a role for coatomer in GTP hydrolysis.",
Cell 96:893-902(1999).
[7]
CC -1- FUNCTION: GTPase-activating protein (GAP) for the ADP ribosylation
CC factor 1 (ARF1). Involved in membrane trafficking and/or vesicle
CC transport. Promotes hydrolysis of the ARF1-bound GTP and thus, is
CC required for the dissociation of coat proteins from Golgi-derived
CC membranes and vesicles, a prerequisite for vesicle's fusion with
CC target compartment. Probably regulates ARF1-mediated transport via
CC its interaction with the KDELR proteins and RNP24. Overexpression
CC induces the redistribution of the entire Golgi complex to the
CC endoplasmic reticulum, as when ARF1 is deactivated. Its activity
CC is stimulated by phospholipids and inhibited by
CC phosphatidylcholine.
CC -1- SUBUNIT: Interacts with ARF1. Interacts with the COP1 coat
CC proteins, KDELR1 and RNP24. It is probably a component of the COP1
CC coat protein complex. The interaction with RNP24 inhibits the GAP
CC activity.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic; associates with the Golgi
CC complex.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=3;
CC Comment-Experimental confirmation may be lacking for some
CC isoforms;
CC Name=1;
CC IsoId=Q62848-1; Sequence=Displayed;
CC Name=2; Synonyms=WI5;
CC IsoId=Q62848-2; Sequence=VSP_000300;
CC Name=3; Synonyms=Z5;
CC IsoId=Q62848-3; Sequence=VSP_000301, VSP_000302;
CC -1- TISSUE SPECIFICITY: Widely expressed. Highly expressed in brain and
CC liver.
CC -1- DOMAIN: The region downstream of ARF-GAP domain is essential to
CC GAP activity in vivo. This region may be required for its
CC targeting to Golgi membranes.
CC -1- SIMILARITY: Contains 1 Arf-GAP domain.

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CC -----
DR EMBL: U35776; AAC52337.1; -
DR InterPro: IPR001164; hRIP-like.
DR Pfam: PF01412; ArfGAP.1.
DR PRINTS: PR00405; REVINTRACTING.
DR SMART: SM00105; ArfGAP.1.
DR PROSITE: PS50115; ARFGAP.1.
KW Transport; Protein transport; GTPase activation; Golgi stack;
KW Zinc-finger; Alternative splicing.
FT DOMAIN 7 124 ARF-GAP.

```

FT ZN.FING 22 45 C4-TYPE.
FT VARSPPLIC 21 57 Missing (in isoform 2).
FT VARSPPLIC 280 283 /FTID=VSP_000300.
FT VARSPPLIC 284 415 OGVG -> GLPC (in isoform 3).
FT VARSPPLIC 284 415 /FTID=VSP_000301.
FT VARSPPLIC 284 415 Missing (in isoform 3).
FT VARSPPLIC 284 415 /FTID=VSP_000302.
FT MUTAGEN 22 22 C->A: LOSS OF GAP ACTIVITY.
FT MUTAGEN 25 25 C->A: LOSS OF GAP ACTIVITY.
FT MUTAGEN 25 25 C->A: LOSS OF GAP ACTIVITY.
SQ SEQUENCE 415 AA; 45442 MW; 90015417E3E717BB CRC64;

Query Match
Best Local Similarity 71.4%; Score 33; DB 1; Length 415;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDITTFY 7
Db 288 RDVTFY 294

RESULT 4
NCAP_FIPV STANDARD; PRT; 377 AA.
ID NCAP_FIPV P25909;
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Nucleocapsid protein (N structural protein).
GN N.
OS Feline infectious peritonitis virus (strain 79-1146) (FIPV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronaviruses.
NCBI_TaxID=33734;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=91134997; PubMed=1847259;
RA Venema H., de Groot R.J., Harbour D.A., Horzinek M.C.,
RA Spaan W.J.M.;
RT "Primary structure of the membrane and nucleocapsid protein genes of
RT feline infectious peritonitis virus and immunogenicity of recombinant
RT vaccinia viruses in kittens."
RL Virology 181:327-335(1991).
CC -1- SIMILARITY: Belongs to the coronavirus nucleocapsid protein
CC family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X56496; CAA39851.1; -
CC PIR: B38498; VHIH79.
CC InterPro: IPR001218; Corona_nucleocap.
CC Pfam: PF00937; Corona_nucleoca. 1.
CC Nucleocapsid.
CC KW SEQUENCE 377 AA; 42745 MW; D76382AE688059B CRC64;

Query Match
Best Local Similarity 84.2%; Score 32; DB 1; Length 377;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DITTFY 7
Db 241 DVTFY 246

RESULT 5
IF41_RABIT STANDARD; PRT; 398 AA.
ID IF41_RABIT P29562;
AC P29562;

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DT 01-APR-1993 (Rel. 25, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Eukaryotic initiation factor 4A-1 (eIF-4A-1) (Fragment).
GN EIF4A1 OR EIF4A.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
RN [1]
RP SEQUENCE OF 5-398 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=91053155; PubMed=2241157;
RA Conroy S.C., Deyer T.E., Owens C.L., Merrick W.C.;
RT "Characterization of the 46,000-dalton subunit of eIF-4F."
RL Arch. Biochem. Biophys. 282:363-371(1990).
CC -1- FUNCTION: EIF-4A IS BOTH A SUBUNIT OF A HIGH MOLECULAR WEIGHT
CC PROTEIN COMPLEX INVOLVED IN CAP RECOGNITION AND IS REQUIRED AS A
CC SINGLE POLYPEPTIDE CHAIN FOR mRNA BINDING TO RIBOSOME. IT IS AN
CC ATP-DEPENDENT SINGLE STRANDED DNA-BINDING PROTEIN WITH A SEQUENCE-
CC INDEPENDENT UNWINDING ACTIVITY (HELICASE).
CC -1- SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY.
CC HSP; 058083; 1HV8.
CC InterPro: IPR001410; DEAD.
CC InterPro: IPR000629; DEAD_box.
CC Pfam: PF00270; DEAD; 1.
CC Pfam: PF00271; helicase_C.
CC DR SMART; SM00487; DEXDC; 1.
CC DR SMART; SM00490; HELIC; 1.
CC DR PROSITE: PS00039; DEAD_ATP_HELICASE; 1.
KW Initiation factor; Protein biosynthesis; ATP-binding; RNA-binding;
KW DNA-binding; Helicase.
FT NON_TER 1
FT NP_BIND 68 75 ATP (BY SIMILARITY).
FT SITE 174 177 DEAD BOX.
SQ SEQUENCE 398 AA; 45291 MW; 8CE1C18DE7AC7D37 CRC64;

Query Match
Best Local Similarity 84.2%; Score 32; DB 1; Length 398;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RDITTFY 7
Db 377 RDITTFY 383

RESULT 6
IF41_HUMAN STANDARD; PRT; 406 AA.
ID IF41_HUMAN P04765; 061516.
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Eukaryotic initiation factor 4A-1 (eIF-4A-1) (eIF4A-1).
GN EIF4A1 OR EIF4A OR DDXX2A.
OS Homo sapiens (Human), and
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606, 10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93261841; PubMed=8493113;
RA Kim N.-S., Kato T., Abe N., Kato S.;
RT "Nucleotide sequence of human cDNA encoding eukaryotic initiation
RT factor 4A1."
RL Nucleic Acids Res. 21:2012-2012(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buttefield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences".
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES-MOUSE;
 RX MEDLINE=86041884; PubMed=3840589;
 RA Nielsen P.J., Mcmaster G.K., Trachsel H.,
 RT "Cloning of eukaryotic protein synthesis initiation factor genes:
 RT isolation and characterization of cDNA clones encoding factor
 RT eIF-4A.";
 RL Nucleic Acids Res. 13:6867-6880(1985).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES-MOUSE;
 RX MEDLINE=89108007; PubMed=3215517;
 RA Reddy N.S., Roth W.W., Bragg P.W., Mahba A.J.,
 RT "Isolation and mapping of a gene for protein synthesis initiation
 RT factor 4A and its expression during differentiation of murine
 RT erythroleukemia cells".
 RL Gene 70:231-243(1988).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC SPECIES-MOUSE; STRAIN=129;
 RA Miyashita A., Shimizu N., Nakajima T., Odani S., Kuwano R.,
 RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
 RN [6]
 RP MUTAGENESIS.
 RC SPECIES-MOUSE;
 RX MEDLINE=92331617; PubMed=1378397;
 RA Pause A., Sonnenberg N.,
 RT "Mutational analysis of a DEAD box RNA helicase: the mammalian
 RT translation initiation factor eIF-4A.";
 RL EMBO J. 11:2643-2654(1992).
 CC -1- FUNCTION: EIF-4A IS BOTH A SUBUNIT OF A HIGH MOLECULAR WEIGHT
 CC PROTEIN COMPLEX INVOLVED IN CAP RECOGNITION AND IS REQUIRED AS A
 CC SINGLE POLYPEPTIDE CHAIN FOR MRNA BINDING TO RIBOSOME. IT IS AN
 CC ATP-DEPENDENT SINGLE STRANDED DNA-BINDING PROTEIN WITH A SEQUENCE-
 CC INDEPENDENT UNWINDING ACTIVITY (HELICASE).
 CC -1- SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY.
 CC -----
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 CC -----
 DR EMBL, D13748; BAA02897.1; -;
 DR EMBL, BC009585; AAH09585.1; -;
 DR EMBL, X03039; CAA26842.1; ALT_INIT.
 DR EMBL, X03039; CAA26843.1; ALT_INIT.
 DR EMBL, X03040; CAA26845.1; ALT_INIT.
 DR EMBL, X03040; CAA26846.1; ALT_INIT.
 DR EMBL, L36611; AAA50407.1; -;
 DR EMBL, M2873; AAA50407.1; JOINED.

DR EMBL, L36608; AAA50407.1; JOINED.
 DR EMBL, L36609; AAA50407.1; JOINED.
 DR EMBL, L36610; AAA50407.1; JOINED.
 DR EMBL, AB011595; BAA25075.1; -;
 DR PIR, S00039; FIMSA4.
 DR PIR, S33681; S33681.
 DR HSSP, Q58083; IHV8.
 DR Genew; HGNC:3282; EIF4A1.
 DR GK; P04765; -;
 DR MIM; 602641; -;
 DR MGD; MGI:95303; EIf4a1.
 DR GO; GO:0008306; C:eukaryotic translation initiation factor 4 . . .; TAS.
 DR GO; GO:0003729; F:mRNA binding activity; TAS.
 DR GO; GO:0006441; P:binding to mRNA cap; TAS.
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR006629; DEAD_box.
 DR InterPro; IPR001650; Helicase_C.
 DR Pfam; PF00270; DEAD; 1.
 DR Pfam; PF00271; Helicase_C; 1.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00490; HELICC; 1.
 DR PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
 KW Initiation factor; Protein biosynthesis; ATP-binding; RNA-binding;
 KW DNA-binding; Helicase.
 FT NP_BIND 76 83 ATP (BY SIMILARITY).
 FT SITE 182 185 DEAD BOX.
 FT CONFLICT 300 300 S -> C (IN REF. 4).
 SQ SEQUENCE 406 AA; 46154 MW; 6EF89939F3045420 CRC64;

 QY 1 RDIITFY 7 84.2% Score 32; DB 1; Length 406;
 Db 385 RDIITFY 391 Best Local Similarity 85.7% Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 RESULT 7
 IF42_HUMAN STANDARD; PRT; 407 AA.
 AC Q14240; O96B90; -;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Eukaryotic initiation factor 4A-II (eIF-4A-II).
 DE EIF4A2 OR DDXXB.
 GN EIF4A2 OR DDXXB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=96103476; PubMed=8521730;
 RA Sudo K., Takahashi E., Nakamura Y.,
 RT "Isolation and mapping of the human EIF4A2 gene homologous to the
 RT murine protein synthesis initiation factor 4A-II gene EIf4a2.";
 RL Cytogenet. Cell Genet. 71:385-388(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,

RA Villalón D.R., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko I., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: EIF-4A IS BOTH A SUBUNIT OF A HIGH MOLECULAR WEIGHT
 CC PROTEIN COMPLEX INVOLVED IN CAP RECOGNITION AND IS REQUIRED AS A
 CC SINGLE POLYPEPTIDE CHAIN FOR MRNA BINDING TO RIBOSOME. IT IS AN
 CC ATP-DEPENDENT SINGLE STRANDED DNA-BINDING PROTEIN WITH A SEQUENCE-
 CC INDEPENDENT UNWINDING ACTIVITY (HELICASE).
 CC -1- SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY.
 CC -1- DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobiogen.fr/services/chromosome/genet/EIF4A2ID262.html".
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CC EMBL: D30655; BAA06336.1; -;
 DR EMBL: BC015842; AAH15842.1; -;
 DR HSSP: Q58083; IHV8.
 DR Genew: HGNC:3284; EIF4A2.
 DR GK: 014240; -;
 DR WIM: 601102; -;
 DR GO: GO:0008304; C:eukaryotic translation initiation factor 4 . . .; TAS.
 DR GO: GO:0003743; F:translation initiation factor activity; TAS.
 DR GO: GO:0006446; P:regulation of translational initiation; TAS.
 DR InterPro: IPR001410; DEAD.
 DR InterPro: IPR000629; DEAD_box.
 DR InterPro: IPR001650; Helicase_C.
 DR Pfam: PF00270; DEAD; 1.
 DR Pfam: PF00271; Helicase_C; 1.
 DR SMART: SM00487; DEXDC; 1.
 DR SMART: SM00490; HELIC; 1.
 DR PROSITE: PS00039; DEAD_ATP_HELICASE; 1.
 KW Initiation factor; Protein biosynthesis; ATP-binding; RNA-binding;
 KW DNA-binding; Helicase.
 FT NP_BIND 77 84 ATP (BY SIMILARITY).
 FT SITE 183 186 DEAD BOX.
 FT CONFLICT 27 27 N -> S (IN REF. 2).
 FT CONFLICT 212 213 FA -> LT (IN REF. 2).
 SO SEQUENCE 407 AA; 46394 MW; 046BA69D25ED5A87 CRC64;

Query Match 84.2%; Score 32; DB 1; Length 407;
 Best Local Similarity 85.7%; Pred. NO. 14;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RDITTEY 7
 DB 386 RDITTEY 392

RESULT 8
 IF42_MOUSE STANDARD; PRT; 407 AA.
 AC P10630; Q61513; Q61514;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Eukaryotic initiation factor 4A-II (EIF-4A-II) (EIF4A-II).
 GN EIF4A2 OR DDX2B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI-TaxID-10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND VARIANT SER-9 INS.
 RX MEDLINE-8832898; PubMed-3046931;
 RA Nielsen P.J., Trachsel H.;
 RT "The mouse protein synthesis initiation factor 4A gene family
 RT includes two related functional genes which are differentially
 RT expressed".
 RL EMBO J. 7:2097-2105(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6; TISSUE-Liver;
 RA Nielsen P.J.,
 RN Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE OF 291-323 FROM N.A.
 RC TISSUE-Liver;
 RX MEDLINE-97248616; PubMed-9092667;
 RA Selvamurugan N., Joost O.H., Haas E.S., Brown J.W., Galvin N.J.,
 RA Ellicott G.L.;
 RT "Intracellular localization and unique conserved sequences of three
 RT small nucleolar RNAs".
 RL Nucleic Acids Res. 25:1591-1596(1997).
 CC -1- FUNCTION: EIF-4A IS BOTH A SUBUNIT OF A HIGH MOLECULAR WEIGHT
 CC PROTEIN COMPLEX INVOLVED IN CAP RECOGNITION AND IS REQUIRED AS A
 CC SINGLE POLYPEPTIDE CHAIN FOR MRNA BINDING TO RIBOSOME. IT IS AN
 CC ATP-DEPENDENT SINGLE STRANDED DNA-BINDING PROTEIN WITH A SEQUENCE-
 CC INDEPENDENT UNWINDING ACTIVITY (HELICASE).
 CC -1- SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY.
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CC EMBL: X12507; CAA31025.1; -;
 DR EMBL: X14422; CAA32585.1; -;
 DR EMBL: X56953; CAA40269.1; -;
 DR EMBL: X56953; CAA40268.1; -;
 DR EMBL: U64706; AAC53180.1; -;
 DR PTR: S00985; S00985.
 DR HSSP: Q58083; IHV8.
 DR MGD: MGI:106906; EIF4a2.
 DR InterPro: IPR001410; DEAD.
 DR InterPro: IPR000629; DEAD_box.
 DR InterPro: IPR001650; Helicase_C.
 DR Pfam: PF00270; DEAD; 1.
 DR Pfam: PF00271; Helicase_C; 1.
 DR SMART: SM00487; DEXDC; 1.
 DR SMART: SM00490; HELIC; 1.
 DR PROSITE: PS00039; DEAD_ATP_HELICASE; 1.
 KW Initiation factor; Protein biosynthesis; ATP-binding; RNA-binding;
 KW DNA-binding; Helicase.
 FT NP_BIND 77 84 ATP (BY SIMILARITY).
 FT SITE 183 186 DEAD BOX.
 FT VARIANT 9 9 IF -> RV (IN REF. 1).
 FT CONFLICT 200 201 IF -> RV (IN REF. 1).
 FT CONFLICT 294 297 HARD -> QATY (IN REF. 1).
 FT CONFLICT 387 387 D -> H (IN REF. 1).
 FT CONFLICT 403 403 V -> G (IN REF. 1).
 SO SEQUENCE 407 AA; 46402 MW; FAAVD3BA9D8C6DA0 CRC64;

Query Match 84.2%; Score 32; DB 1; Length 407;
 Best Local Similarity 85.7%; Pred. NO. 14;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RDITTEY 7
 DB 386 RDITTEY 392

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RESULT 9
MSMR_STRMU STANDARD: PRT: 278 AA.
ID MSMR_STRMU STANDARD: PRT: 278 AA.
AC 000753;
DT 01-JUN-1994 (Rel. 29, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mem operon regulatory protein.
GN MSMR OR SMU.876.
OS Streptococcus mutans.
OC Bacteria: Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1309;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ingbritt;
RX MEDLINE=92165821; PubMed=1537846;
RA Russell R.R.B., Aduse-Opoku J., Sutcliffe I.C., Tao L.,
RA Ferretti J.J.;
RT "A binding protein-dependent transport system in Streptococcus mutans
RT responsible for multiple sugar metabolism."
RL J. Biol. Chem. 267:4631-4637(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=0A159 / ATCC 700610 / Serotype C;
RX MEDLINE=22295063; PubMed=12397186;
RA Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin Y.,
RA Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferretti J.J.;
RT "Genome sequence of Streptococcus mutans 0A159, a cariogenic dental
RT pathogen."
RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
CC -1- FUNCTION: REGULATORY PROTEIN FOR THE MSM OPERON FOR MULTIPLE
CC SUGAR METABOLISM. ACTIVATES THE TRANSCRIPTION OF THE MSMERG,
CC AGA, DEXA AND GFTA GENES.
CC -1- SIMILARITY: BELONGS TO THE ARAC/XLIS FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
CC -----
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CC -----
DR EMBL: M77351; AAA26932.1; -
DR EMBL: AB014929; AAN58591.1; -
DR InterPro: IPR000005; HTHARAC.
DR Pfam: PF00165; HTH_ARAC; 2.
DR PRINTS: PR00032; HTHARAC.
DR SMART: SM00342; HTH_ARAC; 1.
DR PROSITE: PS00041; HTH_ARAC_FAMILY_1; 1.
DR PROSITE: PS01124; HTH_ARAC_FAMILY_2; 1.
KM Transcription regulation; DNA-binding; Activator; Complete proteome.
FT DNA_BIND 192 211
FT CONFLICT 4 4 L-T-H MOTIF (BY SIMILARITY).
FT CONFLICT 94 110 GSKRAENTKSSLEFR -> RVQKPRFLSSQAVLNL
FT (IN REF. 1).
SO SEQUENCE 278 AA; 31967 MW; 9A8E28ABEF6CCCEA CRC64;

Query Match 81.6%; Score 31; DB 1; Length 278;
Best Local Similarity 71.4%; Pred. No. 16;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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ID NISK_LACIA STANDARD: PRT: 447 AA.
AC P42707;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Nisin biosynthesis sensor protein nisk (EC 2.7.3.-).
GN NISK.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria: Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=63;
RX MEDLINE=94213458; PubMed=8161176;
RA Engelke G., Gutowski-Eckel Z., Klesau P., Siegers K.,
RA Hammelmann M., Ertlan R.-D.;
RT "Regulation of nisin biosynthesis and immunity in Lactococcus lactis
RT 63."
RL Appl. Environ. Microbiol. 60:814-825(1994).
CC -1- FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM NISK/NISR
CC INVOLVED IN THE REGULATION OF THE BIOSYNTHESIS OF LANTIBIOTIC
CC NISIN. NISK MAY FUNCTION AS A MEMBRANE-ASSOCIATED PROTEIN
CC KINASE THAT PHOSPHORYLATES NISR IN RESPONSE TO ENVIRONMENTAL
CC SIGNALS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: Contains 1 histidine kinase domain.
CC -----
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CC -----
DR EMBL: X76884; CA54212.1; -
DR PIR: S44133; S44133.
DR InterPro: IPR003594; ATPbind_ATPase.
DR InterPro: IPR003661; His_KinA.
DR InterPro: IPR005467; His_Kinase.
DR Pfam: PF02518; HATPase_C; 1.
DR Pfam: PF00512; HSKA; 1.
DR SMART: SM00387; HATPase_C; 1.
DR SMART: SM00388; HSKA; 1.
DR PROSITE: PS0109; HIS_KIN; 1.
KM Sensory transduction; Transferase; Kinase; Transmembrane;
FT Phosphorylation.
FT TRANSMEM 15 35
FT TRANSMEM 147 167 POTENTIAL.
FT DOMAIN 235 447 HISTIDINE KINASE.
FT MOD_RES 238 238 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 305 305 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SO SEQUENCE 447 AA; 51319 MW; 47E10533F5A9685D CRC64;

Query Match 81.6%; Score 31; DB 1; Length 447;
Best Local Similarity 83.3%; Pred. No. 26;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

RESULT 10
NISK_LACIA

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RESULT 11
BACC_BACLI STANDARD: PRT: 6359 AA.
ID BACC_BACLI STANDARD: PRT: 6359 AA.
AC 068008;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bactracin synthetase 3 (Ba3) [Includes: ATP-dependent isoleucine
DE adenylation (IleA) (isoleucine activase); ATP-dependent D-phenylalanine
DE adenylation (D-PheA) (D-phenylalanine activase); ATP-dependent histidine

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DE adenylation (HSA) (Histidine activase); ATP-dependent D-aspartate
 DE adenylation (D-AspA) (D-aspartate activase); ATP-dependent asparagine
 DE adenylation (AsnA) (Asparagine activase); Aspartate racemase
 DE (EC 5.1.1.13); Phenylalanine racemase [ATP hydrolyzing]
 DE (EC 5.1.1.11).
 GN BACC.
 OS Bacillus licheniformis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID:1402.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 10716;
 RX MEDLINE-98089193; PubMed-9427658;
 RA Konz D., Klens A., Schoegendorfer K., Marahiel M.A.;
 RT "The bacitracin biosynthesis operon of Bacillus licheniformis ATCC
 10716: molecular characterization of three multi-modular peptide
 synthetases.";
 RT Chem. Biol. 4:927-937(1997).
 CC -1- FUNCTION: INDUCES PEPTIDE SYNTHESIS, ACTIVATES AND INCORPORATES
 CC FIVE AMINO ACIDS, FORMS A THIAZOLINE RING BETWEEN THE FIRST TWO
 CC AMINO ACIDS AND INCORPORATES A D-GLUTAMINE IN THE FOURTH POSITION.
 CC -1- CATALYTIC ACTIVITY: L-aspartate -> D-aspartate.
 CC -1- CATALYTIC ACTIVITY: ATP + L-phenylalanine -> AMP + diphosphate + D-
 CC phenylalanine.
 CC -1- COFACTOR: CONTAINS 5 COVALENTLY BOUND PHOSPHOPANTETHEINES
 CC (PORENTIAL).
 CC -1- PATHWAY: Cyclic peptide antibiotic bacitracin biosynthesis.
 CC -1- SUBUNIT: LARGE MULTISUBUNIT COMPLEX OF BAI, BA2 AND BA3.
 CC -1- DOMAIN: CONSISTS OF FIVE MODULES WITH TWO EPIMERIZATION DOMAINS IN
 CC THE SECOND AND FOURTH MODULES, AND A PUTATIVE C-TERMINAL
 CC THIOESTERASE DOMAIN. EACH MODULE INCORPORATES ONE AMINO ACID INTO
 CC THE PEPTIDE PRODUCT AND CAN BE FURTHER SUBDIVIDED INTO DOMAINS
 CC RESPONSIBLE FOR SUBSTRATE ADENYLATION, THIOYLATION, CONDENSATION
 CC (NOT FOR THE INITIATION MODULE), AND EPIMERIZATION (OPTIONAL), AND
 CC N-METHYLATION (OPTIONAL).
 CC -1- MISCELLANEOUS: BACITRACIN IS A MIXTURE OF AT LEAST TEN CYCLIC
 CC DODECAPETIDES, THAT DIFFER BY ONE OR TWO AMINO ACIDS. THE MOST
 CC ABUNDANT IS BACITRACIN A, A BRANCHED CYCLIC DODECAPETIDE. IT
 CC CONTAINS AN N-TERMINAL LINEAR PENTAPEPTIDE MOTIF (ILE-CYS-LEU-D-
 CC GLU-ILE) WITH AN ISOLEUCINE-CYSTEINE-THIAZOLINE CONDENSATION
 CC PRODUCT AND A C-TERMINAL HEPTAPEPTIDE RING (LYS-D-ORN-ILE-D-PHE-
 CC HIS-D-ASP-ASN), IN WHICH THE FREE ALPHA-CARBOXY GROUP OF THE C-
 CC TERMINAL ASN IS BOUND TO THE EPSILON-AMINO GROUP OF LYSINE. IT
 CC CONTAINS FOUR AMINO ACIDS IN THE D-CONFIGURATION (GLU-4, ORN-7,
 CC PHE-9, AND ASP-11).
 CC -1- SIMILARITY: BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYME
 CC FAMILY.
 CC -1- SIMILARITY: Contains 5 acyl carrier domains.
 CC -----
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 CC -----
 CC EMBL: AF007865; AAC06348.1; .
 CC DR PIR: T31679; T31679.
 CC DR HSSP: P14687; 1AMU.
 CC DR InterPro: IPR000873; AMP-bind.
 CC DR InterPro: IPR001242; Condensatn.
 CC DR InterPro: IPR006163; PP_bind.
 CC DR InterPro: IPR006162; Phantse-attach.
 CC DR InterPro: IPR001031; Thioesterase.
 CC DR Pfam: PF00501; AMP-binding; 5.
 CC DR Pfam: PF00668; Condensation; 7.
 CC DR Pfam: PF00550; PP-binding; 5.
 CC DR Pfam: PF00975; Thioesterase; 1.
 CC DR PROSITE: PS00012; PHOSPHOPANTETHEINE; 4.
 CC DR PROSITE: PS00455; AMP-BINDING; 5.
 CC DR PROSITE: PS00075; ACP DOMAIN; 5.
 CC DR Lysase; Isomerase; Hydrolase; Antibiotic biosynthesis;
 CC KM

KW Phosphopantetheine; Multifunctional enzyme; Repeat.
 FT REPEAT 461 1034
 FT REPEAT 1517 2064
 FT REPEAT 2999 3570
 FT REPEAT 4047 4612
 FT REPEAT 5549 6129
 FT REPEAT 5549 6129
 FT DOMAIN 966 1033
 FT DOMAIN 1998 2064
 FT DOMAIN 3502 3569
 FT DOMAIN 4544 4610
 FT DOMAIN 6052 6119
 FT BINDING 966 996
 FT BINDING 2028 2028
 FT BINDING 3532 3532
 FT BINDING 4574 4574
 FT BINDING 6082 6082
 SQ SEQUENCE 6359 AA; 722923 MW; 82A273C546253074 CRC64;
 Query Match 81.6%; Score 31; DB 1; Length 6359;
 Best Local Similarity 71.4%; Pred. No. 4e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 1 IDITFFY 7
 Db 4305 RDVETFF 4311
 ID PAL_PSEPK STANDARD; PRT; 166 AA.
 ID PAL_PSEPK
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Peptidoglycan-associated lipoprotein precursor.
 GN PAL OR PAL1 OR OPR1 OR PPI23.
 OS Pseudomonas putida (strain KT2440), and
 OS Pseudomonas putida.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID:160488, 303;
 [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN-KT2440.
 RX MEDLINE-22423060; PubMed-12534463;
 RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
 RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
 RA Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
 RA Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
 RA Chris Lee P., Holtzapple E., Scanlan D., Tran K., Kozaczek A.,
 RA Ueberbach T., Rizzo M., Lee K., Kosack D., Mestl D., Wedler H.,
 RA Lauber J., Stjepandic D., Hohnselt J., Straetz M., Helm S.,
 RA Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuenmler B.,
 RA Fraser C.M.;
 RT "Complete genome sequence and comparative analysis of the
 RT metabolically versatile Pseudomonas putida KT2440".
 RT Environ. Microbiol. 4:799-808(2002).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN-mt-2.
 RC MEDLINE-96198174; PubMed-8626299;
 RX Rodriguez-Herva J.J., Ramos-Gonzalez M.I., Ramos J.L.;
 RT "The Pseudomonas putida peptidoglycan-associated outer membrane
 RT lipoprotein is involved in maintenance of the integrity of the cell
 RT cell envelope".
 RT J. Bacteriol. 178:1699-1706(1996).
 CC -1- FUNCTION: VERY STRONGLY ASSOCIATED WITH THE PEPTIDOGLYCAN (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
 CC anchor.
 CC -1- SIMILARITY: BELONGS TO THE OMPA FAMILY. PAL SUBFAMILY.
 CC -----
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CC -----
DR EMBL; AE016778; AAN66847.1; -.
DR EMBL; X74218; CA52294.1; -.
DR PIR; S52308; S52308.
DR TIGR; PPI223; -.
DR InterPro: IPR006664; Bac.Ompa.
DR InterPro: IPR006665; Ompa.MotB.
DR InterPro: IPR006690; Ompa.Like.
DR Pfam; PF00691; Ompa; 1.
DR PRINTS; PRO1021; OMPADOMAIN.
DR PRODOM; PD000930; OMPA/MotB; 1.
DR PROSITE; PS00013; PROKAR.LIPOPROTEIN; 1.
DR PROSITE; PS01068; OMPA; 1.
KW Outer membrane; Signal; Lipoprotein; Complete proteome.
FT SIGNAL 1 21
FT CHAIN 1 21
FT LIPID 22 22
FT DOMAIN 98 142
FT SEQUENCE 166 AA; 17833 MW; 1735318143555A01 CRC64;

Query Match 78.9%; Score 30; DB 1; Length 166;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DITTFY 7
DB 60 RAITTFY 66

RESULT 13
PUR2_STRSU STANDARD; PRT; 420 AA.
ID PUR2_STRSU
AC Q9F1S9;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Phosphoribosylamine-glycine ligase (EC 6.3.4.13) (GARS) (glycinamide
DE ribonucleotide synthetase) (Phosphoribosylglycinamide synthetase).
GN PURD.
OS Streptococcus suis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1307;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DAT1 / Serotype 2;
RX MEDLINE=20576151; PubMed=11133943;
RA Sekizaki T., Otani Y., Osaki M., Takamatsu D., Shimoi Y.;
RT "Evidence for horizontal transfer of the Suidat1 restriction-
RT modification genes to the Streptococcus suis genome.";
RL J. Bacteriol. 183:500-511(2001).
CC -1- CATALYTIC ACTIVITY: ATP + 5-phospho-D-riboseylamine + glycine = ADP
CC + phosphate + N(1)-(5-phospho-D-riboseyl)glycinamide.
CC -1- PATHWAY: De novo purine biosynthesis; second step.
CC -1- SIMILARITY: Belongs to the GARS family.
CC -----
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CC -----
DR EMBL; AB045609; BAB20832.1; -.
DR HSSP; P15640; IGSO.
DR HAMAP; MF_00138; -; 1.

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DR InterPro: IPR000115; Gars.
DR Pfam; PF01071; GARS; 1.
DR Pfam; PF02842; GARS_B; 1.
DR Pfam; PF02843; GARS_C; 1.
DR Pfam; PF02844; GARS_N; 1.
DR TIGRfams; TIGR00877; purD; 1.
DR PROSITE; PS00184; GARS; 1.
KW Purine biosynthesis; Ligase.
SQ SEQUENCE 420 AA; 45333 MW; 14E9C2D29CDF6B9F CRC64;

Query Match 78.9%; Score 30; DB 1; Length 420;
Best Local Similarity 83.3%; Pred. No. 40;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DITTFY 7
DB 355 DITTFY 360

RESULT 14
RAS1_RHRA STANDARD; PRT; 203 AA.
ID RAS1_RHRA
AC P22278;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ras-like protein 1.
GN RAS1.
OS Rhizomucor racemosus (Mucor circinelloides f. lusitanicus).
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
OC Mucor.
OX NCBI_TaxID=4841;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 1216B;
RX MEDLINE=91061774; PubMed=1701021;
RA Casale W.L., McConnell D.G., Wang S.-Y., Lee Y.-J., Linz J.E.;
RT "Expression of a gene family in the dimorphic fungus Mucor racemosus
RT which exhibits striking similarity to human ras genes.";
RL Mol. Cell. Biol. 10:6654-6663(1990).
CC -1- ENZYME REGULATION: ALTERNATE BETWEEN AN INACTIVE FORM BOUND TO GDP
CC AND AN ACTIVE FORM BOUND TO GTP. ACTIVATED BY A GUANINE
CC NUCLEOTIDE-EXCHANGE FACTOR (GEF) AND INACTIVATED BY A GTPASE-
CC ACTIVATING PROTEIN (GAP).
CC -1- SUBCELLULAR LOCATION: Plasma membrane.
CC -1- DEVELOPMENTAL STAGE: IN ALL DEVELOPMENTAL STAGES ANALYZED. ITS
CC SIGNAL WAS MORE INTENSE IN SPOROULATING MYCELIA.
CC -1- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RAS FAMILY.
CC -----
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CC -----
DR EMBL; M55175; AAA83378.1; -.
DR PIR; A36365; A36365.
DR HSSP; P01112; IPL.
DR InterPro: IPR003577; GTPase_Ras.
DR InterPro: IPR001806; Ras_trnsmfmg.
DR InterPro: IPR005225; Small_GTP.
DR Pfam; PF00071; ras; 1.
DR PRINTS; PRO0449; RASTRNSFRANG.
DR SMART; SM00173; RAS; 1.
DR TIGRfams; TIGR00231; small_gtp; 1.
KW GTP-binding; Prenylation; Lipoprotein.
FT NP_BIND 17 24
FT NP_BIND 64 68
FT NP_BIND 123 126
FT DOMAIN 39 47
FT LIPID 200 200

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SO SEQUENCE 203 AA: 23236 MW: 52098F53F396A54 CRC64;

Query Match 76.3%; Score 29; DB 1; Length 203;
Best Local Similarity 83.3%; Pred. No. 32;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 DITTFY 7
:|||||
DB 99 EITTFY 104

RESULT 15

PCYB_PSEPA
ID PCYB_PSEPA STANDARD; PRT; 302 AA.
AC P22636;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protocatechuate 4,5-dioxygenase beta chain (EC 1.13.11.8) (4,5-PCD).
GN LIGB
OS Pseudomonas paucimobilitis (Sphingomonas paucimobilitis).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Sphingomonas.
OX NCBI_TaxID=13689;
RN (1)
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-9.
RC STRAIN-SKK-6;
RX MEDLINE=90236935; PubMed=2185230;
RA Noda Y., Nishikawa S., Shiozuka K.-I., Kadokura H., Nakajima H.,
RA Yoda K., Katayama Y., Morohoshi N., Haraguchi T., Yamasaki M.;
RT "Molecular cloning of the protocatechuate 4,5-dioxygenase genes of
RT Pseudomonas paucimobilitis.";
RT J. Bacteriol. 172:2704-2709(1990).
CC -1- FUNCTION: RESPONSIBLE FOR THE AROMATIC RING FISSION OF
CC PROTOCATECHUATE.
CC -1- CATALYTIC ACTIVITY: Protocatechuate + O(2) -> 4-carboxy-2-
CC hydroxymuconate semialdehyde.
CC -1- COFACTOR: FERROUS ION.
CC -1- SUBUNIT: COMPOSED OF TWO SUBUNITS (ALPHA AND BETA) IN A 1:1 RATIO.
CC -----
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CC -----
CC EMBL: M34835; AAA17728.1; -
DR PIR: B35271; B35271.
DR PDB: 1BAU; 27-AUG-99.
DR PDB: 1B0U; 04-MAY-99.
DR InterPro: IPR004183; LIGB.
DR Pfam: PF02900; LIGB; 1.
KW Aromatic hydrocarbons catabolism; Oxidoreductase; Dioxygenase; Iron;
KW 3D-structure.
SQ SEQUENCE 302 AA: 33292 MW: 0552B3B0E59702E5 CRC64;

Query Match 76.3%; Score 29; DB 1; Length 302;
Best Local Similarity 71.4%; Pred. No. 48;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RDIITTFY 7
||:||||
DB 258 RDLITTFY 264

Search completed: October 7, 2003, 19:15:04
Job time : 2.42414 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 19:04:06 ; Search time 6.97586 Seconds
(without alignments)
258.946 Million cell updates/sec

Title: US-09-988-013A-4_COPY_99_105
Perfect score: 38
Sequence: 1 RDITTFY 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	89.5	98	16	099VG9
2	33	86.8	315	2	052517
3	33	86.8	333	10	09MOV1
4	33	86.8	392	11	08BMW6
5	33	86.8	410	10	09XE75
6	33	86.8	414	11	08BMQ7
7	33	86.8	422	10	09XE77
8	33	86.8	438	10	09XE79
9	33	86.8	753	3	08JIE3
10	33	86.8	760	3	08JIE2
11	33	86.8	2644	4	013535
12	32	84.2	39	13	090506
13	32	84.2	68	11	099LRO
14	32	84.2	179	4	096B07
15	32	84.2	242	6	095KJ3
16	32	84.2	312	4	09NZB6

17	32	84.2	343	2	08RTS8	08RTS8 candidatus
18	32	84.2	407	13	08JFE1	08JFE1 gallus gall
19	32	84.2	408	4	096EA8	096EA8 homo sapien
20	32	84.2	473	4	09BRH1	09BRH1 homo sapien
21	32	84.2	565	16	08R7J7	08R7J7 thermoaer
22	32	84.2	565	16	08R6J9	08R6J9 thermoaer
23	32	84.2	565	16	08R6J2	08R6J2 thermoaer
24	32	84.2	764	16	08PMW9	08PMW9 xanthomonas
25	32	84.2	816	10	08W5E9	08W5E9 oryza sativ
26	32	84.2	892	2	09LAF1	09LAF1 bacillus ce
27	31	81.6	35	16	097RE8	097RE8 streptococ
28	31	81.6	166	3	09UTC3	09UTC3 schizosacch
29	31	81.6	267	11	091W78	091W78 mus musculu
30	31	81.6	279	17	027027	027027 methanobact
31	31	81.6	307	17	028263	028263 archaeoglob
32	31	81.6	376	5	08SMI7	08SMI7 encytopallito
33	31	81.6	447	2	048675	048675 lactococcus
34	31	81.6	543	2	093GZ4	093GZ4 streptococ
35	31	81.6	579	16	08CZD8	08CZD8 oceanobacill
36	31	81.6	695	16	09A901	09A901 caulobacter
37	31	81.6	830	10	065482	065482 arabidopsis
38	31	81.6	1395	5	09W2J3	09W2J3 drosophila
39	31	81.6	1395	5	044924	044924 drosophila
40	30	78.9	168	2	051489	051489 pseudomonas
41	30	78.9	168	16	0914Z4	0914Z4 pseudomonas
42	30	78.9	192	17	08ZUV5	08ZUV5 pyrobaculum
43	30	78.9	281	2	09ZFL6	09ZFL6 bacillus st
44	30	78.9	297	16	092K18	092K18 rhizobium m
45	30	78.9	336	13	091669	091669 xenopus lae

ALIGNMENTS

RESULT 1

ID	099VG9	PRELIMINARY:	PRT:	98 AA.
DC	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Hypothetical protein SAV0836 (MW0789, protein).			
GN	SAV0836 OR SA0768.1 OR SAS023 OR MM0789.			
OS	Staphylococcus aureus (strain Mu50 / ATCC 700699),			
OS	Staphylococcus aureus (strain N315), and			
OC	Bacteria: Firmicutes: Bacillales; Staphylococcus.			
OX	NCBI_TaxID=158878, 158879, 196620;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Mu50, and N315;			
RX	MEDLINE=21311952; PubMed=11418146;			
RA	Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,			
RA	Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,			
RA	Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,			
RA	Mikutani-Oi Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,			
RA	Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,			
RA	Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,			
RA	Hattori M., Ogasawara N., Hayashi H., Hiratake K.,			
RT	"Whole genome sequencing of methicillin-resistant Staphylococcus			
RT	aureus";			
RL	Lancet 357:1225-1240(2001).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MM2;			
RX	MEDLINE=22040717; PubMed=12044378;			
RA	Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,			
RA	Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,			
RA	Yamamoto K., Hiratake S. K.,			
RT	"Genome and virulence determinants of high virulence community-			
RT	acquired MRSA";			
RL	Lancet 359:1819-1827(2002).			
DR	EMBL; AP003360; BAB56998.1; -.			

DR EMBL: AP003131; BAB42007.1; -
DR EMBL: AP004824; BAB94654.1; -
DR Interpro: IPR006663; Thiorodox_dom2.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 98 AA; 11454 MW; D33BDF1D6392C139 CRC64;

Query Match
Best Local Similarity 89.5%; Score 34; DB 16; Length 98;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDITTFY 7
DB 8 KDVTTFY 14

RESULT 2
ID 052517 PRELIMINARY; PRT; 315 AA.
AC 052517;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE VIRL.
GN VIRL.
OS Agrobacterium tumefaciens.
OC Plasmid T1.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=358;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99009000; PubMed=9791116;
RA Kalligeraki V.S., Winans S.C.;
RT Wound-released chemical signals may elicit multiple responses from an
RT Agrobacterium tumefaciens strain containing an octopine-type T1
RT plasmid.
RL J. Bacteriol. 180:5660-5667(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Winans S.C., Zhu J., Oger P.M., Schrammelfer B., Hooykaas P.J.,
RA Fairard S.R.;
RT Octopine-type T1 plasmid sequence.
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF242881; AAC72016.1; -
KW Plasmid.
SQ SEQUENCE 315 AA; 36474 MW; 324B565C43B04A365 CRC64;

Query Match
Best Local Similarity 86.8%; Score 33; DB 2; Length 315;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDITTFY 7
DB 139 RDVTTFY 145

RESULT 3
ID 09MOV1 PRELIMINARY; PRT; 333 AA.
AC 09MOV1;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE D123-1-like protein.
GN AT4G05440.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Spliegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vili D.M.,

RA Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M.,
RA Shekher M., Schultz K., See L.H., Swaby I., Habermann K., Dedhia N.N.,
RA Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.

RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL161503; CAB81086.1; -
SQ SEQUENCE 333 AA; 38777 MW; 85DBA4B4F38703D2 CRC64;

Query Match
Best Local Similarity 86.8%; Score 33; DB 10; Length 333;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDITTFY 7
DB 198 REVITTFY 204

RESULT 4
ID 08BMM6 PRELIMINARY; PRT; 392 AA.
AC 08BMM6;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE ADP-ribosylation factor 1 GTPase activating protein homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Plutary;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RT Nature 420:563-573(2002).
DR EMBL: AK030520; BAC27002.1; -
SQ SEQUENCE 392 AA; 42956 MW; FC2BDDA150130CA2 CRC64;

Query Match
Best Local Similarity 86.8%; Score 33; DB 11; Length 392;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDITTFY 7
DB 266 RDVTTFY 272

RESULT 5
ID 09XE75 PRELIMINARY; PRT; 410 AA.
AC 09XE75;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Patatin-like protein.
OS Sorghum bicolor (Sorghum) (Sorghum vulgare).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Sorghum.
OX NCBI_TaxID=4556;
RN [1]
RP SEQUENCE FROM N.A.
RA Liaca V., Lou A., Messing J.W.;
RT "Microsynteny analysis of 22-kDa zein cluster in maize and sorghum."
DR EMBL: AF061282; AAD22170.1; -
DR Interpro: IPR002641; Patatin.

DR Pfam: PF01734; Patatin; 1.
SQ SEQUENCE 410 AA; 44564 MW; 46405E0A445CE994 CRC64;

Query Match 86.8%; Score 33; DB 10; Length 410;
Best Local Similarity 71.4%; Pred. No. 50;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDITTFY 7
:|||||
Db 95 KDLTTFY 101

RESULT 6

Q8BMQ7 PRELIMINARY; PRT; 414 AA.
AC Q8BMQ7;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE ADP-ribosylation factor 1 GTPase activating protein homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary, and uterus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK030295; BAC26883.1; -
SQ SEQUENCE 414 AA; 45288 MW; 72A3279D185714C0 CRC64;

Query Match 86.8%; Score 33; DB 11; Length 414;
Best Local Similarity 71.4%; Pred. No. 50;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDITTFY 7
:|||||
Db 288 RDVTTF 294

RESULT 7

Q9XE77 PRELIMINARY; PRT; 422 AA.
AC Q9XE77;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Patatin-like protein.
OS Sorghum bicolor (Sorghum) (Sorghum vulgare).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
OX NCBI_TaxID=4558;
RN [1]
RP SEQUENCE FROM N.A.
RC Llaça V., Lou A., Messing J.W.;
RT "Microsynteny analysis of 22-kDa zein cluster in maize and sorghum";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF061282; AAD22169.1; -
DR InterPro; IPR002641; Patatin.
DR Pfam; PF01734; Patatin; 1.
SQ SEQUENCE 422 AA; 45766 MW; 742128BB0A37F479 CRC64;

Query Match 86.8%; Score 33; DB 10; Length 422;
Best Local Similarity 71.4%; Pred. No. 51;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDITTFY 7

Db 94 KDLTTFY 100
:|||||

RESULT 8

Q9XE79 PRELIMINARY; PRT; 438 AA.
AC Q9XE79;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Patatin-like protein.
OS Sorghum bicolor (Sorghum) (Sorghum vulgare).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
OX NCBI_TaxID=4558;
RN [1]
RP SEQUENCE FROM N.A.
RC Llaça V., Lou A., Messing J.W.;
RT "Microsynteny analysis of 22-kDa zein cluster in maize and sorghum";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF061282; AAD22149.1; -
DR InterPro; IPR002641; Patatin.
DR Pfam; PF01734; Patatin; 1.
SQ SEQUENCE 438 AA; 47495 MW; EF5EB650E2186044 CRC64;

Query Match 86.8%; Score 33; DB 10; Length 438;
Best Local Similarity 71.4%; Pred. No. 54;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDITTFY 7
:|||||
Db 95 KDLTTFY 101

RESULT 9

Q8JIE3 PRELIMINARY; PRT; 753 AA.
AC Q8JIE3;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Cellulase Cel48A precursor.
OS Cel48A.
OS Plomycetes sp. E2.
OC Eukaryota; Fungi; Chytridiomycota; Neocallimasticales;
OC Neocallimasticeae; Plomycetes.
OX NCBI_TaxID=73868;
RN [1]
RP SEQUENCE FROM N.A.
RC Steenbakkers P.J.M., Freelove A., van Cranenbroek B., Sweegers B.M.C.,
RA Harhangi H.R., Vogels G.D., Hazlewood G.P., Gilbert H.J.,
RA Op den Camp H.J.W.;
RT "The Major Component of the Cellulosomes of Anaerobic Fungi from the
RT Genus Plomycetes is a Family 48 Glycoside Hydrolase."
RL DNA Seq. 13:313-320(2002).
DR EMBL; AF449412; AAN75734.1; -
KM SIGNAL.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 753 CELLULASE CEL48A.
SQ SEQUENCE 753 AA; 83489 MW; D7C28317A4AB7BBF CRC64;

Query Match 86.8%; Score 33; DB 3; Length 753;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DITTFY 7
:|||||
Db 414 DITTFY 419

RESULT 10

```
08J1E2
ID 08J1E2      PRELIMINARY;      PRT;      760 AA.
AC 08J1E2;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Cellulase Cel48a precursor.
GN CEL48A.
OS Pteromyces equi.
OC Eukaryota; Fungi; Chytridiomycota; Neocallimastixales;
OC Neocallimastixaceae; Pteromyces.
OX NCBI_TaxID=99929;
RN [1]
RP SEQUENCE FROM N.A.
RA Steenhakkers P.J.M., Freelove A., van Cranenbroek B., Sweegers B.M.C.,
RA Harhangi H.R., Vogels G.D., Hazlewood G.P., Gilbert H.T.,
RA Op den Camp H.J.M.;
RT "The Major Component of the Cellulosomes of Anaerobic Fungi from the
RT Genus Pteromyces is a Family 48 Glycoside Hydrolase.";
RL DNA Seq. 13:313-320(2002).
DR EMBL; AF49413; MAM76735.1; -.
KW SIGNAL.
FT CHAIN
FT SIGNAL
SQ SEQUENCE 760 AA; 84648 MW; B7AF925F95EB0271 CRC64;

Query Match
Best Local Similarity 100.0%; Score 33; DB 3; Length 760;
Pred. No. 96;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DIFFY 7
DB 415 DIFFY 420

RESULT 11
013535
ID 013535      PRELIMINARY;      PRT;      2644 AA.
AC 013535; Q93051;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBlrel. 22, Last annotation update)
DE FRAP-related protein (Protein kinase ATR).
DE ATR OR FRPL.
GN ATR OR FRPL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-96181495; PubMed-8610130;
RA Clamprich K.A., Shio T.B., Keith C.T., Schreiber S.L.;
RT "cDNA cloning and gene mapping of a candidate human cell cycle
RT checkpoint protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:2850-2855(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Bentley N.J., Holtzman D.A., Flagg G., Keegan K.S., Demaggio A.,
RA Ford J.C., Hoekstra M., Carr A.M.;
RT Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DE EMBL; U49844; AAC50405.1; -.
DE EMBL; Y09077; CAA70298.1; -.
DE EMBL; U76308; AAC50929.1; -.
DE Genes; HGNC:882; ATR.
DR InterPro; IPR003151; FAT.
DR InterPro; IPR003152; FATC.
DR InterPro; IPR000357; HEAT_repeat.
DR InterPro; IPR000403; PI3_Pi4_kinase.
DR Pfam; PF02259; FAT; 1.
DR Pfam; PF02260; FATC; 1.
DR Pfam; PF00454; PI3_Pi4_kinase; 1.
DR SMART; SM00146; PI3Kc; 1.
DR PROSITE; PSS0077; HEAT_REPEAT; 1.
```

```
DR PROSITE; PSS00916; PI3_4_KINASE_2; 1.
DR PROSITE; PSS0290; PI3_4_KINASE_3; 1.
KW Kinase; Transferase.
FT CONFLICT 92 R -> A (IN REF. 1).
SQ SEQUENCE 2644 AA; 301449 MW; 3889CAB930E630A CRC64;

Query Match
Best Local Similarity 86.8%; Score 33; DB 4; Length 2644;
Pred. No. 3; 6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIFFY 7
DB 1814 RDITAFY 1820

RESULT 12
090506
ID 090506      PRELIMINARY;      PRT;      39 AA.
AC 090506;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Initiation factor (Fragment).
GN EIF-4A.
OS Fundulus heteroclitus (Killifish) (Mummichog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopteleostei; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Fundulidae; Fundulus.
OX NCBI_TaxID=8078;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue-Pituitary;
RA Price D.A., Lin Y.-W.P.;
RT "PCR fragment from Killifish that is homologous to mouse EIF-4A.";
DR EMBL; M89792; AAA49287.1; -.
FT NON_TER
SQ SEQUENCE 39 AA; 4530 MW; 824F368975B22686 CRC64;

Query Match
Best Local Similarity 84.2%; Score 32; DB 13; Length 39;
Pred. No. 7;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RDITFY 7
DB 18 RDITFY 24

RESULT 13
099LR0
ID 099LR0      PRELIMINARY;      PRT;      68 AA.
AC 099LR0;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Hypothetical 7.9 kDa protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RA Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DE EMBL; BC002266; AAH02266.1; -.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 68 AA; 7882 MW; BDD7476AB5499E88 CRC64;

Query Match
Best Local Similarity 84.2%; Score 32; DB 11; Length 68;
Pred. No. 13;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

OY 1 RDITTFY 7
 ||| |||
 DB 47 RDITTFY 53

RESULT 14

Q96B07 PRELIMINARY; PRT; 179 AA.
 ID Q96B07;
 AC Q96B07;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=uterus;
 RA Strausberg R.;
 RL Submitted (Oct-2001) to the EMBL/GenBank/DDbJ databases.
 DR EMBL, BC016295; AAH16295.1; -.
 DR InterPro: IPR001410; DEAD.
 DR InterPro: IPR001650; Helicase_C.
 DR Pfam: PF00271; helicase_C; 1.
 DR SMART: SM00490; HELIC; 1.
 KW Hypothetical protein; ATP-binding; Helicase; Hydrolase.
 SQ SEQUENCE 179 AA: 21039 MW: 325A790227A89C35 CRC64;

Query Match 84.2%; Score 32; DB 4; Length 179;
 Best Local Similarity 85.7%; Pred. No. 35;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RDITTFY 7
 ||| |||
 DB 158 RDITTFY 164

RESULT 15

Q95KJ3 PRELIMINARY; PRT; 242 AA.

ID Q95KJ3;
 AC Q95KJ3;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Hypothetical 28.5 kDa protein.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_Taxid=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Temporal cortex;
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RT *Isolation of full-length cDNA clones from macaque brain cDNA
 RT libraries.*;
 RL Submitted (Apr-2001) to the EMBL/GenBank/DDbJ databases.
 CC -1- SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY.
 DR EMBL, AB060830; BAB46863.1; -.
 DR InterPro: IPR001410; DEAD.
 DR InterPro: IPR000629; DEAD_box.
 DR InterPro: IPR001650; Helicase_C.
 DR Pfam: PF00270; DEAD; 1.
 DR Pfam: PF00271; helicase_C; 1.
 DR SMART: SM00490; HELIC; 1.
 DR PROSITE: PS00039; DEAD_ATP_HELICASE; 1.
 KW Hypothetical protein; ATP-binding; Helicase; Hydrolase.
 SQ SEQUENCE 242 AA: 28492 MW: 03D02D3A7B405A21 CRC64;

Query Match 84.2%; Score 32; DB 6; Length 242;
 Best Local Similarity 85.7%; Pred. No. 48;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RDITTFY 7
 ||| |||
 DB 221 RDITTFY 227

Search completed: October 7, 2003, 19:20:05
 Job time : 8.97586 secs

